

Result No.	Query			Description		
	Score	Match	Length	ID	DB	Description
1	1746	100.0	1746	3	US-09-147-405B-12	Sequence 12, Appl
2	1746	100.0	3600	3	US-09-147-405B-14	Sequence 14, Appl
3	1745	99.9	1781	3	US-09-147-405B-10	Sequence 10, Appl
4	1613.8	92.4	2793	3	US-09-134-001C-2477	Sequence 2477, Ap
5	1613.8	92.4	2976	3	US-09-386-962C-7	Sequence 7, Appli
6	1613.8	92.4	2976	3	US-09-386-959-7	Sequence 7, Appli
7	507.2	29.0	837	3	US-09-710-279-2699	Sequence 2699, Ap
8	507.2	29.0	3236	3	US-09-710-279-3492	Sequence 3492, Ap
9	364.4	20.9	3498	3	US-09-200-650B-8	Sequence 8, Appli
10	126	7.2	3945	3	US-09-200-650B-6	Sequence 6, Appli
11	122.2	7.0	3619	3	US-09-710-279-4157	Sequence 6, Appli
12	110.2	6.3	2957	3	US-09-710-279-4135	Sequence 4135, Ap
13	110.2	6.3	3132	3	US-09-710-279-3455	Sequence 3455, Ap
14	110.2	6.3	3465	3	US-09-710-279-1779	Sequence 1779, Ap
15	108.6	6.2	5406	3	US-09-386-962C-1	Sequence 1, Appli
16	108.6	6.2	5406	3	US-09-386-959-1	Sequence 1, Appli
17	98.4	5.6	2841	3	US-09-200-650B-4	Sequence 4, Appli
18	98.4	5.6	4358	3	US-08-956-171E-454	Sequence 454, App
19	98.4	5.6	4358	3	US-08-781-986A-454	Sequence 454, App
20	95.8	5.5	1039	3	US-09-902-540-1280	Sequence 1280, Ap
21	88.8	5.1	612	3	US-09-902-540-1357	Sequence 1357, Ap
22	81.6	4.7	13794	3	US-08-956-171E-54	Sequence 54, Appl
23	81.6	4.7	13794	3	US-08-781-986A-54	Sequence 54, Appl

```
QY 241 TCCTCAATTCATCAATTGATGACTGCCCAACCAACCATCTCCACCAACAATAAATAGAGAA 300
DB 241 TCCTCAATTCATCAATTGATGACTGCCCAACCAACCATCTCCACCAACAATAAATAGAGAA 300
QY 301 GAATCTGTTCAAAACAAGTGATTAATGTAGAAAGATTCAACAGTATCAGATTTTGGCTAACTCT 360
DB 301 GAATCTGTTCAAAACAAGTGATTAATGTAGAAAGATTCAACAGTATCAGATTTTGGCTAACTCT 360
QY 361 AAAATAAAGAGAGTAACAACCTGAATCTGGTAAAGAGAGAAATATATATAGAGCAACCTAAT 420
DB 361 AAAATAAAGAGAGTAACAACCTGAATCTGGTAAAGAGAGAAATATATATAGAGCAACCTAAT 420
QY 421 AAAGTAAAGAGAGATTCAACAACCAAGTCAAGCGCTCGGCTATACAAATATATAGATGAAAAA 480
DB 421 AAAGTAAAGAGAGATTCAACAACCAAGTCAAGCGCTCGGCTATACAAATATATAGATGAAAAA 480
QY 481 ATTTCAAATCAAGATGAGTTATTAATTTTACCNAATAAATGAATATGAAAAATAAGGCTAGA 540
DB 481 ATTTCAAATCAAGATGAGTTATTAATTTTACCNAATAAATGAATATGAAAAATAAGGCTAGA 540
QY 541 CCATTATCTACAACATCTGCCCAACCATCGATTAAACCGTGAACCGTAAATCAATTTAGCG 600
DB 541 CCATTATCTACAACATCTGCCCAACCATCGATTAAACCGTGAACCGTAAATCAATTTAGCG 600
QY 601 GCGGAACAAGGTTCCGAATGTTAAACCATTTAATTAAGTTACTGATCAAGATATTACTGAA 660
DB 601 GCGGAACAAGGTTCCGAATGTTAAACCATTTAATTAAGTTACTGATCAAGATATTACTGAA 660
QY 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 GTAACCTTTTGAAGTAGATGATAAGGTGAAATCTCGTGATACGATGACAGTGGATATAGAT 780
DB 721 GTAACCTTTTGAAGTAGATGATAAGGTGAAATCTCGTGATACGATGACAGTGGATATAGAT 780
QY 781 AAGATACAGTTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 AAGATACAGTTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TCTGAGAAATCATCGCTACAGTACTTATGATACAAATAAATAAATAAATAAATAAATAAATAA 900
DB 841 TCTGAGAAATCATCGCTACAGTACTTATGATACAAATAAATAAATAAATAAATAAATAAATAA 900
QY 901 TTTACAGATTTATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 TTTACAGATTTATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 ATTTGATAAATCAAGGTTCCAAATATATACCAAGTTAGATGATGATGATGATGATGATGATGAT 1020
DB 961 ATTTGATAAATCAAGGTTCCAAATATATATACCAAGTTAGATGATGATGATGATGATGATGATGAT 1020
QY 1021 CTTTTCATCAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1080
DB 1021 CTTTTCATCAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1080
QY 1081 GCTAACCTTTCAAAGTATGTTTACAAATATAGATACGAAATAATATATATATATATATATATAT 1140
DB 1081 GCTAACCTTTCAAAGTATGTTTACAAATATAGATACGAAATAATATATATATATATATATATAT 1140
QY 1141 ATTTATATTAACCTTCTCGTTTATTTACGCAAGGAAACAAATGTTAAATATTTTCAGGGAAT 1200
DB 1141 ATTTATATTAACCTTCTCGTTTATTTACGCAAGGAAACAAATGTTAAATATTTTCAGGGAAT 1200
QY 1201 GGTGATGAAGGTTCAACAATATAGACGATAGACAAATAATTAAGTTTATAAGGTTGGA 1260
DB 1201 GGTGATGAAGGTTCAACAATATAGACGATAGACAAATAATTAAGTTTATAAGGTTGGA 1260
QY 1261 GATAATCAAAATTTTACCAGATAGTAAACAGAAATTTTATGATTTACAGTGAATATGAAGATGTC 1320
DB 1261 GATAATCAAAATTTTACCAGATAGTAAACAGAAATTTTATGATTTACAGTGAATATGAAGATGTC 1320
```

```
QY 1321 ACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 ACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 ATAGATTCACCATATATTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTT 1440
DB 1381 ATAGATTCACCATATATTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTT 1440
QY 1441 ACAGTATATACAGCAAACTGTGACAAATGACAGACGATATTAATGATGATGATGATGATGATGAT 1500
DB 1441 ACAGTATATACAGCAAACTGTGACAAATGACAGACGATATTAATGATGATGATGATGATGATGAT 1500
QY 1501 AGACAGATCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1501 AGACAGATCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 GACTTGCTCTCGTGAATAAATCTTATAAATCGGAGATACGATGATGATGATGATGATGATGATGAT 1620
DB 1561 GACTTGCTCTCGTGAATAAATCTTATAAATCGGAGATACGATGATGATGATGATGATGATGATGAT 1620
QY 1621 GATGATATCAAAATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 GATGATATCAAAATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 ACATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 ACATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1741 GATGGA 1746
DB 1741 GATGGA 1746
```

## RESULT 2

```
US-09-147-405B-14
; Sequence 14, Application US/09147405B
; Patent No. 6733758
; GENERAL INFORMATION:
; APPLICANT: Guss, Bengt
; APPLICANT: Nilsson, Martin
; APPLICANT: Frykberg, Lars
; APPLICANT: Flock, Jan-Ingmar
; APPLICANT: Lindberg, Martin
; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from
; TITLE OF INVENTION: Coagulase-Negative Staphylococcus
; FILE REFERENCE: Guss 09/147405
; CURRENT APPLICATION NUMBER: US/09/147,405B
; CURRENT FILING DATE: 1999-04-11
; PRIOR APPLICATION NUMBER: PCT/SE97/10191
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: SE 9602496-3
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 3600
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)..(3308)
US-09-147-405B-14
```

Query Match 100.0%; Score 1746; DB 3; Length 3600;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TCTAGTCATGAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
DB 255 TCTAGTCATGAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 314
QY 61 AATAACCAAAATTAATTAATAAAGAAAGAAACGAAATTAACCTACGATGGCATAGAAAAACGCTCA 120
```









```
; NAME/KEY: CDS
; LOCATION: (3) .. (2975)
US-09-386-962C-7

Query Match      92.4%; Score 1613.8; DB 3; Length 2976;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1670; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 1 TCTAGTGATGAAGAAAGATGATGTGATCAATAATAATCAATGATCGATCAATAAAGACCGACGAT 60
DB 318 TCCAGTAATGAAGAAAGAAAGATGATGTAATCAATAATAGTCAGTCATTAATAAAGACCGATGAT 377
QY 61 AATAACCAAAATTAATAAAGAAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 378 GATAACCAAAATA---AAAAAGAAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 434
QY 121 GAAATAGAAACAGAGTCACAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 435 AAAGATATAACACAGTCACAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 494
QY 181 ACCCTCAAGATATACTCATCTTTACAGAAAGAGAGGTTAAAGAAATCTCTCATCATGATCGAA 240
DB 495 ACCCTCAAGATATACTCATCTTTAAAGAAAGAGGTTAAAGAAATCTCTCATCATGATCGAA 554
QY 241 TCCTCAAAATTCATCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 555 TCCTCAAAATTCATCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 614
QY 301 GAAATCTGTTCAAAACAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 615 GCATCTATTCAAACAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 674
QY 361 AAAATAAGAGAGTAAACCTGAATCTCGGTAAAGAAAGATGATGATGATGATGATGATGATGATGAT 420
DB 675 AAAATAAGAGAGTAAACCTGAATCTCGGTAAAGAAAGATGATGATGATGATGATGATGATGATGAT 734
QY 421 AAAGTAAAGAGAGTAAACCTGAATCTCGGTAAAGAAAGATGATGATGATGATGATGATGATGATGAT 480
DB 735 AAAGTAAAGAGAGTAAACCTGAATCTCGGTAAAGAAAGATGATGATGATGATGATGATGATGATGAT 794
QY 481 ATTTCAAAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 795 ATTTCAAAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 854
QY 541 CCAATATCTACAACTCTGCCCAACCATCGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 855 CCGTTATCTACAACTCTGCCCAACCATCGATGATGATGATGATGATGATGATGATGATGATGATGAT 914
QY 601 GCGGAACAAGGTTCCGAATGTTAAACCATTTAATTTAAAGTTTACTGATCAAAAGTATTACTGAA 660
DB 915 GCGAACAAGGTTCCGAATGTTAATTTAATTTAAAGTTTACTGATCAAAAGTATTACTGAA 974
QY 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 975 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1034
QY 721 GTAACCTTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
DB 1035 GTAACCTTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1094
QY 781 AAGATACAGTTCCATCAGATTTAAACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 1095 AAGATACAGTTCCATCAGATTTAAACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154
QY 841 TCTGAGAAATCATCGCTACAGGTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 1155 TCTGAGAAATCATCGCTACAGGTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1214
QY 901 TTTACAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 1215 TTTACAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1274
QY 961 ATTGATAAATCAAAGGTTCCAAATTAATAATACCAAGTTTAGATGATGATGATGATGATGATGATGAT 1020
```

```
RESULT 6
US-09-386-959-7
; Sequence 7, Application US/09386959
; Patent No. 6703025
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; APPLICANT: FOSTER, Timothy J.
; APPLICANT: HOOK, Magnus
; TITLE OF INVENTION: MULTICOMPONENT VACCINES
; FILE REFERENCE: P0633051/BAS
; CURRENT APPLICATION NUMBER: US/09/386.959
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: 60/098.439
; EARLIER FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
```

```
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(2976)
US-09-386-959-7

Query Match      92.4%; Score 1613.8; DB 3; Length 2976;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1670; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 1 TCTAGTGATGAGAGAAAGATGATGATCAATAATAATCACTCAATTAACAGTCAATTAACACCGACGAT 60
Db 318 TCACGTAATGAGAAAGAAAGATGATGTAATCAATAATAGTCAGTCAATTAACACCGATGAT 377

QY 61 AATAACCAATAATTAATAAAGAAAGAAAGCAATTAACAGTGGCAGTAAAGAAAGCCTCA 120
Db 378 GATACCAATA---AAAAAGAGAAAGCAATAGCAACGATGCCATAGAAATCGCTCT 434

QY 121 GAAGATAGAACAGAGTCAACAAATGTAGATGAAAGCAAGCAACATTTTACAAAAG 180
Db 435 AAAGATATAACACAGTCAACAAATGTAGATGAAAGCAAGCAACATTTTACAAAG 494

QY 181 ACCCTCAAGATAATCTCATCTTACAGAAAGAGGTAAAGATCTCATCAGTCGAA 240
Db 495 ACCCTCAAGATAATCTCAGCTTAAAGAAAGGTGTTAAAGAAAGCCCTCATCAGTCGAA 554

QY 241 TCTCAAAATTCATCAATTCATCTGCTCCCAACCAACCATCTCACACCAACCAATTAATAGAA 300
Db 555 TCTCAAAATTCATCAATTCATCTGCTCCCAACCAACCATCTCACACCAACCAATTAATAGTAA 614

QY 301 GAATCTGTTCAACCAAGTGATTAATGTAGAAAGATTCACACGATATCAGATTTTCTCAACTCT 360
Db 615 GCATCTATTTCAACCAAGTGATTAATGAAGAAATTTCCGGGTATCAGATTTTCTCAACTCT 674

QY 361 AAAATAAAGAGAGTAACTGTAATCTGTTAAAGAGAGAAATCTATAGAGCAACTAAT 420
Db 675 AAAATAAAGAGAGTAACTGTAATCTGTTAAAGAGAGAAATCTATAGAGCAACTAAT 734

QY 421 AAGTAAAGAGAGTAACTAACAACAGTCAGCCGCTCTGGCTATACAAATATAGATCAAAA 480
Db 735 AAGTAAAGAGAGTAACTAACAACAGTCAGCCGCTCTGGCTATACAAATATAGATCAAAA 794

QY 481 ATTTCAAAATCAAGATGAGTTTAAATTTACCAATTAATGAATATGAAATTAAGGCTAGA 540
Db 795 ATTTCAAAATCAAGATGAGTTTAAATTTACCAATTAATGAATATGAAATTAAGGCTAGA 854

QY 541 CAATATCTAACAATCTGCCCAACATCGATTTAAACCGTGAACCGTAAATCAATTAGCG 600
Db 855 CGTTATCTAACAATCTGCCCAACATCGATTTAAACCGTGAACCGTAAATCAATTAGCG 914

QY 601 GCGGAACAGGTTCCGAATGTTAAACCAATTAATTAAGTTACTGATCAAAAGTATTACTGAA 660
Db 915 GCGGAACAGGTTCCGAATGTTAAATTAATTAAGTTACTGATCAAAAGTATTACTGAA 974

QY 661 GGATATGATGATGAGAGGTTGTTAAAGCACATGATGCTGAAACCTTAATCTATGAT 720
Db 975 GGATATGATGATGAGAGGTTGTTAAAGCACATGATGCTGAAACCTTAATCTATGAT 1034

QY 721 GTAATTTTGAAGTATAGATGAAGGTGAATCTGGTGATACGATGACAGTGGATATAGAT 780
Db 1035 GTAATTTTGAAGTATAGATGAAGGTGAATCTGGTGATACGATGACAGTGAATATAGAT 1094

QY 781 AAGATACAGTTCCATCAGATTTAACCGATAGCTTTACATACCAAAAATAAAGATAT 840
Db 1095 AAGATACAGTTCCATCAGATTTAACCGATAGCTTTTGAATACCAAAAATAAAGATAT 1154

QY 841 TCTGAGAAATCATCGCTACAGTACTTATGATTAACAAAATAAACAATCACCTACT 900
Db 1155 TCTGAGAAATCATCGCTACAGTACTTATGATTAACAAAATAAACAATCACCTACT 1214

QY 901 TTACAGATTATGTAGATAAGTATGAAAAATATTAAGACACACCTTTAAATTAACGTCATAC 960
```

## RESULT 7

```
US-09-710-279-2699
; Sequence 2699, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
```

## US-09-710-279-2699

```
US-09-710-279-2699
; Sequence 2699, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
```

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2699

; LENGTH: 837

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: nucleic acid sequence

US-09-710-279-2699

Query Match 29.0%; Score 507.2; DB 3; Length 837;  
Best Local Similarity 97.5%; Pred. No. 9.6e-99;  
Matches 515; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TCTAGTGATGAAGAAAAGAAATGATGTGATCAATTAATAATCAAGTCAATTAATAACCGACGAT 60  
Db 223 TCTAGTGATGAAGAAAAGAAATGATGTGATCAATTAATAATCAAGTCAATTAATAACCGAT 282  
Qy 61 AATAACCAATAATTAATAAAGAAAGAAAGCAATTAATCAAGTCAATTAATAACCGATCA 120  
Db 283 AATAACCAATAATTAATAAAGAAAGAAAGCAATTAATCAAGTCAATTAATAACCGATCA 342  
Qy 121 GAAGATAGACAGAGTCAACAAACAATGTAGATGAAGAAAGCAAGCAACATTTTACAAAAG 180  
Db 343 GAAGATAGACAGAGTCAACAAACAATGTAGATGAAGAAAGCAAGCAACATTTTACAAAAG 402  
Qy 181 ACCCTCAAGATAATCACTCTTACAGAAAGAGGTAAGAAAGCAACATTTTACAAAAG 240  
Db 403 ACCCTCAAGATAATCACTCTTACAGAAAGAGGTAAGAAAGCAACATTTTACAAAAG 462  
Qy 241 TCCTCAAAATTCATCAATTTGATACTGCCCCAACCAACCATCTCACAAACAATAAATAGAAA 300  
Db 463 TCCTCAAAATTCATCAATTTGATACTGCCCCAACCAACCATCTCACAAACAATAAATAGAAA 522  
Qy 301 GAATCTGTTCAACAAGTGAATCTGTTAGAAAGTTCACACGATATCAGATTTTGCCTAACTCT 360  
Db 523 GAATCTGTTCAACAAGTGAATCTGTTAGAAAGTTCACACGATATCAGATTTTGCCTAACTCT 582  
Qy 361 AAAATAAAGAGAGTAACACTGAAATCTGTTAAAGAGAGATATCTATAGAGCAACCTAAT 420  
Db 583 AAAATAAAGAGAGTAACACTGAAATCTGTTAAAGAGAGATATCTATAGAGCAACCTAAT 642  
Qy 421 AAAGTAAAGAGAGTTCACAAACCAAGTTCAGCGCTGCTGCTATACAAATATAGATGAAAAA 480  
Db 643 AAAGTAAAGAGAGTTCACAAACCAAGTTCAGCGCTGCTGCTATACAAATATAGATGAAAAA 702  
Qy 481 ATTTCAAAATCAAGATGAGTTATTAATTTACCAATAAATGAATATGAA 528  
Db 703 ATTTCAAAATCAAGATGAGTTATTAATTTACCAATAAATGAATATGAA 750

RESULT 8

US-09-710-279-3492

; Sequence 3492, Application US/09710279

; Patent No. 6703492

; GENERAL INFORMATION:

; APPLICANT: KIMMERLY, WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

; FILE REFERENCE: PU3480US

; CURRENT APPLICATION NUMBER: US/09/710,279

; PRIOR FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: 60/164,258

; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3492

; LENGTH: 3236

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: nucleic acid sequence

US-09-710-279-3492

Query Match 29.0%; Score 507.2; DB 3; Length 3236;

Best Local Similarity 97.5%; Pred. No. 1.3e-98;

Matches 515; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TCTAGTGATGAAGAAAAGAAATGATGTGATCAATTAATAATCAAGTCAATTAATAACCGACGAT 60  
Db 1807 TCTAGTGATGAAGAAAAGAAATGATGTGATCAATTAATAATCAAGTCAATTAATAACCGAT 1866  
Qy 61 AATAACCAATAATTAATAAAGAAAGAAAGCAATTAATCAAGTGGCATAGAAAAACGCTCA 120  
Db 1867 AATAACCAATAATTAATAAAGAAAGAAAGCAATTAATCAAGTGGCATAGAAAAACGCTCA 1926  
Qy 121 GAAGATAGACAGAGTCAACAAACAATGTAGATGAAGAAAGCAAGCAACATTTTACAAAAG 180  
Db 1927 GAAGATAGACAGAGTCAACAAACAATGTAGATGAAGAAAGCAAGCAACATTTTACAAAAG 1986  
Qy 181 ACCCTCAAGATAATCACTCTTACAGAAAGAGGTAAGAAAGCAACATTTTACAAAAG 240  
Db 1987 ACCCTCAAGATAATCACTCTTACAGAAAGAGGTAAGAAAGCAACATTTTACAAAAG 2046  
Qy 241 TCCTCAAAATTCATCAATTTGATACTGCCCCAACCAACCATCTCACAAACAATAAATAGAAA 300  
Db 2047 TCCTCAAAATTCATCAATTTGATACTGCCCCAACCAACCATCTCACAAACAATAAATAGAAA 2106  
Qy 301 GAATCTGTTCAACAAGTGAATCTGTTAGAAAGTTCACACGATATCAGATTTTGCCTAACTCT 360  
Db 2107 GAATCTGTTCAACAAGTGAATCTGTTAGAAAGTTCACACGATATCAGATTTTGCCTAACTCT 2166  
Qy 361 AAAATAAAGAGAGTAAACACTGAAATCTGTTAAAGAGAGATATCTATAGAGCAACCTAAT 420  
Db 2167 AAAATAAAGAGAGTAAACACTGAAATCTGTTAAAGAGAGATATCTATAGAGCAACCTAAT 2226  
Qy 421 AAAGTAAAGAGAGTTCACAAACCAAGTTCAGCGCTGCTGCTATACAAATATAGATGAAAAA 480  
Db 2227 AAAGTAAAGAGAGTTCACAAACCAAGTTCAGCGCTGCTGCTATACAAATATAGATGAAAAA 2286  
Qy 481 ATTTCAAAATCAAGATGAGTTATTAATTTACCAATAAATGAATATGAA 528  
Db 2287 ATTTCAAAATCAAGATGAGTTATTAATTTACCAATAAATGAATATGAA 2334

RESULT 9

US-09-200-650E-8

; Sequence 8, Application US/09200650E

; Patent No. 6680195

; GENERAL INFORMATION:

; APPLICANT: Patti, Joseph M.

; APPLICANT: Foster, Timothy J.

; APPLICANT: Hook, Magnus A.O.

; APPLICANT: Eidhinn, Deirdre Ni

; APPLICANT: Perkins, Samuel L.

; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus

; FILE REFERENCE: P06283US2/BAS

; CURRENT APPLICATION NUMBER: US/09/200,650E

; PRIOR FILING DATE: 1998-11-25

; PRIOR APPLICATION NUMBER: 60/066,815

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: 60/098,427

; PRIOR FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 3498

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-09-200-650E-8

Query Match 20.9%; Score 364.4; DB 3; Length 3498;

Best Local Similarity 52.7%; Pred. No. 3.1e-68;

Matches 931; Conservative 0; Mismatches 796; Indels 39; Gaps 5;

Qy 10 GAAGAAAAGAAATGATGTGATCAATAATAATCAAGTCAATAAAGCAACCGACGATAATAACCAA 69

Db 229 GAAACTGAAATTAATTCGCAACAGAAAAATAATTCAACAAATCAATTAAGAAGAAACA 288  
QY 70 ATAATTAAGAAAGAGAAACGAATAACTACGATGGCATAGAAAAACGCTCAGAGATAGA 129  
Db 289 AATACTGATTCAACAACAGAGAGCTAAAGAGATCAATCTCATCAAGTACTCAAAACAG 348  
QY 130 ACGAGTCAACAACAAATGTAGATGAAGAAAGCAACAACTTTTACAAAGACCCCTCAA 189  
Db 349 CAAATAAAGCTTACAGCTACAACTGAACCTAAAGCTCAAAACATTCGAAAAAGAAATGTT 408  
QY 190 GATAAATCACTCATCTTACAGAGAGAGGTAAAGAAATCCTCATCACTCGAATCCTCAAT 249  
Db 409 AAACCTTCACTGATAAACTGCGACAGAGATACATCTGTTATTTTGAAGAGAGAA 468  
QY 250 TCATCAATTTGATATCTGCCAAACCAACCATCTCAACAACAATAAATAGAGAAGAAATCTGTT 309  
Db 469 GCACCAATAATACAAATACAGATGTAATCAACAACCATCTACAAGTGACCATCTACA 528  
QY 310 CAAACAAAGTGATAATGTAGAGATTCACACGATACAGATTTTGTCTAACTCTAAATAAAA 369  
Db 529 AGTGAATTTCAAAACAAACCAACTACACCTCAAGAAATCTACAAATATTGAAATTCACAA 588  
QY 370 GAGAGTAAACACTGAACTCTGGTAAAGAGAGATACATATAGAGCAACCTAATAAGTAA 429  
Db 589 CCGCAACCAACGCTTTCAAAAGTAGACAATCAAGTTTACAGATGCAACTAATCCAAAGAA 648  
QY 430 GAAGATTTCAACAACAGTCAGCGCTCTGGCTATACAAATATAGATGAAAAAATTTCAAAT 489  
Db 649 CCAGTAATGTCTAAAGAGAGAACTTAAATATATCTTGAGAAATTAAGAAATTTGGTT 708  
QY 490 CAAAGATGATTAATTAATTAACAATAATGAATATGAATAATAGCTAGACCATTTATCT 549  
Db 709 AGAAATGATAGCAATACAGATCAATCAACTAAACCAAGTTGCTACAGCTCCAACAAGTGT 768  
QY 550 ACAACATCTGCCCAACCATCGATTAAACGTGTAAACGTHAATCAATAGCGCGGGAACAA 609  
Db 769 GCACCAAAACGTTGTAACCCAAAAATGCGCTTTGCAGTTTGCACCAACGACGAGTTGCT 828  
QY 610 GGTTCGAATGTTAAACCATTTAATTAAGTTTACTGATCAAGTATTACTGAAGGATATGAT 669  
Db 829 TCAACAAATGTAATGATTAATTAAGTGACGAGCAACAACTCA ---AAGTTGCGCAT 885  
QY 670 GATAGTGAAGTGTATTAAAGCACATGATGCTGAAAACTTAATCTATGATGTAACCTTTT 729  
Db 886 GGTAAAGATAATGTGCGCAGCAGCATGACGTTAAAGATATTGAATATGATACAGATTT 945  
QY 730 GNAGTAGATGATAAGTGAATCTGGTGATACGATGACGTGGATATAGATAAGAAATACA 789  
Db 946 ACAATTTGCAATAAAGTCAAAAAGCGGATACAAATGACGATTAATATGATAAGAAATGTA 1005  
QY 790 GTTCCATCAGATTTAAACCGATAGCTTTACAATACCAAAAATAAAGATAATTTCTGGANA 849  
Db 1006 ATTCTCTCGATTTAAACAGATAAATAATGATCTCTATCGATATTACTGATCCATCAGAGAG 1065  
QY 850 ATCACTCGCTACAGGTACTTATGATAACAAAAATAAACAACCACTATCTATCTTTACAGAT 909  
Db 1066 GTCATTGCTAAAGGAACATTTGATTAAGCAACTAAGCAAAATCACATATACATTTACAGAC 1125  
QY 910 TATGTAGATAGTATGAATAATTAAGCACACCTTTAAATTAACGTCTATACATTTGATAAA 969  
Db 1126 TATGTAGATAAATATGAAGATAAATAATCAACGCTTTAACTCTATATTCGTATATATGATA 1185  
QY 970 TCAAGAGTTTCCAAATAATAATACCAAGTTTATAGATGATAGATAAATAACCGCCCTTTCA 1029  
Db 1186 AAAACAGTTCCA ---AATGAGACAAGTTTGAATTTAAACATTTGCTACAGCAGGTAAGAA 1242  
QY 1030 GTAAATAAACAATTAACGTTTGAATATCAAGACCTTAACGAAATTCGGAATCGTAACCTT 1089  
Db 1243 ACAAGCCAAAATGTCACTGTTGATTTATCAAGATCCAAATGCTGATGATTCAAACATT 1302  
QY 1090 CAAAGTATGTTTACAAATATAGATACGAAATAATCATACAGTTGACCAACAGATTTATAT 1149

Db 1303 CAATCTATCTTTTACAAAATTAGATGAAGATAAGCAAACTATTGAAACAACAAATTTATGTT 1362  
QY 1150 AACCCCTCTTCTGTTATTTCAGCCAGGAAACAAAATGTAAATATTTCAGGGAAATCGTGATG 1207  
Db 1363 AACCCATTTGAAAAAATCAGAACCACTAAAGTTGATATAGCTGGTAGTCAAGTAGAT 1422  
QY 1208 -----AAGGTTTCAACAAATTTATAGACCATAGCACAATAAAT 1242  
Db 1423 GATTATGGAATATTAAACCTAGGAAATGCTAGCACCATTATTGACCANAATACAGAAATA 1482  
QY 1243 AAAGTTTATAAGGTTGGAGATAATCAAAATTTTACAGATAGTAAACAGAAATTTATGATATAC 1302  
Db 1483 AAAGTTTATAAAGTTTAACTCTGATCAACAAATTTGCCCTCAAGTAATAGAAATCTATGATTT 1542  
QY 1303 AGTGAATATGAAGATGTCACAAATGA ---TGATTAATGCCCAATTTAGGAATAATAATGAT 1359  
Db 1543 AGTCAATACGAAGATGTAACAAGTCAATTTGATAATAAAAAATCATTTAGTAATAATGTA 1602  
QY 1360 GTGAATATTAATTTTGGTAATATAGATTCCACCATATATTATTAAAGTTATTAGTAAATAT 1419  
Db 1603 GCAACATTTGGAATTTTGGTGATATTAAATTCAGCCTATATTATCAAGTTGTTAGTAAATAT 1662  
QY 1420 GACCCTAATAAGGATGATTACAGACTATAACAGCAAACTGTGACAAATGACAGCACTATA 1479  
Db 1663 ACACCTATACATCAGATGGCGAACTAGATATTGCCAAGGTACTAGTATGAGAAACAACT 1719  
QY 1480 AATGATGATACCTGAGTTTGAACAGCATCCTATGATAATAACAAATTCCTTCTCTACA 1539  
Db 1720 GATAAATATGGTTATTATTAATTTATGAGGATATTCAACTTCATCGTAATCTTAATGAC 1779  
QY 1540 AGTTCAGGTCAAGGACAAGGTGACTTGCCTCTGAAAAAACTTATAAAAAATCGGAGATTAC 1599  
Db 1780 ACTGCGGTGGCGACGCTACTGTTAAACCTGGAAGAAAGTTATACAAAATTTGTTGACTAT 1839  
QY 1600 GTATGGGAGATGATAGATAAGATGGTATTTCAAAAATACAAATGATAATGAAAAACCGCTT 1659  
Db 1840 GTATGGGAGACGTTGATAAAGACGCTGTTCAAGGTACAGATTCAAAAGAAAAAACCAATG 1899  
QY 1660 AGTAATGATTTGGTAACTTTGACGCTATCTGATGAACTTCAAAATCAGTCAGACAGAT 1719  
Db 1900 GCAACGTTTATGTTTACATTAATTTACCGGACGCTACTACAAAATCAGTAAGACAGAT 1959  
QY 1720 GAAGATGGGAATATCAATTTTATGATGG 1745  
Db 1960 GCTAATGCTCATTAATGAAATTCGGTGG 1985

## RESULT 10

US-09-200-650E-6  
; Sequence 6, Application US/09200650E  
; Patent No. 6680195  
; GENERAL INFORMATION:  
; APPLICANT: Fatti, Joseph M.  
; APPLICANT: Foster, Timothy J.  
; APPLICANT: Hook, Magnus A.O.  
; APPLICANT: Eidehinn, Deirdre Ni  
; APPLICANT: Perkins, Samuel L.  
; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus  
; FILE REFERENCE: P0628302/BAS  
; CURRENT APPLICATION NUMBER: US/09/200,650E  
; CURRENT FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: 60/066,815  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: 60/098,427  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 3945  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus  
US-09-200-650E-6

Query Match 7.2%; Score 126; DB 3; Length 3945;  
Best Local Similarity 44.0%; Pred. No. 1.7e-17;  
Matches 727; Conservative 0; Mismatches 915; Indels 12; Gaps 4;

QY 86 AAACGAATAACTACGATGGCATAGAAAACGCTCAGAAAGATAGAACAGAGTCAACAACAA 145  
DB 212 AATCGAGTAAAGTTGATATGCGCAACTAAATCAAGAGACAACTACTAAATGATA 271  
QY 146 ATGTAGATGAAAACGAAGCAACATTTTACAAAAGACCCCTCAAGATATATCTCATCTTA 205  
DB 272 ATCAAAAAGAAATGGTATCATCTCAAGGTAATGAACGACTTCAATGGGAATAAATTA 331  
QY 206 CAGAAGAGAGGTAAAGAAATCCTCATCAGTCGAATCCTCAAAATTCATCAATTCGACTG 265  
DB 332 TAGAAAAGAAAGTGTACATCTCACTGGAATTAAGTTGAAATTTCAACTGCCAAT 391  
QY 266 CCCAACCAACCATCTCACAAACAATAMATAGAGAAGAACTCTGTTCAAAACAAGTGATG 325  
DB 392 CAGATGACCAAGCT---TCACCAAAATCTACGAATGAAGATTTAAACACTAAACAACTA 448  
QY 326 TAGAAGATTCACAGTATCAGATTTTGCTAACTCTTAAATAAAGAGAGTAACTGAAT 385  
DB 449 TAAGTAATCAAGAGCGTTACAACTGATTTGCAAGAGATAAATCAGTGTAAATGTTTC 508  
QY 386 CTGGTAAAGAGAGAACTACTAGAGCAACCTTAATAAGTAAAGAAAGATTCACAACAA 445  
DB 509 AACCAACTAATAGAGGAAACAAAGGTAGATGCCAAACCTGAATCAACTACATTAATG 568  
QY 446 GTCAGCCCTCGGCTATACAAATATAGATGAAAAATTTCAAAATCAAGATGAGTTATTA 505  
DB 569 TTAAAGTGATGCTATCAAGAGTAATGATGAACCTCTTGTTGATAACAATAGTAATCAA 628  
QY 506 ATTTACCAATAAATGAATATGAATAAAGGTAGACCAATATCTACAACTCTGCCCAAC 565  
DB 629 ATAATGAAAATAATCAGATATCATTTTGCAAAAGATPACAGCACTTAAACGTTTGA 688  
QY 566 CATCGATTAACGTTGTAACCGTAAATCAATTAGCGGCGGAACAAGTTTCAAGATGTTA 625  
DB 689 CA---AGATGCGTATACGACGATACAGCCATCATCAACGAGGCTTAAATGTTTATG 745  
QY 626 ATTTAAATTAAGTTACTGATCAAGATATTAATCTGAAGGATATGATGATAGTGAAGTG 685  
DB 746 ATTTAATCACATCAAAATCAACATTAATCTGCTGTTGATGCGAGATAAACAATAAATCG 805  
QY 686 TTAAGCAGATGATGCTGAAAACCTTAATCTATGATGTAACCTTTTGAAGTAGATGAAGG 745  
DB 806 TACCAGCCCAAGATATTTATCATTTAAATACAAATTTACAGATTTGATGACAAAGTTAA 865  
QY 746 TGAATCTGGTGATACGATGACAGTGGATATAGATAAGAAATACAGTTCCATCAGATTAA 805  
DB 866 CAGGTGATTTTCAAAATTAATTAATCTCAGATACAGTACAGTATATGGATTGAATCCGG 925  
QY 806 CCGATAGCTTTACATATACCAAAATAAAGAT---AATTCGGAGAAATCATCGCTACAG 862  
DB 926 AAGATATTAATAAATATGTTGATATTAAGATCCAAATAATGGTGAACAATTTGGCACTG 985  
QY 863 GTACTTATGATAAATAAATAAACAATCACTATACCTTTTACAGATTTATGATAGTAAGT 922  
DB 986 CAAAACATGATCTGCAAAATTAATTAATACATATACATTTTACAGATTTATGTTGATCAT 1045  
QY 923 ATGAAAATATTAAGCACACCTTAAATTAAGTCAATACATATGATAAATCAAAAGTTCCAA 982  
DB 1046 TTAATCTGTACAAATGGGAATTAATTAATTTCAATTTATATGATGCTGATACAAATCTCTG 1105  
QY 983 ATAATAATACCAAGTTAGATGTAGAAATATAAAGCGCCCTTTTCATCAGTAATAAACA 1042  
DB 1106 TTAGTAAACCGATGTTGAGTTAATGTTTACGATAGGTAATTAACAACAACAACTG 1165  
QY 1043 TTACGGTTGAATATCAAGACCTAACGAATACGAAGTCTTAACCTTCAAGATATGTTA 1102  
DB 1166 CTAACATTTCAATATCCAGATTTATGTTGTAATAGAGAAAAATTCATTTGGATCAGCGTTCA 1225  
QY 1103 CAAATATAGATACGAAAAAT---CATACAGTTGACAAACGATTTTATATTAACCCCTCTTC 1159

DB 1226 CTGAAACAGTTTCACATGTTGGAAATAAAGAAATCCAGGTACTATATAACCAACGATTT 1285  
QY 1160 GTTATTCAGCAAGAAACAAATGTAATATTTTTCAGGAATGGTGAAGAGTTCAACAA 1219  
DB 1286 ATGTAAATCCATCGAAAAATTTCTTTAAACAAATGCAAACTAAAGTTTCAAGCTTACC 1345  
QY 1220 TTATAGCAGTAGCAGCAATAATTAAGCTTTTATAGGTTGGAGATAAATCAAAATTTACC 1279  
DB 1346 CAAGTTATCTTAATAATATCGGCAAAATAAATAAGATGTAACAGATATAAATAATATATC 1405  
QY 1280 ATAGTAACAGAAATTTATGATTTACAGTGAATATGAAGATGTCAAAATGATGATTTATG 1339  
DB 1406 AAGTTCTCTAAAGTTTATACATTAATAAAGGATACGATGTGAATTAAGAGCTTACAG 1465  
QY 1340 AATTAGGAATAATAATGATGTGAATATTAATTTTGGTAATATAGATTCACCATATATTA 1399  
DB 1466 ATGTAAACAAATCAATCTTCAGAAAAATTAATATGCGGCAACAATATAGCGCTGTATTG 1525  
QY 1400 TTAAGTTATAGTAAATATGACCCCTAATAAGGATGATTAACGACTATACAGCAAACTG 1459  
DB 1526 ATTTGGAAATGCGAGATTCGCTTATGTTGTAATGTTTAACAAAATTCCAATATACAA 1585  
QY 1460 TGACAATGCGACGACTATAAATGAGTATATCTGCTGAGTTTAGAACAGCATCTTATGATA 1519  
DB 1586 ATAGCGAAAGCCCAACACTGTTCAAAATGGCTACTTTTCTTCAACAGGTAATAAATCCG 1645  
QY 1520 ATACAATTTGCTTTCTTACAGTTTCAGGTCAAGGACAGGAGTGTGCTCTCTGAAAAA 1579  
DB 1646 TTTCTACTGCGCAATGCTTTAGGATTTACTAATAACCAAGAGTGGCGAGCTGGTCAAG 1705  
QY 1580 CTTATAAATCGGAGATTCAGTATGCGAAGATGATAGATAAAGATGGTATTCAAAATACAA 1639  
DB 1706 TATATAAATTTGGTAATCTAGTATGCGAAGATACATAAATAACGGTGTTCAGAAATTA 1765  
QY 1640 ATGATAATGAAAAACCGCTTAGTAAATGTTTGGTAACTTTTGACGTATCTCTGATGGA 1699  
DB 1766 GAGAAAAGCGTTGGCAATGTAATCTGTAATGATTAATAATAACAAATACAAAG 1825  
QY 1700 CAAATCAGTCAGAACAGATGAAGATCGGAATA 1733  
DB 1826 TAGGAGAAGCAGTTTACTTAAAGAGATGGGTCTATA 1859

RESULT 11  
US-09-710-279-4157/c  
; Sequence 4157, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710, 279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4157  
; LENGTH: 3619  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-09-710-279-4157

Query Match 7.0%; Score 122.2; DB 3; Length 3619;  
Best Local Similarity 94.1%; Pred. No. 1.1e-16;  
Matches 127; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1612 GTAGATAAAGATGGTATTTCAAAATACAAATGATTAATGAAAAACCGCTTAGTAATGTTATG 1671

Db 3170 GTGAACACCAATATTATTCAAAATACAAATGATAAAGTAAAGAAAACCGCTTAGTAATGATTG 3111  
QY 1672 GTAACCTTTCAGTATCTCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGAAA 1731  
Db 3110 GTTATTTGACGTATCTCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGAAA 3051  
QY 1732 TATCAATTTTCATGGA 1746  
Db 3050 TATCAATTTTCATGGA 3036

## RESULT 12

US-09-710-279-4135  
; Sequence 4135, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4135  
; LENGTH: 2957  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-09-710-279-4135

Query Match 6.3%; Score 110.2; DB 3; Length 2957;  
Best Local Similarity 46.3%; Pred. No. 3.6e-14;  
Matches 361; Conservative 0; Mismatches 418; Indels 0; Gaps 0;  
QY 608 AAGGTTTCAATGTTAAACCACTTTAAATTAAGTTACTGATCAAAAGTATTACTGAAGGATATG 667  
Db 905 AAAATGTGAATGATAAGTTAAATCAAAACCTTACGCTTTCACCTTAATAGAGTAATA 964  
QY 668 ATGATAGTAGAGTGTTTAAAGCAATGCTGAAACCTTAACTAATGATGTAATCTT 727  
Db 965 ATCACTTAATACGTAATATGCGCAACCAAGTAAACCAATTTAAATTTAAAGCAAAAT 1024  
QY 728 TTGAAGTATGATAGGTTGAATCTGTTGATACGATGACAGTGGATATAGTAAGAATA 787  
Db 1025 ATGAATTTAGATGACATATAAGAGGAGATACCTTTTACTATTAAGTATGTCAGTATA 1084  
QY 788 CAGTTCCATCAGATTTAAACCGATAGCTTTTCAATACCAAAATATAAAGATTAATCTCGGAG 847  
Db 1085 TTAGACCGGGTGGTTTAGAATCTTCTGCAATATAAAACTCACTACGTAGTAGGCTT 1144  
QY 848 AATATCATCGTACAGTACTTTATGATAACAAAATATAACAAATACCTATACCTTTTACAG 907  
Db 1145 CTATTCTAGCTAATGTTGATATGATAAAACTACAAATACGACGACTTATACATTTACTA 1204  
QY 908 ATTATGATAGTATGAATATAATTAAGACACACCTTAAATTAAGCTATACATTTGATA 967  
Db 1205 ACTATGTTGATCAATATCAAAATATTAACAGGTAGTTTTCATTTAATTTGCGACGCTAAGA 1264  
QY 968 AATCAAGGTTCCAAATATAATACCAAGTTAGATGTAGATATAAAGCGGCTTTTCAT 1027  
Db 1265 GGGAAACAGCAATTAAGGATATATCAGANTATCTATGGAATGACGATTTGTAACGAG 1324  
QY 1028 CAGTAAATATAAACAATTAACGTTTGAATATCAAGACCTTAACGAAATTCGAGCTGCTAAC 1087  
Db 1325 TAGTCAAAAAGAACTTTCATTGTGGATTATGGTAAATAAAGGACAAATACAACTACAGCAG 1384  
QY 1088 TTCAAGATGTTTACAAATATAGATACGAAATATCATCAGTTTGGAGCAACGATTTATA 1147  
Db 1385 CGGTAGCAATGTGGATATGTAATTAATTAACATAAACGAAAGTTGTTTATCTTAAACCAA 1444

QY 1148 TTAACCCCTCTTCGTTATTTCAGCCAGGAAACAAATGTAATATTTTCAGGGAATGGTGATG 1207  
Db 1445 ATACCCAAATCTTAATATGCTAAATATTTCTCAACAGTAAAAAATGGTAATTTATAC 1504  
QY 1208 AAGGTTCAACAATATTAGACGATAGCACAAATATTAAAGTTTATAAAGTTGGAGATAATC 1267  
Db 1505 CAGGTGAAGTGAAGTTTACGAAGTACGATACCAATGCGATGGTAGATAGCTTCAATC 1564  
QY 1268 AAAATTTACCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAGATGTCCACAATG 1327  
Db 1565 CTGAATTTAAATAGTCTTAATGTAAAGATGTGCAAGTCAATTTACACCTTAAAGTAAGTG 1624  
QY 1328 ATGATTATGCCAAATTAGGAAATAATAATGATGTAATTAATTTTGGTAAATATAGAT 1386  
Db 1625 CAGATGGTACTAGAGTTGATATCAATTTTGTAGAGATATGGCAATGGTAAAAAGTAT 1683

## RESULT 13

US-09-710-279-3455  
; Sequence 3455, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3455  
; LENGTH: 3132  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-09-710-279-3455

Query Match 6.3%; Score 110.2; DB 3; Length 3132;  
Best Local Similarity 46.3%; Pred. No. 3.6e-14;  
Matches 361; Conservative 0; Mismatches 418; Indels 0; Gaps 0;  
QY 608 AAGGTTTCAATGTTAAACCACTTTAAATTAAGTTACTGATCAAAAGTATTACTGAAGGATATG 667  
Db 761 AAAATGTGAATGATAAGTTAAATTAAGTAAACCTTCACTTAAATAAGAGTAATA 820  
QY 668 ATGATAGTGAAGGTGTTAATTAAGGACATGATGCTGAAACCTTAATCTATGATTAACCTT 727  
Db 821 ATCACTGTAATTAACGTTAATATGCGCAACAAAGTAAACGAACTTTAATTTAAAGCAAT 880  
QY 728 TTGAAGTATGATGAATGAAGTGAATCTGTTGATACGATGACAGTGGATATAGATAAGAATA 787  
Db 881 ATGAATTTAGATGACAGCATAAAGAGGAGATACCTTTTACTATTAAGTATGTCAGTATA 940  
QY 788 CAGTTCCATCAGATTTAACCAGTACTTTTACAAATACCAAAATATAAAGATTAATCTCGGAG 847  
Db 941 TTAGACCGGGTGGTTTAGAATCTTCTGCAATATAAACTCACTACGTAGTAGGATGGCT 1000  
QY 848 AATCATCTCCTCAGTACTTATGATAACAAAATATAACAAATACCTATCTATCTTTTACAG 907  
Db 1001 CTATTGTTAGTAAATGGTGTATATGATATAAACTCAAAATACGACGACTTATATCAATTACTA 1060  
QY 908 ATTATGATAGATGAATGAAAAATATTAAAGCAACCTTAAATTAACGTCATACATTTGATA 967  
Db 1061 ACTATGTTGATCAATATCAAAATATTACAGGTAGTTTTCATTTAATTTGCGACGCTAAGA 1120  
QY 968 AATCAAGGTTCCAAATATAATATCAAGTTAGATGTAGATATAAAGCGGCTTTTCAT 1027  
Db 1121 GGGAAACAGCAATTAAGGATATAATCAGAATTTATCTTATGGAAGTACGATTTGTTAAACGAA 1180



```
QY 1028 CAGTAAATAAACAATTACGGTTGTAATATCAAGACCTAAACGAAATCGGACTGCTAACC 1087
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1181 TAGTCAAAAAGACCTTCATTGTTGGATTATGGTAATAAAAAGGACAATAACAACACAGCAG 1240
QY 1088 TTCAAAGTAGTGTTCACAAATATAGATACGAAAAATCATACAGTTGAGCAAAAGCATTTATA 1147
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1241 CGGTAGCAAAATGCGGATATGTAATATAATAACATAACGAGTTGTTTATCTAAACCAA 1300
QY 1148 TTAACCCCTCTCGTTATTACAGCAAGGAAACAAATGTAAATATTTACAGGGAATGGTGATG 1207
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1301 ATAACCAAAATCCTAAATATGCTAAATATTTCTCAACAGTAAATAATGTTAAATTTATAC 1360
QY 1208 AAGGTTCAACAAATATAGACGATACCAATAATTTAAAGTTTATAAGTTGAGATATC 1267
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1361 CAGGTGAAGTGAAGTTTACGAAAGTGACGATACCAATGCGATGTAGTAGTCTTCAATC 1420
QY 1268 AAAATTTTACCAGATAGTACACAAATTTATGATTACAGTCAATATCAAGATGTCAAAATG 1327
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1421 CTGATTTAAATAGTTCTAATGTAAGATGTGACAAAGTCAATTTACACCTTAAAGTAAAGTG 1480
QY 1328 ATGATTATGCCCAATAGGAAATAATAATGATGTGAATATTAATTTTGGTAAATATAGAT 1386
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1481 CAGATGGTACTAGAGTTGATATCAATTTTGTGAGAAGTATGCAAAATGTTAAAGATAT 1539

RESULT 14
US-09-710-279-1779
; Sequence 1779, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1779
; LENGTH: 3465
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-1779

Query Match 6.3%; Score 110.2; DB 3; Length 3465;
Best Local Similarity 46.3%; Pred. No. 3.7e-14; Mismatches 418; Indels 0; Gaps 0;
Matches 361; Conservative 0;

QY 608 AAGGTTTCAATGTTAAACCAATTTAATTAAGTTTACTGATCAAAAGTATTACTGAAGGATATG 667
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1094 AAAATGTGAATGATAAAGTTAAATCAACAAACCTTACGCTTTCACCTTAATAAGAGTAATA 1153
QY 668 ATGATAGTGAAGGTGTTATTAAGCACATGATGCTGGAACCAATTAATCTATGATGTAACCTT 727
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1154 ATCAGGCTAAATACGCTTAATATGCGCAACAAAGTAACGAACAATTTAATTTAAAGCAAAAT 1213
QY 728 TTGAAGTAGATCATAGGTGAATCTGGTGATACGATGACAGTGTAGATATAGATAAGAATA 787
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1214 ATGAATTAGATGACAGCATAAAGAGGGAGATCTTTTACTATTAAAGTATGGTCAGTATA 1273
QY 788 CAGTTCCTCATCAGATTAAACCGATAGCTTTTACAAATACCAAAAATAAAGATATTTCTGGAG 847
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1274 TTAGACCGGGTGGTTTGAAGACTTCTGCAATAAAACTCAACTAGTAGTAAGGTGCT 1333
QY 848 AAATCATCGCTACAGTACTTATGATACAAAAAATAAACAATCAACATCACTTACTTTTACAG 907
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1334 CTATTGTAGCTAATGGTGATATGATAAAACTTACAATAACGACGACTTATACATTTACTA 1393
QY 908 ATTATGTAGATAAGTGAATAATATTAAAGCACACCTTTAAATTAACGTATCATATTGATA 967
```

```
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1394 ACTATGTTGATCAATATCAAAATATTACAGTAGTTTGTGATTTAATTCGGACGCCTAAGA 1453
QY 968 AATCAAAAGGTTCCAAAATAATAATACCAAGTTAGATGTAGAATATAAAAAACGGCCCTTTTCA 1027
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1454 GGGAAACAGCAAAATTAAGGATTAATCAGAATTATCTCTGGAAGTGACGATTGCTAACGAAG 1513
QY 1028 CAGTAAATAAACAATTTACGGTTGAAATATCAAGACCTTAACGAAATCGGACTGCTAACC 1087
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1514 TAGTCAAAAAAGACTTCATTGTGGATTATGTTAAATAAAAAAGGACAATAACAACACAGCAG 1573
QY 1088 TTCAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAAAAGCATTTATA 1147
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1574 CGGTAGCAAAATGCGGATATGTAATATAATAACATAACGAAGTTGTTTATCTAAACCAA 1633
QY 1148 TTAACCCCTCTCGTTATTACGCCAAAGGAAACAAATGTAAATATTTACAGGGAATGGTGATG 1207
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1634 ATAACCAAAATCCTAAATATGCTAAATATTTCTCAACAGTAAAAAATGTTAAATTTATAC 1693
QY 1208 AAGGTTCAACAAATTTATAGACGATAGCAAAATTTATGATTTACAGTGAATATGAAGTTTATAAGGTTGGAGATAATC 1267
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1694 CAGGTGAAGTGAAAGTTTACGAAGTGACGATACCAATGCGATGTAGTAGTCTTCAATC 1753
QY 1268 AAAATTTACCAGATAGTAAACAGAATTTATGATTTACAGTGAATATGAAGTGTCAAAAATG 1327
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1754 CTGATTTAAATAGTTCTAATGTAAGATGTGACAAAGTCAATTTACACCTTAAAGTAAAGTG 1813
QY 1328 ATGATTATGCCCAATTAGGAAATAATAATGATGTGAATATTAATTTTGGTAAATATAGAT 1386
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1814 CAGATGGTACTAGAGTTGATATCAATTTTGTCTAGAAGTATGCAAAATGTTAAAGATAT 1872
```

```
RESULT 15
US-09-386-962C-1
; Sequence 1, Application US/09386962C
; Patent No. 6635473
; GENERAL INFORMATION:
; APPLICANT: POSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCUS EPIDERMIDIS
; FILE REFERENCE: P06335US2/BAS
; CURRENT APPLICATION NUMBER: US/09/386,962C
; CURRENT FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5406
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(5406)
US-09-386-962C-1
```

```
Query Match 6.2%; Score 108.6; DB 3; Length 5406;
Best Local Similarity 46.2%; Pred. No. 8.9e-14; Mismatches 419; Indels 0; Gaps 0;
Matches 360; Conservative 0;

QY 608 AAGGTTTCAATGTTAAACCAATTTAATTAAGTTTACTGATCAAAAGTATTACTGAAGGATATG 667
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1205 AAAATGTGAATGATAAAGTTAAATATCAACAACTTACGCTTTCACCTTAATAAGAGTAATA 1264
QY 668 ATGATAGTGAAGGTGTTTATTAAGCACATGATGCTGAAAACTTAATCTATGATGTAACCTT 727
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1265 ATCAGCTTAATAACGTTAATATATGCGCAACAAAGTAAACGAACAATTTAATTTAAAGCAAAAT 1324
QY 728 TTGAAGTAGATGATAAGGTGAATCTGGTGATACGATGACAGTGTAGTATAGATAAGAATA 787
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1325 ATGAATTAGATGACAGCATAAAGAGGGAGATACTTTTACTATTAAAGTATGGTCAAGTATA 1384
```

Search completed: August 14, 2006, 06:00:01  
Job time : 479 secs

**This Page Blank (uspto)**

61 AATAACCAAAATAATTAAAAAGAGAAACGAATAACTACGATGGCATAGAAAAACGCTCA 120

```
QY 121 GAAGATAGAACAGAGTCAACAACTGTAGATGAAGCAAGCAATTTTACAAAAG 180
DB 121 GAAGATAGAACAGAGTCAACAACTGTAGATGAAGCAAGCAATTTTACAAAAG 180
QY 181 ACCCTCTCAAGATAAATCTCATCTTACAGAAAGAGGTAAAGAAATCTCTCATCAGTCGAA 240
DB 181 ACCCTCTCAAGATAAATCTCATCTTACAGAAAGAGGTAAAGAAATCTCTCATCAGTCGAA 240
QY 241 TCTTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCCACAACTAAATAGAGAA 300
DB 241 TCTTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCCACAACTAAATAGAGAA 300
QY 301 GAATCTGTTCAAAACAGGTAAATGTAGAGAAATTCACACGTTATCAGATTTTGTCAACTCT 360
DB 301 GAATCTGTTCAAAACAGGTAAATGTAGAGAAATTCACACGTTATCAGATTTTGTCAACTCT 360
QY 361 AAAATAAAGAGAGTAACACTGAATCTGTGAAGAGAGAACTACTATAGAGCAACTAAT 420
DB 361 AAAATAAAGAGAGTAACACTGAATCTGTGAAGAGAGAACTACTATAGAGCAACTAAT 420
QY 421 AAAGTAAAGAGAGTTCAACAAAGTCAAGCGTCTGCGCTATACAAATATAGATGAAAAA 480
DB 421 AAAGTAAAGAGAGTTCAACAAAGTCAAGCGTCTGCGCTATACAAATATAGATGAAAAA 480
QY 481 ATTTCAAAATCAAGATGAGTTTAAATTTTCAACAAATGAATATGAATAAAGGCTAGA 540
DB 481 ATTTCAAAATCAAGATGAGTTTAAATTTTCAACAAATGAATATGAATAAAGGCTAGA 540
QY 541 CAAATATCTACAAATCTGCCCAACCATCTGATTAACCGTGAACCGTAAATCAATTAGCG 600
DB 541 CAAATATCTACAAATCTGCCCAACCATCTGATTAACCGTGAACCGTAAATCAATTAGCG 600
QY 601 GCGGAACAAGGTTTCAAGTTTAAACCAATTTAAATTTAAAGTTTACTGATCAAAAGTATTCTGAA 660
DB 601 GCGGAACAAGGTTTCAAGTTTAAACCAATTTAAATTTAAAGTTTACTGATCAAAAGTATTCTGAA 660
QY 661 GGATATGATGATGAGTGAAGGTGTTTAAAGCACATGATGCTGGAACCTTAATCTATGAT 720
DB 661 GGATATGATGATGAGTGAAGGTGTTTAAAGCACATGATGCTGGAACCTTAATCTATGAT 720
QY 721 GTAACCTTTTGAAGTAGATGATGAAGTGAATCTGCTGATACGATCAGATGATATAGAT 780
DB 721 GTAACCTTTTGAAGTAGATGATGAAGTGAATCTGCTGATACGATCAGATGATATAGAT 780
QY 781 AAGAAATACAGTTCCATCAGATTTAAACCGATAGCTTTTACAATAACCAAAATATAAAGATAAT 840
DB 781 AAGAAATACAGTTCCATCAGATTTAAACCGATAGCTTTTACAATAACCAAAATATAAAGATAAT 840
QY 841 TCTGAGAAATCATCGCTACAGGTACTTATGATAACAAATAAACAATGACCTATACT 900
DB 841 TCTGAGAAATCATCGCTACAGGTACTTATGATAACAAATAAACAATGACCTATACT 900
QY 901 TTTACAGATTATGATAGATAAGTATGAAATATTTAAAGCACACCTTAAATTAACGTCATAC 960
DB 901 TTTACAGATTATGATAGATAAGTATGAAATATTTAAAGCACACCTTAAATTAACGTCATAC 960
QY 961 ATTGATAAATCAAAAGGTTCCAAATTAATAATACAAAGTTAGATGTAAGATAATAAAGCGCC 1020
DB 961 ATTGATAAATCAAAAGGTTCCAAATTAATAATACAAAGTTAGATGTAAGATAATAAAGCGCC 1020
QY 1021 CTTTCATCAGTAAATAAACAATTAACGGTTGAATATCAAGACCTTAACGAAATTCGGACT 1080
DB 1021 CTTTCATCAGTAAATAAACAATTAACGGTTGAATATCAAGACCTTAACGAAATTCGGACT 1080
QY 1081 GCTAACCTTTCAAGGTATGTTTACAAATATAGATACGAAATATCATACAGTTGAGCAACG 1140
DB 1081 GCTAACCTTTCAAGGTATGTTTACAAATATAGATACGAAATATCATACAGTTGAGCAACG 1140
QY 1141 ATTTATATTAACCTCTTCGTTTATTCAGCCAAAGGAAACAAATGTAAATTTTTCAGGGAAT 1200
DB 1141 ATTTATATTAACCTCTTCGTTTATTCAGCCAAAGGAAACAAATGTAAATTTTTCAGGGAAT 1200
```

```
QY 1201 GGTGATGAAGGTTCAACAAATTTATAGACGATAGCACTAAATTTAAAGTTTATTAAGGTTGGA 1260
DB 1201 GGTGATGAAGGTTCAACAAATTTATAGACGATAGCACTAAATTTAAAGTTTATTAAGGTTGGA 1260
QY 1261 GATAATCAAAATTTTACACGATAGTAAACAGAAATTTATGATTACAGTGAATATGAAGATGTC 1320
DB 1261 GATAATCAAAATTTTACACGATAGTAAACAGAAATTTATGATTACAGTGAATATGAAGATGTC 1320
QY 1321 ACAAATGATGATTATGCCAAATAGGAAATTAATATGATGTGAATTTTAAATTTTGGTAAT 1380
DB 1321 ACAAATGATGATTATGCCAAATAGGAAATTAATATGATGTGAATTTTAAATTTTGGTAAT 1380
QY 1381 ATAGATTCACCATATATTTAAAGTTTATTAAGTAAATATGACCCCTAAATGAAGATGATTAC 1440
DB 1381 ATAGATTCACCATATATTTAAAGTTTATTAAGTAAATATGACCCCTAAATGAAGATGATTAC 1440
QY 1441 ACAGTATACAGCAAACTGTGACAAATGCAGACGACTATAAAATGAGTACTCTGGTGAGTTT 1500
DB 1441 ACAGTATACAGCAAACTGTGACAAATGCAGACGACTATAAAATGAGTACTCTGGTGAGTTT 1500
QY 1501 AGAACAGCATCTATGATAATAACAATTTCTTCACAAGTTCAGGTCAGGCAAGGACAAGGT 1560
DB 1501 AGAACAGCATCTATGATAATAACAATTTCTTCACAAGTTCAGGTCAGGCAAGGACAAGGT 1560
QY 1561 GACTTGCTCTCTGAAAGAACTTTATAAAATCGGAGATTACGTTATGGAAGATGTAGATAAA 1620
DB 1561 GACTTGCTCTCTGAAAGAACTTTATAAAATCGGAGATTACGTTATGGAAGATGTAGATAAA 1620
QY 1621 GATGGTATTTCAAAATACAAATGATAAATGAAACCGCTTAGTAAATGTTTGGTAACTTTG 1680
DB 1621 GATGGTATTTCAAAATACAAATGATAAATGAAACCGCTTAGTAAATGTTTGGTAACTTTG 1680
QY 1681 ACGTATCTGATGAACCTTCAAAATCAGTACAGACAGATGAAGTGGGAAATATCAATTT 1740
DB 1681 ACGTATCTGATGAACCTTCAAAATCAGTACAGACAGATGAAGTGGGAAATATCAATTT 1740
QY 1741 GATGGA 1746
DB 1741 GATGGA 1746
```

## RESULT 2

```
US-10-806-288-14
; Sequence 14, Application US/10806288
; Publication No. US20040209326A1
; GENERAL INFORMATION:
; APPLICANT: Guss, Bengt
; APPLICANT: Nilesen, Martin
; APPLICANT: Frykberg, Lars
; APPLICANT: Flock, Jan-Ingmar
; APPLICANT: Lindberg, Martin
; TITLE OF INVENTION: Coagulase-Negative Staphylococcus
; FILE REFERENCE: Guss 09/147405
; CURRENT APPLICATION NUMBER: US/10/806,288
; PRIOR FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/147,405
; PRIOR FILING DATE: 1999-04-11
; PRIOR APPLICATION NUMBER: PCT/SE97/10191
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: SE 9602496-3
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 3600
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33) .. (3308)
US-10-806-288-14
```

Query Match	100.0%; Score 1746; DB 9; Length 3600;
Best Local Similarity	100.0%; Pred. No. 1.3e-292;
Matches 1746; Conservative	0; Mismatch 0; Indels 0; Gaps 0;
Qy	1 TCTAGTGTGAAGAAAAGAAATGATGTGTATCAATAATACATCAGTCATCAGTCAATAAACCACGCAGAT 60
Dd	255 TCTAGTGTGAAGAAAAGAAATGATGTGTATCAATAATACATCAGTCAATAAACCACGCAGAT 314
Qy	61 AATAACCAAATAATTAAAAAGAGAAGAAACGAATAACTACGATGGCATAGAAAAACCGTCA 120
Dd	315 AATAACCAAATAATTAAAAAGAGAAGAAACGAATAACTACGATGGCATAGAAAAACCGTCA 374
Qy	121 GAAGATAGAACAGAGTCAACAACAATGTAGATGAAAAAGAAAGAAAGAAAGAAAGAAAG 180
Dd	375 GAAGATAGAACAGAGTCAACAACAATGTAGATGAAAAAGAAAGAAAGAAAGAAAGAAAG 434
Qy	181 ACCCTCTCAAGATAATACATCATCTTTACAGAAGAGGGTAAGAAGATCCTCATCAGTCGAA 240
Dd	435 ACCCTCTCAAGATAATACATCATCTTTACAGAAGAGGGTAAGAAGATCCTCATCAGTCGAA 494
Qy	241 TCCTCAAATTCATAATTGATACCTGCCCAACCAACCATCTCACAAACAATAAATAGAGAA 300
Dd	495 TCCTCAAATTCATAATTGATACCTGCCCAACCAACCATCTCACAAACAATAAATAGAGAA 554
Qy	301 GAATCTGTTCAAACAAGTGATAATGTAGAGATTACAACGTTACAGATTCTGCTTAACCTCT 360
Dd	555 GAATCTGTTCAAACAAGTGATAATGTAGAGATTACAACGTTACAGATTCTGCTTAACCTCT 614
Qy	361 AAAATAAAGAGAGTAAACATCGAATCTGGTAAAGAGNGATATCTATAGAGCAACCTAAT 420
Dd	615 AAAATAAAGAGAGTAAACATCGAATCTGGTAAAGAGAGAAATCTATAGAGCAACCTAAT 674
Qy	421 AAAGTAAAGAGAGATTCAACAACAAGTCAGCCGCTCTGGCTATACAAATATAGATGAAAAA 480
Dd	675 AAAGTAAAGAGAGATTCAACAACAAGTCAGCCGCTCTGGCTATACAAATATAGATGAAAAA 734
Qy	481 ATTTCAAATCAAAGTAGATTAAATTTTACCAATAAATGAATATGAAAAATPAAGGCTAGA 540
Dd	735 ATTTCAAATCAAAGTAGATTAAATTTTACCAATAAATGAATATGAAAAATPAAGGCTAGA 794
Qy	541 CCATTATCTCAAACATCTGCCCAACCATCGAATTAAACGTTAAACCGTAAATCAATTAGCG 600
Dd	795 CCATTATCTCAAACATCTGCCCAACCATCGAATTAAACGTTAAACCGTAAATCAATTAGCG 854
Qy	601 GCGGAAACAAGTTCGAAATGTTTAAACCATTTAATTAAGGTTACTGATCAAAAGTATTACTGAA 660
Dd	855 GCGGAAACAAGTTCGAAATGTTTAAACCATTTAATTAAGGTTACTGATCAAAAGTATTACTGAA 914
Qy	661 GGATATGATGATGTAAGGAGTGTATTAAAGCAATGATGCTGAAAACTTAACTCTATGAT 720
Dd	915 GGATATGATGATGTAAGGAGTGTATTAAAGCAATGATGCTGAAAACTTAACTCTATGAT 974
Qy	721 GTAACCTTTGAAGTAGATGATAAGGTGAAATCTCGGTGATACGATGACAGTGGATATAGAT 780
Dd	975 GTAACCTTTGAAGTAGATGATAAGGTGAAATCTCGGTGATACGATGACAGTGGATATAGAT 1034
Qy	781 AAGAATACAGTTCATCAGATTTTAAACCGATAGCTTTTAAATACCAAAAATAAAGAATAAT 840
Dd	1035 AAGAATACAGTTCATCAGATTTTAAACCGATAGCTTTTAAATACCAAAAATAAAGAATAAT 1094
Qy	841 TCTGGAGAAATCATCGCTACAGGTACTTATGATAACAAAAATAAACAATCACCCTATACT 900
Dd	1095 TCTGGAGAAATCATCGCTACAGGTACTTATGATAACAAAAATAAACAATCACCCTATACT 1154
Qy	901 TTTTACAGATTATGTAGATAGATGAAAAATTTAAAGCAACCTTTAAATTTAAACGTCTATAC 960
Dd	1155 TTTTACAGATTATGTAGATAGATGAAAAATTTAAAGCAACCTTTAAATTTAAACGTCTATAC 1214
Qy	961 ATTTCATAAATCAAAGGTTCCAATAAATAAACAAGTTAGATGTAGATATATAAACCAGCC 1020
Dd	1215 ATTTCATAAATCAAAGGTTCCAATAAATAAACAAGTTAGATGTAGATATATAAACCAGCC 1274
Qy	1021 CTTTTATCAGTAAAAATAAAACAAATTTACGGTTGAAATATCAAGAGCCTAACGAAAAATCGGACT 1080

RESULT 3  
US-10-806-288-10  
: Sequence 10, Application US/10806288  
: Publication No. US20040209326A1  
: GENERAL INFORMATION:  
: APPLICANT: Guss, Bengt  
: APPLICANT: Nilsson, Martin  
: APPLICANT: Prykberg, Lars  
: APPLICANT: Flock, Jan-Ingmar  
: APPLICANT: Lindberg, Martin  
: TITLE OF INVENTION: Fibrinogen Binding Protein Originating from  
: TITLE OF INVENTION: Coagulase-Negative Staphylococcus  
: FILE REFERENCE: Guss 09/147405  
: CURRENT APPLICATION NUMBER: US/10/806, 288  
: CURRENT FILING DATE: 2004-03-23  
: PRIOR APPLICATION NUMBER: US/09/147, 405  
: PRIOR FILING DATE: 1999-04-11  
: PRIOR APPLICATION NUMBER: PCT/SE97/10191  
: PRIOR FILING DATE: 1997-06-18  
: PRIOR APPLICATION NUMBER: SE 9602496-3  
: PRIOR FILING DATE: 1996-06-20

RESULT 4  
US-282-122A-34297  
; Sequence 34297, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselebeck, Robert  
; APPLICANT: Ohlsen, Karl



APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 34297  
LENGTH: 2676  
TYPE: DNA  
ORGANISM: Staphylococcus epidermidis  
US-10-282-122A-34297  
Query Match 92.4%; Score 1613.8; DB 8; Length 2676;  
Best Local Similarity 95.7%; Pred. No. 9.6e-270;  
Matches 1670; Conservative 0; Mismatches 72; Indels 3; Gaps 1;  
QY 1 TCTAGTGATGAAGAAAGATGATGTGATCAATAATAATCAGTCAATAAACAACCGACGAT 60  
DB 103 TCCAGTAAATGAAGAAAGATGATGTAATCAATATAGTCAATCAATCAACCGATGAT 162  
QY 61 AATAACCAATTAATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120  
DB 163 GATAACCAATAA- - -AAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 219  
QY 121 GAAGATAGAACAGAGTCAACACAAATGTAGATGAAGAAAGAAAGAAAGAAAGAAAGAAAG 180  
DB 220 AAGATATTAACAGAGTCAACACAAATGTAGATGAAGAAAGAAAGAAAGAAAGAAAGAAAG 279  
QY 181 ACCCTTCAAGATAAATACTCATCTTACAGAAAGAGAGTAAAGAAAGTCAATCATCAGTCGAA 240  
DB 280 ACCCTTCAAGATAAATACTCATCTTACAGAAAGAGAGTAAAGAAAGTCAATCATCAGTCGAA 339  
QY 241 TCTCAAAATTCATCAATTCATCTGTCGCAACCAACCAATCTCAACAAATAAATAGAGAA 300  
DB 340 TCTCAAAATTCATCAATTCATCTGTCGCAACCAACCAATCTCAACAAATAAATAGAGAA 399  
QY 301 GAATCTGTTCAACAGTGTATGTAGAGATTCACAGTATCAGATTTTGTCACTCT 360  
DB 400 GAATCTTATTCACAAAGTGTATGTAGAGATTCACAGTATCAGATTTTGTCACTCT 459  
QY 361 AAAAAAGAGAGTAACTGATCTGCTGTAAGAGAGAGTAACTATAGAGCAACCTAAT 420  
DB 460 AAAAAAGAGAGTAACTGATCTGATCCATTAAGAGAGAGTAACTATAGAGCAACCTAAT 519  
QY 421 AAGTAAAGAGAGTTCACAAAGTCAAGCCGCTGCTGCTATACAAATATAGATGAAGAA 480

DB 520 AAAGTAAGAGAGAGATTCAATAACAGTCAACCGCTAGCTATATAAAATATAGATGAAGAA 579  
QY 481 ATTTTCAAAATCAAGATGAGTTTATAATTTTACCATAAATGAATATGAATATGAATATGAAT 540  
DB 580 ATTTTCAAAATCAAGATGAGTTTATAATTTTACCATAAATGAATATGAATATGAATATGAAT 639  
QY 541 CCATTATCTACAACTCTCCCAACCATCGATTAAACGTTAAACGTTAAACCGTTAAATCAATTAGCG 600  
DB 640 CGGTTATCTACAACTCTCCCAACCATCGATTAAACGTTAAACCGTTAAATCAATTAGCG 699  
QY 601 GCGGAACAAGGTTGCAATGTTTAAACCAATTTAAATTAAGTTTACTGATCAAAAGTATTAATCTGAA 660  
DB 700 GCAGAAACAAGGTTGCAATGTTTAAATTTAAATTTAAAGTTTACTGATCAAAAGTATTAATCTGAA 759  
QY 661 GGNATATGATGATGAGTGAAGGTTGTTTAAAGACACATGATGCTGGAACCTTTAAATCTATGAT 720  
DB 760 GGNATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 819  
QY 721 GTAACTTTTGAAGTAGATGATGAAGGTTAAATCTGGTGATACGATGACAGTGGATATAGAT 780  
DB 820 GTAACTTTTGAAGTAGATGATGAAGGTTAAATCTGGTGATACGATGACAGTGGATATAGAT 879  
QY 781 AAGAATACAGTTTCCATCAGATTTAACCGATAGCTTTTAAATACCAAAATAAAGATAAT 840  
DB 880 AAGAATACAGTTTCCATCAGATTTAACCGATAGCTTTTAAATACCAAAATAAAGATAAT 939  
QY 841 TCTGGAGAAATCATCGTACAGTACTTATGATACAAATAAATAAATAAATAAATAAATAAATAA 900  
DB 940 TCTGGAGAAATCATCGTACAGTACTTATGATACAAATAAATAAATAAATAAATAAATAAATAA 999  
QY 901 TTTACAGATTATGTAGATAAGTATGAAATATTAAGACACACCTTTAAATTAACGTCATAC 960  
DB 1000 TTTACAGATTATGTAGATAAGTATGAAATATTAAGACACACCTTTAAATTAACGTCATAC 1059  
QY 961 ATTGATAAATCAAGGTTCCAAATTAATAATACAAAGTTAGATGTAGATAAATAAATAAATAA 1020  
DB 1060 ATTGATAAATCAAGGTTCCAAATTAATAATACAAAGTTAGATGTAGATAAATAAATAAATAA 1119  
QY 1021 CTTTCATCAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1080  
DB 1120 CTTTCATCAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1179  
QY 1081 GCTAACCTTTCAAAGTATGTTTACAAATATAGATACGAAATAATCATAAGTTCAGCAAAACG 1140  
DB 1180 GCTAACCTTTCAAAGTATGTTTACAAATATAGATACGAAATAATCATAAGTTCAGCAAAACG 1239  
QY 1141 ATTTATATTAACCTTCTCGTTTATTCAGCCAAAGGAAACAAATGTAAATTTTCAGGGAAT 1200  
DB 1240 ATTTATATTAACCTTCTCGTTTATTCAGCCAAAGGAAACAAATGTAAATTTTCAGGGAAT 1299  
QY 1201 GGTGATGAAGGTTCAACAAATTTATAGACGATACGATACGATACGATACGATACGATACGAT 1260  
DB 1300 GCGGATGAAGGTTCAACAAATTTATAGACGATACGATACGATACGATACGATACGATACGAT 1359  
QY 1261 GATAATCAAAATTTTACCAGATAGTAAACAGAAATTTATGATTAACAGTAAATCAAGATGTC 1320  
DB 1360 GATAATCAAAATTTTACCAGATAGTAAACAGAAATTTATGATTAACAGTAAATCAAGATGTC 1419  
QY 1321 ACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
DB 1420 ACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1479  
QY 1381 ATAGATTCACCATATATTTTAAAGTATTTAGTAAATATGACCCCTTAATGAAGTATGATTAAC 1440  
DB 1480 ATAGATTCACCATATATTTTAAAGTATTTAGTAAATATGACCCCTTAATGAAGTATGATTAAC 1539  
QY 1441 ACAGCTATACAGCAAACTGTGCAATGTGACAGATCTATAAAATGAGTATATCTGTCAGTTT 1500  
DB 1540 ACAGCTATACAGCAAACTGTGCAATGTGACAGATCTATAAAATGAGTATATCTGTCAGTTT 1599  
QY 1501 AGAACAGCATCTTATGATAAATCAATTTGCTTTCTCTCAAGTTTCAGGTCAGGTCAGGTCAGGTC 1560

Db 1600 AGAACAGCATCCTATGATATAACAATTCGTTTCTCTCAAGTTCAGGTCACAGGCAAGGT 1659  
Qy 1561 GACTTGCCTCTCGAAGAACTTATATAATCGGAGATTACGTATCGGAAGATGTAGATAAA 1620  
Db 1660 GACTTGCCTCTCGAAGAACTTATATAATCGGAGATTACGTATCGGAAGATGTAGATAAA 1719  
Qy 1621 GATGCTATTCAAATAACAAATGATATGAAGAACCGCTTAGTAAATGTTTGGTAACCTTG 1680  
Db 1720 GATGCTATTCAAATAACAAATGATATGAAGAACCGCTTAGTAAATGTTTGGTAACCTTG 1779  
Qy 1681 ACCTATCTCGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT 1740  
Db 1780 AGTATCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT 1839  
Qy 1741 GATGG 1745  
Db 1840 GATGG 1844

RESULT 5  
US-10-724-972A-1537  
; Sequence 1537, Application US/10724972A  
; Publication No. US20040147734A1  
; GENERAL INFORMATION:  
; APPLICANT: Doucette-Stamm, Lynen  
; APPLICANT: Bush, David  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: PATH03-16  
; CURRENT APPLICATION NUMBER: US/10/724,972A  
; CURRENT FILING DATE: 2003-12-01  
; PRIOR APPLICATION NUMBER: 09/450,969  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/134,001  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 7544  
; SEQ ID NO 1537  
; LENGTH: 2793  
; TYPE: DNA  
; ORGANISM: S.epidermidis  
US-10-724-972A-1537

Query Match 92.4%; Score 1613.8; DB 8; Length 2793;  
Best Local Similarity 95.7%; Pred. No. 9,8e-270;  
Matches 1670; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

Qy 1 TCTAGTGAAGAAAGATGATGTGATCAATTAATATAGTCATTAATAACACCGAGAT 60  
Db 217 TCCAGTAATAGAAAGAAAGATGATGTAATCAATATAGTCATCAATTAACACCGAGAT 276  
Qy 61 AATACCAAAATTAATTAAGAAAGAAAGATGATGTAATCAATATAGTCATTAATAACACCGATCA 120  
Db 277 GATAACCAAAATTAATTAAGAAAGAAAGATGATGTAATCAATATAGTCATCAATTAACACCGAT 333  
Qy 121 GAAAGATAGACAGATCAACAAATGATAGTAAAGAAAGATGATGTAATCAATATAGTCATCAATTAACAAAG 180  
Db 334 AAGATATAGACAGATCAACAAATGATAGTAAAGAAAGATGATGTAATCAATATAGTCATCAATTAACAAAG 393  
Qy 181 ACCCTCAAGATATATCTCATCTTACAGAAAGAGAGGTAAAGAAATCTCATCAGTCGAA 240  
Db 394 ACCCTCAAGATATATCTCATCTTACAGAAAGAGAGGTAAAGAAATCTCATCAGTCGAA 453  
Qy 241 TCCTCAAAATTCATCAATGATCTGCCCAACCAACCATCTCACACAAATTAATAAGAGAA 300  
Db 454 TCCTCAAAATTCATCAATGATCTGCCCAACCAACCATCTCACACAAATTAATAAGAGAA 513  
Qy 301 GAATCTGTTCAACCAAGTGAATATAGTAAGATTCACACGATATCAGATTTTGTCTAATCTCT 360  
Db 514 GCATCTATTCAAACCAAGTGAATATAGTAAGATTCACACGATATCAGATTTTGTCTAATCTCT 573

Qy 361 AAAATAAAGAGAGATTAACACACTCGTAAATCTGGTAAAGAGAGAAATATCTATAGAGCAACCTAAT 420  
Db 574 AAAATAAAGAGAGATTAACACACTCGTAAATCTGGTAAAGAGAGAAATATCTATAGAGCAACCTAAT 633  
Qy 421 AAAGTAAAGAGAGATTAACACCAAGTCAGCCGCTCTGGCTATACAAAATATAGATCAAAA 480  
Db 634 AAAGTAAAGAGAGATTAACAAAGTCACCGCTAGCTATATAAATAATATAGATCAAAA 693  
Qy 481 ATTTCAAATCAAGATGAGTTAATAATTTTCAATTAATGAATATGAATAATAAGGCTAGA 540  
Db 694 ATTTCAAATCAAGATGAGTTAATAATTTTCAATTAATGAATATGAATAATAAGGCTAGA 753  
Qy 541 CCATATCTCAACACATCTGCCCAACCATCGATTAACCGTGAACCGTGAACCAATCAATTAGCG 600  
Db 754 CCGTTATCTCAACACATCTGCCCAACCATCGATTAACCGTGAACCGTGAACCAATTAGCG 813  
Qy 601 GCGGAACAAGGTTCCGAATGTTAAACCATTTAATTTAAAGTTTACTGTATCAAAAGTATTACTGAA 660  
Db 814 GCAGAACCAAGGTTCCGAATGTTAATTTAATTTAAAGTTTACTGTATCAAAAGTATTACTGAA 873  
Qy 661 GGATATGATGATAGTAGGAGGTGTTTATTAAAGCACATGATCTGAAACCTTAAATCTATGAT 720  
Db 874 GGATATGATGATAGTAGGAGGTGTTTATTAAAGCACATGATCTGAAACCTTAAATCTATGAT 933  
Qy 721 GTAACTTTTGAAGTAGATGATGAAGTGAATCTGGTGAACGATGACAGTGAATATAGAT 780  
Db 934 GTAACTTTTGAAGTAGATGATGAAGTGAATCTGGTGAACGATGACAGTGAATATAGAT 993  
Qy 781 AAGAAATCAGTTCATCAGATTTTAAACGATAGCTTTTACAATACCAAAAATAAAGATAT 840  
Db 994 AAGAAATCAGTTCATCAGATTTTAAACGATAGCTTTTGCATACCAAAAATAAAGATAT 1053  
Qy 841 TCTCGAGAAATCATCGCTACAGGTACTTATGATTAACAAAAATAACAAATCACCTATACT 900  
Db 1054 TCTCGAGAAATCATCGCTACAGGTACTTATGACAACACAAATAAACAATTAACCTACT 1113  
Qy 901 TTTACAGATTTAGTAGATAGTATGAATTAATTAAGCACACCTTAAATTTAACGTCATAC 960  
Db 1114 TTTACAGATTTAGTAGATAGTATGAATTAATTAAGCACACCTTAAATTTAACCATCATAC 1173  
Qy 961 ATTGATAAATCAAAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATAATAAACAACGCC 1020  
Db 1174 ATTGATAAATCAAAAGGTTCCAAATAATAATTAACACTAAGTTAGATGTAGATAATAAGACGCC 1233  
Qy 1021 CTTTCATCAGTAAATAAACAATTAACGTTGAATATCAAAAAACCTTAACGAAAAATCGGACT 1080  
Db 1234 CTTTCATCAGTAAATAAACAATTAACGTTGAATATCAAAAAACCTTAACGAAAAATCGGACT 1293  
Qy 1081 GCTAACCTTCAAGATAGTATTAACAATATAGATACGAAAAATCATACAGTTTGAGCAACG 1140  
Db 1294 GCTAACCTTCAAGATAGTATTAACAATATAGATACGAAAAACCTTAACAGTTTGAGCAACG 1353  
Qy 1141 ATTTATATTAACCTCTCTCGTTATTTCAGCCCAAGGAAACAAATGTAAAATATTTTCAGGAAAT 1200  
Db 1354 ATTTATATTAACCTCTCTCGTTATTTCAGCCCAAGGAAACAAATGTAAAATATTTTCAGGAAAT 1413  
Qy 1201 GGTGATGAAGGTTCAACAAATTTATAGACGATAGCAATATAATTAAGTTTATAGAGTTGGA 1260  
Db 1414 GCGGATGAAGGTTCAACAAATTTATCGACGATAGTACAATCATTTAAAGTTTATAGAGTTGGA 1473  
Qy 1261 GATTAATCAAAATTTTACAGATAGTAAACAGAAATTTATGATTTACAGTGAATATGAAGATGTC 1320  
Db 1474 GATTAATCAAAATTTTACAGATAGTAAACAGAAATTTATGATTTACAGTGAATATGAAGATGTC 1533  
Qy 1321 ACAATGATGATTTATGCCCAATTAAGGAAATTAATATGATGTGAATTTAAATTTTGGTAAAT 1380  
Db 1534 ACAATGATGATTTATGCCCAATTAAGGAAATTAATATGACGTTGAATTTAAATTTTGGTAAAT 1593  
Qy 1381 ATAGATTCACCATATATTTATTAAGGTTTATTAAGTAAATATGACCTTAATTAAGATGATAC 1440  
Db 1594 ATAGATTCACCATATATTTATTAAGGTTTATTAAGTAAATATGACCTTAATTAAGATGATAC 1653

Qy	1441	ACGACATATACAGCAAACTGTGCAAAATGACAGCATATAAATGAGTATAC	TGTTGAGTTT	1500
Db	1654	ACGACGATACAGCAAACTGTGCAAAATGCAAAACGACTAAATGAGTATAC	TGTTGAGTTT	1713
Qy	1501	AGAACAGCATCCTATGATAATACAAATTCCTTCTCAAGTTTCAGGTCAAGGACAGGT		1560
Db	1714	AGAACAGCATCCTATGATAATACAAATTCCTTCTCAAGTTTCAGGTCAAGGACAGGT		1773
Qy	1561	GACTTGCTCCTCGAAAAAATTTATAAAATCGGAGATTACGTATGCGGAAGATGTAGATAAA		1620
Db	1774	GACTTGCTCCTCGAAAAAATTTATAAAATCGGAGATTACGTATGCGGAAGATGTAGATAAA		1833
Qy	1621	GATGGTATTCAAAAATACAAATGATAATGAAAAACCGCTTAGTAATGTATTGGTAACTTTG		1680
Db	1834	GATGGTATTCAAAAATACAAATGATAATGAAAAACCGCTTAGTAATGTATTGGTAACTTTG		1893
Qy	1681	ACGTATCCTGATGGAACCTTCAAAATCAGTCGAAACAGATGAAGATGCGGAATATCAATTT		1740
Db	1894	ACGTATCCTGATGGAACCTTCAAAATCAGTCGAAACAGATGAAGATGCGGAATATCAATTT		1953
Qy	1741	GATGG 1745		
Db	1954	GATGG 1958		

RESULT 6  
 US-10-615-383-7  
 ; Sequence 7, Application US/10615383  
 ; Publication No. US20040038327A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FOSTER, Timothy  
 ; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCI  
 ; FILE REFERENCE: P06335US03/BAS  
 ; CURRENT APPLICATION NUMBER: US/10/615,383  
 ; CURRENT FILING DATE: 2003-07-09  
 ; PRIOR APPLICATION NUMBER: 09/386,962  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: 60/098,443  
 ; PRIOR FILING DATE: 1998-08-31  
 ; PRIOR APPLICATION NUMBER: 60/117,119  
 ; PRIOR FILING DATE: 1999-01-25  
 ; NUMBER OF SEQ ID NOS: 39  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 2976  
 ; TYPE: DNA  
 ; ORGANISM: Staphylococcus epidermidis  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (3)..(2975)  
 ; OTHER INFORMATION:  
 US-10-615-383-7

Query Match 92.4%; Score 1613.8; DB 8; Length 2976;

Best Local Similarity 95.7%; Pred. No. 1e-269;

Matches 1670; Conservative 0; Mismatches 72; Indels 3;

[illegible]

1 TCTAGTGATGAAGAAAGATGATGTGATCAATAATAATCAGTCAATAAACACCGACGAT 60

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

b  
318 TCCAGTAATGAAGAAAGAAATGATGTAATCAATAATAGTCAGTCAATAAACACCGATGAT 377

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84

61 AATAACCAATAATTAAAGAGAAACGAATACTACGATGGCATAGAAAAACGCTCA 120

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84

b  
378 GATAACCAAATA--AAAGAGAGAAACGAATAGCAACGATGCCATAGAAATCGCTCT 434

[illegible]

121 GAAGATAGAACAGAGTCAACAACAATGTAGATGAAAACGAAGCAACATTTTACAAAAG 180

[illegible]

b 435 AAAGATATTAACACAGTCAACACAAATGTAGATGAAACGAAGCAACATTTTTACAAAAG 494

181 ACCCCCTCAGATAATACTCATCTTACAGAGAAGAGGTAAGAATCCTCATCAGTCCAA 240

Y 181 ACCCCICAGGATAATACICATCTTACAGGAAGAAGAGGTAAAAGAAATCCCTCATCAGTCGAA 240

b  
495 ACCCCTCAGATAATACTCAGCTTAAGAAGAAGTGGTAAAGAACCCTCATCAGTCGAA 554

D 433 ACCCCCTCAAGATATATACCTCAGCTTAAAGAGAGAGTGGTAAATAGAACCCCTCATCAGTCGAA 354

[illegible]



```
Db 1515 GCGGATGAAGTTCAACAATATTCGACGATAGTACAAATCAATTAAGTTTATAAGTTGGA 1574
QY 1261 GATAATCAAAATTTACCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGTC 1320
Db 1575 GATAATCAAAATTTACCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGTC 1634
QY 1321 ACAATGATGATTTATGCCCAATTTAGGAATAATAATGATGTGAATATTAATTTTGGTAAT 1380
Db 1635 ACAATGATGATTTATGCCCAATTTAGGAATAATAATGATGTGAATATTAATTTTGGTAAT 1694
QY 1381 ATAGATTCCACATATATTATTAAGTTTATTAGTAAATATGACCCCTAATAGGATGATTAC 1440
Db 1695 ATAGATTCCACATATATTATTAAGTTTATTAGTAAATATGACCCCTAATAGGACGATTAC 1754
QY 1441 ACAGCTATACAGCAAACTGTGACAAATCGACAGACTATATAATGAGTATATCTGGTGAGTTT 1500
Db 1755 ACAGCTATACAGCAAACTGTGACAAATCGACAAACGACTATATAATGAGTATATCTGGTGAGTTT 1814
QY 1501 AGAAGAGATCCCTATGATTAATACAAATGCTTCTCTACAGTTTCAGGTCAAGGACAAAGGT 1560
Db 1815 AGAAGAGATCCCTATGATTAATACAAATGCTTCTCTACAGTTTCAGGTCAAGGACAAAGGT 1874
QY 1561 GACTTGCCTCCTGAAAAAATTTATAAATCGGAGATTACGTATGCGAAGATGTAGATAAA 1620
Db 1875 GACTTGCCTCCTGAAAAAATTTATAAATCGGAGATTACGTATGCGAAGATGTAGATAAA 1934
QY 1621 GATGGTATTTCAAAATACAAATGATTAATGAAAAACCCCTTAGTAACTGTTTGGTAACTTTG 1680
Db 1935 GATGGTATTTCAAAATACAAATGATTAATGAAAAACCCCTTAGTAACTGTTTGGTAACTTTG 1994
QY 1681 ACCTATCCCTGATGGAATTTCAAAATCAGTCAGAACAGATGGAAGGGGGAATATCAATTT 1740
Db 1995 ACCTATCCCTGATGGAATTTCAAAATCAGTCAGAACAGATGGAAGGGGGAATATCAATTT 2054
QY 1741 GATGG 1745
Db 2055 GATGG 2059

RESULT 8
US-10-689-082-7
; Sequence 7, Application US/10689082
; Publication No. US20040142348A1
; GENERAL INFORMATION:
; APPLICANT: FOSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLO
; FILE REFERENCE: P06335US04/BAS
; CURRENT APPLICATION NUMBER: US/10/689,082
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 09/386,962
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(2975)
; OTHER INFORMATION:
US-10-689-082-7

Query Match 92.4%; Score 1613.8; DB 8; Length 2976;
Best Local Similarity 95.7%; Pred. No. 1e-269;
Matches 1670; Conservative 72; Mismatches 3; Gaps 1;

QY 1 TCTAGTGTGAAGAAAGATGATGTGATCAATAATAATCAGTCAATAAACACCGACGAT 60
```

```
Db 318 TCCAGTAATGAAGAAAGATGATGTAAATCAATAATAGTCAGTCAATAAACACCGATGAT 377
QY 61 AATAACCAAAATTAATAAAAAAGAGAAACGAATAAATCTACGATGGCATAGAAAAACGCTCA 120
Db 378 GATNACCAATA---AAAAAGAGAGAAACGAATAGCAACGATGCCATAGAAAATCGCTCT 434
QY 121 GAAGATAGAACAGAGTCAACAAATGTAGATGAAAAAGCAACAAATTTTACAAAAG 180
Db 435 AAAGATATTAACACAGTCAACAAATGTAGATGAAAAAGCAACAAATTTTACAAAAG 494
QY 181 ACCCTCTACAGATAATACTCATCTTACAGAAAGAGAGGTAAAGAAATCTCATCAGTCGAA 240
Db 495 ACCCTCTCAAGATAATACTCAGCTTTAAAGAGAGAGGTGTTAAAGAGAACCTCATCAGTCGAA 554
QY 241 TCTCAAAATTCATCAATTCATCTGCTTCCCAACCAACCATCTCACACAACAATAAATAGAGAA 300
Db 555 TCTCAAAATTCATCAATTCATCTGCTTCCCAACCAACCATCTCACACAACAATAAATAGAGAA 614
QY 301 GAATCTGTTCAAAACAGTGATTAATGTAGAAAGATTCAACGATATCAGATTTTGTCTAACTCT 360
Db 615 GCATCTATTTCAAAACAGTGATTAATGAAGAAATTTCCCGGTATCAGATTTTGTCTAACTCT 674
QY 361 AAAATAAAGAGAGATTAACCTGAATCTGTTAAAGAGAGAAATCTATAGAGCAACCTAAT 420
Db 675 AAAATAAAGAGAGATTAACCTGAATCTGTTAAAGAGAGAAATCTATAGAGCAACCTAAT 734
QY 421 AAGTAAAGAGAGATTTCAACACAGTCAAGCGCTCTGCTGTATCAAAATATAGATGAAGAA 480
Db 735 AAGTAAAGAGAGATTTCAATAACAGTCAACCGCTAGCTATATAAAATATAGATGAAGAA 794
QY 481 ATTTCAAAATCAAGATGAGTTTAAATTTTCAAAATGAATATGAATATGAATATGAATATGA 540
Db 795 ATTTCAAAATCAAGATGAGTTTAAATTTTCAAAATGAATATGAATATGAATATGAATATGA 854
QY 541 CAATATATCAACATCTGCCCAACCATCGATTTAAACCGTGAACCGTGAATCAATTTAGCG 600
Db 855 CCGTTATCTACAAACATCTGCCCAACCATCGATTTAAACCGTGAACCGTGAATCAATTTAGCG 914
QY 601 GCGAACAGGTTCCGAATGTTAAACCAATTTAAATTAAGTTTACTGATCAAGATATTTACTGAA 660
Db 915 GCAGAACAGGTTCCGAATGTTAAATTTAAATTTAAAGTTTACTGATCAAGATATTTACTGAA 974
QY 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 975 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1034
QY 721 GTAACTTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 1035 GTAACTTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1094
QY 781 AAGATACAGTTCATCAGATTTTAAACCGATAGCTTTTACAAATACCAAAATTAAGATTAAT 840
Db 1095 AAGATACAGTTCATCAGATTTTAAACCGATAGCTTTTAAACCGATAGCTTTTAAACCGATTA 1154
QY 841 TCTGGAGAAATCATCGCTACAGTACTTATGATTAACAAATAAATAAATAAATAAATAAATAA 900
Db 1155 TCTGGAGAAATCATCGCTACAGTACTTATGATTAACAAATAAATAAATAAATAAATAAATAA 1214
QY 901 TTTACAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 1215 TTTACAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1274
QY 961 ATTGATAAATCAAGGTTCCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
Db 1275 ATTGATAAATCAAGGTTCCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1334
QY 1021 CTTTCATCAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1080
Db 1335 CTTTCATCAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1394
QY 1081 GCTAAACCTTTCAAGATGATGTTTCAAAATATAGATGATGATGATGATGATGATGATGATGATGAT 1140
```







```

; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-5

Query Match      49.6%; Score 866; DB 7; Length 951;
Best Local Similarity 96.7%; Pred. No. 3e-140;
Matches 884; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 602 CGGAACAAGGTCGAAATGTAACCAATTTAAATTAAGTTACTGATCAAAAGTATTACTGAAG 661
DB 35 CCGAACAAGGTCGAAATGTAATCAATTTAAATTAAGTTACTGATCAAAAGTATTACTGAAG 94

QY 662 GATATGATGATGTAAGGCTGTTATTAAGACACATGATGCTGAAACCTTAATCTATGATG 721
DB 95 GATATGATGATGATGATGATGATTTATTAAGACACATGATGCTGAAACCTTAATCTATGATG 154

QY 722 TAACTTTTGAAGTAGATGATGAAGTGAATCTGTGATACGATGACAGTGAATATAGATA 781
DB 155 TAACTTTTGAAGTAGATGATGAAGTGAATCTGTGATACGATGACAGTGAATATAGATA 214

QY 782 AGAATACAGTTCATCAGATTAAACCGATAGCTTTTACAATACCAAAATAAAGNATTT 841
DB 215 AGAATACAGTTCATCAGATTAAACCGATAGCTTTTACAATACCAAAATAAAGNATTT 274

QY 842 CTGGAGAAATCATCGCTACAGTACTTATGATAACAAAAATAAACAATCACTTACTT 901
DB 275 CTGGAGAAATCATCGCTACAGTACTTATGATAACAAAAATAAACAATCACTTACTT 334

QY 902 TTACAGATTATGTAGATAAGTAAATATATTAAGACACACCTTAAATTAACGTCAATACA 961
DB 335 TTACAGATTATGTAGATAAGTAAATATATTAAGACACACCTTAAATTAACGTCAATACA 394

QY 962 TTGATAAATCAAGGTTCCAAATATATATCCAGTTAGATGATAGATAAATAAAGCGCCC 1021
DB 395 TTGATAAATCAAGGTTCCAAATATATATCCAGTTAGATGATAGATAAATAAAGCGCCC 454

QY 1022 TTTTCATCAGTAAATAAACAATTCAGGTTGAAATATCAAAAGCTTAACGAAATCGGACTG 1081
DB 455 TTTTCATCAGTAAATAAACAATTCAGGTTGAAATATCAAAAGCTTAACGAAATCGGACTG 514

QY 1082 CTAACCTTTCAAAGTAGTTTCAAAATATAGATACGAAAAAATCATACAGTTGAGCAAAAGA 1141
DB 515 CTAACCTTTCAAAGTAGTTTCAAAATATAGATACGAAAAAATCATACAGTTGAGCAAAAGA 574

QY 1142 TTTATTTAAACCTCTTCGTTATTCAGCCAGGAAACAAATGTAATATTTTCAGGGAATG 1201
DB 575 TTTATTTAAACCTCTTCGTTATTCAGCCAGGAAACAAATGTAATATTTTCAGGGAATG 634

QY 1202 GTGATGAAGGTTCAACAATTTATAGACGATAGCACAAATTAAGTTTATAGGTTGGAG 1261
DB 635 GCGATGAAGGTTCAACAATTTATCGACGATAGTACAAATCATTAAGTTTATAGGTTGGAG 694

QY 1262 ATAAATCAAAATTTACAGATAGTAAACAGATTTTATGATTTACAGTGAATATGAAGATGCA 1321
DB 695 ATAAATCAAAATTTACAGATAGTAAACAGATTTTATGATTTACAGTGAATATGAAGATGCA 754

QY 1322 CAAATGATGATTTATGCCCAATTTAGGAAATTAATGATGTGATTAATTTTGGTAAATA 1381
DB 755 CAAATGATGATTTATGCCCAATTTAGGAAATTAATGATGTGATTAATTTTGGTAAATA 814

QY 1382 TAGATTCACCATATATTTATTAAGTTTATTAAGTAAATATGACCTTAATGAAGATGATTAACA 1441
DB 815 TAGATTCACCATATATTTATTAAGTTTATTAAGTAAATATGACCTTAATGAAGATGATTAACA 874

QY 1442 CGCACTATACAGCAAACTGTGACAATGCAGACGACTATTAATGAGTATATCTGGTGAGTTTA 1501
DB 875 CGCACTATACAGCAAACTGTGACAATGCAGACGACTATTAATGAGTATATCTGGTGAGTTTA 934

QY 1502 GAACAGCATCCTAT 1515
DB 935 GAACAGCATCCTAT 948
```

```

RESULT 12
US-10-282-122A-34260
; Sequence 34260, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34260
; TYPE: DNA
; LENGTH: 2010
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-34260

Query Match      35.4%; Score 618.2; DB 8; Length 2010;
Best Local Similarity 98.2%; Pred. No. 3.5e-97;
Matches 639; Conservative 0; Mismatches 3; Indels 9; Gaps 1;

QY 1096 ATGTTTCAAAATATAGATACGAAAAATCATACAGTTGAGCAAAACGATTTATTAACCCCT 1155
DB 1 ATGTTTCAAAACATAGATACGAAAAATCATACAGTTGAGCAAAACGATTTATTAACCCCT 60

QY 1156 CTTGCTTATTCAGCCAGGAAACAAATGTAATATTTTCAGGGAATGGTGATGAAGTTTCA 1215
DB 61 CTTGCTTATTCAGCCAGGAAACAAATGTAATATTTTCAGGGAATGGTGATGAAGTTTCA 120

QY 1216 ACAATTATAGACGATAGCACAAATTAATAAGTTTATTAAGTTTGGAGATAATCAAAATTTA 1275
DB 121 ACAATTATAGACGATAGCACAAATTAATAAGTTTATTAAGTTTGGAGATAATCAAAATTTA 180

QY 1276 CCAGATAGTAACAGAAATTTATGATTTACAGTGAATATGAAGATGTCCAAAATGATGATTAT 1335
DB 181 CCAGATAGTAACAGAAATTTATGATTTACAGTGAATATGAAGATGTCCAAAATGATGATTAT 240

QY 1336 GCCCAATAGGAAATAATAATGATGTGAATATTAATTTTGGTAAATATAGATTCACCATAT 1395
DB 241 GCCCAATAGGAAATAATAATGATGTGAATATTAATTTTGGTAAATATAGATTCACCATAT 300
```

QY 1396 ATTATTAAGTTATTAGTAAATATGACCCCTAATAAGGATGATTACAGACTATACAGCAA 1455  
Db |||||  
QY 301 ATTATTAAGTTATTAGTAAATATGACCCCTAATAAGGATGATTACAGACTATACAGCAA 360  
Db |||||  
QY 1456 ACTGTGACAACTGACAGACGACTAATAATGATGATCTGCTGAGTTAGAACAGCCTCTAT 1515  
Db |||||  
QY 361 ACTGTGACAACTGACAGACGACTAATAATGATGATCTGCTGAGTTAGAACAGCCTCTAT 411  
Db |||||  
QY 1516 GATAATACAAATGCTTTCTTCTACAGTTTCAGGTCAGGCAAGGTCGCTCTCTGAA 1575  
Db |||||  
QY 412 GATAATACAAATGCTTTCTTCTACAGTTTCAGGTCAGGCAAGGTCGCTCTCTGAA 471  
Db |||||  
QY 1576 AAAAATTATAAATCGGAGATACGTTATCGGAGAGATGTAGATAAAGATGTTATCAAAAT 1635  
Db |||||  
QY 472 AAAAATTATAAATCGGAGATACGTTATCGGAGAGATGTAGATAAAGATGTTATCAAAAT 531  
Db |||||  
QY 1636 ACAAAATGATAATGAAACCCGCTTAGTAAATGTTAGTAACTTTGATGATCTCTGATGGA 1695  
Db |||||  
QY 532 ACAAAATGATAATGAAACCCGCTTAGTAAATGTTAGTAACTTTGATGATCTCTGATGGA 591  
Db |||||  
QY 1696 ACTTCAAAATCAGTCAGAACAGATGAAGATGCGAAATATCAATTTGATGGA 1746  
Db |||||  
QY 592 ACTTCAAAATCAGTCAGAACAGATGAAGATGCGAAATATCAATTTGATGGA 642  
Db |||||

RESULT 13  
US-10-793-626-2699  
; Sequence 2699, Application US/10793626  
; Publication No. US2005025478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; CURRENT APPLICATION NUMBER: US/10793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2699  
; LENGTH: 837  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-10-793-626-2699

Query Match 29.0%; Score 507.2; DB 10; Length 837;  
Best Local Similarity 97.5%; Pred. No. 4.6e-78;  
Matches 515; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 1 TCTAGTGATGAAGAAAGAAATGATGTGATCAATAATAATCAATCAATCAATCAATCAATCAAT 60  
Db |||||  
QY 223 TCTAGTGATGAAGAAAGAAATGATGTGATCAATAATAATCAATCAATCAATCAATCAATCAAT 282  
Db |||||  
QY 61 AATAACCAATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120  
Db |||||  
QY 283 AATAACCAATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 342  
Db |||||  
QY 121 GAAGATAGAACAGAGTCAACAAATGTAGATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180  
Db |||||  
QY 343 GAAGATAGAACAGAGTCAACAAATGTAGATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 402  
Db |||||  
QY 181 ACCCTCAAGATAAATCTCATCTTACAGAAAGAGAGGTAAAGAAATCTCTCATCAGTCGAA 240  
Db |||||  
QY 403 TCCCTCAAGATAAATCTCATCTTACAGAAAGAGAGGTAAAGAAATCTCTCATCAGTCGAA 462  
Db |||||  
QY 241 TCCCTCAAGATAAATCTCATCTTACAGAAAGAGAGGTAAAGAAATCTCTCATCAGTCGAA 300  
Db |||||  
QY 463 TCCCTCAAGATAAATCTCATCTTACAGAAAGAGAGGTAAAGAAATCTCTCATCAGTCGAA 522  
Db |||||

QY 301 GAATCTGTTCAAAACAAGTGATTAATGTAGAAAGATTCACAGTATCAGATTTTGTCTAACTCT 360  
Db |||||  
QY 523 GAATCTGTTCAAAACAAGTGATTAATGTAGAAAGATTCACAGTATCAGATTTTGTCTAACTCT 582  
Db |||||  
QY 361 AAAATAAAGAGAGTAAACACTCAATCTGCTAAAGAGAGAACTACTATAGAGCAACCTAAT 420  
Db |||||  
QY 583 AAAATAAAGAGAGTAAACACTCAATCTGCTAAAGAGAGAACTACTATAGAGCAACCTAAT 642  
Db |||||  
QY 421 AAAATAAAGAGAGTAAACACTCAATCTGCTAAAGAGAGAACTACTATAGAGCAACCTAAT 480  
Db |||||  
QY 643 AAAATAAAGAGAGTAAACACTCAATCTGCTAAAGAGAGAACTACTATAGAGCAACCTAAT 702  
Db |||||  
QY 481 ATTTCAAAATCAAGATGAGTTTAAATTTTCAAAATGAATGAAGAA 528  
Db |||||  
QY 703 ATTTCAAAATCAAGATGAGTTTAAATTTTCAAAATGAATGAAGAA 750  
Db |||||

RESULT 14  
US-10-793-626-3492  
; Sequence 3492, Application US/10793626  
; Publication No. US2005025478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; CURRENT APPLICATION NUMBER: US/10793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3492  
; LENGTH: 3236  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-10-793-626-3492

Query Match 29.0%; Score 507.2; DB 10; Length 3236;  
Best Local Similarity 97.5%; Pred. No. 7.2e-78;  
Matches 515; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 1 TCTAGTGATGAAGAAAGAAATGATGTGATCAATAATAATCAATCAATCAATCAATCAATCAAT 60  
Db |||||  
QY 1807 TCTAGTGATGAAGAAAGAAATGATGTGATCAATAATAATCAATCAATCAATCAATCAATCAAT 1866  
Db |||||  
QY 61 AATAACCAATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120  
Db |||||  
QY 1867 AATAACCAATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1926  
Db |||||  
QY 121 GAAGATAGAACAGAGTCAACAAATGTAGATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180  
Db |||||  
QY 1927 GAAGATAGAACAGAGTCAACAAATGTAGATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1986  
Db |||||  
QY 181 ACCCTCAAGATAAATCTCATCTTACAGAAAGAGAGGTAAAGAAATCTCTCATCAGTCGAA 240  
Db |||||  
QY 1987 TCCCTCAAGATAAATCTCATCTTACAGAAAGAGAGGTAAAGAAATCTCTCATCAGTCGAA 2046  
Db |||||  
QY 241 TCCCTCAAGATAAATCTCATCTTACAGAAAGAGAGGTAAAGAAATCTCTCATCAGTCGAA 300  
Db |||||  
QY 2047 TCCCTCAAGATAAATCTCATCTTACAGAAAGAGAGGTAAAGAAATCTCTCATCAGTCGAA 2106  
Db |||||  
QY 301 GAATCTGTTCAAAACAAGTGATTAATGTAGAAAGATTCACAGTATCAGATTTTGTCTAACTCT 360  
Db |||||  
QY 2107 GAATCTGTTCAAAACAAGTGATTAATGTAGAAAGATTCACAGTATCAGATTTTGTCTAACTCT 2166  
Db |||||  
QY 361 AAAATAAAGAGAGTAAACACTCAATCTGCTAAAGAGAGAACTACTATAGAGCAACCTAAT 420  
Db |||||  
QY 2167 AAAATAAAGAGAGTAAACACTCAATCTGCTAAAGAGAGAACTACTATAGAGCAACCTAAT 2226  
Db |||||  
QY 421 AAAATAAAGAGAGTAAACACTCAATCTGCTAAAGAGAGAACTACTATAGAGCAACCTAAT 480  
Db |||||

Db 2227 AAAGTAAAGAGATTCAACACCAAGTCAGCGCTGCGTATACAAATATAGATGAAAA 2286  
Qy 481 ATTTCAAAATCAAGATGAGTTATTAATTTTCAAAATTAAGATGAA 528  
Db 2287 ATTTCAAAATCAAGATGAGTTATTAATTTTCAAAATTAAGATGAA 2334

## RESULT 15

US-10-744-672-8  
; Sequence 8, Application US/10744672  
; Publication No. US20040254354A1  
; GENERAL INFORMATION:  
; APPLICANT: Patti, Joseph M.  
; APPLICANT: Foster, Timothy J.  
; APPLICANT: Hook, Magnus A.O.  
; APPLICANT: Eidhinn, Deirdre Ni  
; APPLICANT: Perkins, Samuel L.  
; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from *Staphylococcus aureus*  
; FILE REFERENCE: P06283US2/BAS  
; CURRENT APPLICATION NUMBER: US/10/744,672  
; PRIOR FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: 60/066,815  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: 60/098,427  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 3498  
; TYPE: DNA  
; ORGANISM: *Staphylococcus aureus*  
US-10-744-672-8

Query Match 20.9%; Score 364.4; DB 9; Length 3498;  
Best Local Similarity 52.7%; Pred. No. 4.2e-53;  
Matches 931; Conservative 0; Mismatches 796; Indels 39; Gaps 5;

Qy 10 GAAGAAAGATGATGTCATCAATTAATCAGTCATAAATCAACACCGGAGCAATAACCAA 69  
Db 229 GAAACTGAAATTAATTCGACACGAGAAATAATTCACAAATTCCAATTAAGAAAGAAACA 288  
Qy 70 ATAAATTAAGAAAGAAACGAATAACTACGATGCGATAGAAAAACGCTCAGAGATAGA 129  
Db 289 AATCTGATTCACACCGAGAGCTTAAAGAAATCACTTCATCAAGTACTCAAAACAG 348  
Qy 130 ACAGAGTCAACCAAAATGTAGTGAAGAAAGCAACATTTTACAAAGACCCCTCAA 189  
Db 349 CAAATAACGTTACAGCTACAACCTGAACCTAAGCCTCAAAACATTTGNAAGAAAGAAATGTT 408  
Qy 190 GATTAATCTCATCTTACAGAGAGAGAGTAAAGAAATCCTCATCGTCGAATCCTCAAT 249  
Db 409 AAACCTTCAACTGATATAAACTCGCAGAGAGATACATCTGTTATTTTGAAGAGAGAGAA 468  
Qy 250 TCATCAATGTACTGCCCCCAACCACTCCACACCAATAAATAGAGAAAGATCTGTT 309  
Db 469 GCACCAATAATACAAATAAGATGTAATCACTACAAACCATCTCAAGTGAACCATCTACA 528  
Qy 310 CAAACAGTGAATGTAGAAGATTCACACGTCATCAGATTTTGTCTAACTTAAATAAAAA 369  
Db 529 AGTGAATTCACAAACAAACCAACTACACCTCAAGAACTTACAAATATTGNAATTCACAA 588  
Qy 370 GAGAGTAACTGTAATCTGGTAAAGAGAGAAATCTATATAGAGCAACCTTAATAAGTAAAA 429  
Db 589 CCGCAACCAACGCCCTTCAAAAAGTAGACAAATCAAGTTACAGATGCAACTTAATCCAAAAGAA 648  
Qy 430 GAAGATTCAACCAACAGTCAGCGCTCGCTATACAAATATATAGATGAAAAATTTCAAAT 489  
Db 649 CCAGTAAATGTCTCAAAAGAGAACTTAAATAATATCTCTGAGAAATTAAGAAATTTGGTT 708  
Qy 490 CAAGATGAGTTATTAATTTTACCAATTAATGAATTAAGAAATTAAGGCTAGACCATTAATCT 549  
Db 709 AGAAATGATAGCAATACAGATCAATTCAACTTAAACCCAGTTGCTACAGCTCCAAACAGTGT 768

Qy 550 ACACATCTGCCCAACCATCGATTAAACGCTGTAAACCGTAAATCAATTAGCGCGGAACAA 609  
Db 769 GCACAAAACGCTGTAAACGCAAAAATGCGCTTTCGAGTTGCACACACGACGAGTTGCT 828  
Qy 610 GGTTCGAATGTAAACCATTTAAATTTAAAGTTACTCATCAAAAGTATTACTTGAAGGATATGAT 669  
Db 829 TCAACCAATGTAAATGATTTAAATTTAAAGTGCAGGACCAACAATCA---AAGTTGGCGAT 885  
Qy 670 GATAGTGAAGGTGTTATTAAGCACATGATGCTGAAACCTTAATCTATGATGTAACCTTTT 729  
Db 886 GGTAAAGATAATGTGGCGCAGCGCATACGCGTAAAGATATTGAATATGATACAGAGTTT 945  
Qy 730 GAAGTAGATGATAGGTGAATCTGCTGATACAGTGCAGTGGATATAGATAAGAAATACA 789  
Db 946 ACATTTGACAAATAAGTCAAAAAAGGCGCATACAAATGACGATTAATTTATGATGAATGTA 1005  
Qy 790 GTTCATCAGATTTAAACCGGATAGCTTTTACAATACCAAAAAATAAAGATAAATCTTGGAGAA 849  
Db 1006 ATTCCTTCGGATTTAACAGATAAAAATGATCCTATCGATTACTGTATCCATCAGGAGAG 1065  
Qy 850 ATCATCGCTACAGGTACTTATGATAACAAAAATAAACAATCACCTATACCTTTTACAGAT 909  
Db 1066 GTCATTGCTAAAGGAACATTTGATAAAGCAACTAAGCAAAATCACATATACATTTACAGAC 1125  
Qy 910 TATGTAGATAGTATGAATATTTAAAGCACACCTTAAATTTAACTCATACATTTGATAAA 969  
Db 1126 TATGTAGATAAATATGAAGATATATAAATACGCTTAACTCTATATTGATTTGATANA 1185  
Qy 970 TCAAGGTTCCAAATAATAATACCAAGTTAGATGTAGAATATAAAGCGCCCTTTTCATCA 1029  
Db 1186 AAAACAGTTCCA---AATGAGACAAAGTTTGAATTTAACAATTTGCTACAGCAGGTAAGAA 1242  
Qy 1030 GTAAATAAAACAATTCAGGTTGTAATATCAAGACCTTAACGAAATTCGACCTGCTAACCTT 1089  
Db 1243 ACAGCCAAAATGTCACCTGTTGATTATCAAGATCCAATGGTCCATGGTGATTCAACACTT 1302  
Qy 1090 CAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTTGAGCAAAACGATTTATATT 1149  
Db 1303 CAATCTATCTTTTCAAAATTAGATGAAGATTAAGCAAACTTTTGAAACAAACAATTTATGTT 1362  
Qy 1150 AACCTCTCTGTTATTTCAGCCAGGAAACAAATGTAAATTTTTCAGGGAATGGTGATG-- 1207  
Db 1363 AACCCATTGAAAAAATCAGCAACCAACACATAAGTTGATATAGCTGGTAGTCAAGTAGAT 1422  
Qy 1208 -----AAGTTTCAACAATTTATAGACGATAGACGATAGACGATTAAT 1242  
Db 1423 GATTATGAAATAATTAACACTAGGAAATGGTAGCACTATTATTGACCAAAATACAGAAATA 1482  
Qy 1243 AAGTTTATAGGTTGGAGATTAATCAAAATTTACCAGATAGTAAACAGAAATTTATGATTAC 1302  
Db 1483 AAGTTTATAGGTTAACTCTGATCAACAATTTGCTCAAGTAATAGAAATCTATGATTTT 1542  
Qy 1303 AGTGAATATGAAGATGTCACAAATGA---TGATTTATGCCCAATTTAGGAAATTAATATGAT 1359  
Db 1543 AGTCAATACGAGATGTAAACAGTCAATTTGATAATAAATAATCATTTAGTAAATATGTA 1602  
Qy 1360 GTGAATATTAATTTTGGTAAATATAGATTCACCATATATTTATTTAAAGTTTATTAGTAAATAT 1419  
Db 1603 GCAACATTTGGATTTTGGTGATTAATTTACGCTTATATTTATCAAAAGTTTGTAGTAAATAT 1662  
Qy 1420 GACCTTAATAGGATGATTACACGACTATACAGCAAACTGTGACAAATGCACAGCACTATA 1479  
Db 1663 ACACCTACATCAGATGGGAACTAGATATTGCCCAAGTACTAGTATGAGAACTACT--- 1719  
Qy 1480 AATCAGTATATCTGCTGAGTTTGAACACAGCATCTTATGATTAATACAAATTTGCTTTCTTACA 1539  
Db 1720 GATTAATATGTTTATTAATTTATGAGGATTAATCAAACTTTCATCGTAACTTCTAATGAC 1779  
Qy 1540 AGTTTCAGGTCAAGGACAGGTCATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1599  
Db 1780 ACTGGCGGTGGCGCGGTACTGTTTAAACCTGGAAGAAAGTTTATACAAATTTGGTGACTAT 1839



**This Page Blank (uspto)**

1	1712.4	98.1	2493	9	US-11-348-413-14147	Sequence 14147, A	
2	1613.8	92.0	2976	7	US-11-396-565-7	Sequence 7, Appl	
3	507.2	29.0	834	9	US-11-348-413-14134	Sequence 14134, A	
4	376	21.5	2701	9	US-11-348-413-18342	Sequence 18342, A	
5	126	7.2	4047	6	US-10-471-571A-3351	Sequence 3351, Ap	
6	113.6	6.5	2202	9	US-11-348-413-18343	Sequence 18343, A	
7	110.6	6.3	3300	9	US-11-348-413-14142	Sequence 14142, A	
8	108.6	6.2	5406	7	US-11-396-565-1	Sequence 1, Appl	
9	108.4	6.2	2000	9	US-11-348-413-18494	Sequence 18494, A	
10	98.4	5.6	2885	6	US-10-471-571A-3353	Sequence 3353, Ap	
11	90.6	5.2	2844	6	US-10-471-571A-3351	Sequence 3351, Ap	
C	12	89.2	5.1	5493	6	US-10-517-441-691	Sequence 691, App
	13	88.2	5.1	2596	9	US-11-218-305-12130	Sequence 12130, A
	14	86.8	5.0	1601	9	US-11-348-413-18596	Sequence 18596, A
	15	80.6	4.6	1851	9	US-11-348-413-18588	Sequence 18588, A
C	16	80.6	4.6	5493	6	US-10-517-441-1517	Sequence 417, App
	17	79.2	4.5	10082	9	US-11-021-837-11	Sequence 11, Appl
	18	78	4.5	4857	6	US-10-517-441-698	Sequence 698, App
	19	75.4	4.3	2631	6	US-10-471-571A-3883	Sequence 3883, Ap
C	20	71.8	4.1	18759	6	US-10-517-441-530	Sequence 530, App
	21	71.8	4.1	14147	6	US-10-517-441-540	Sequence 540, App
	22	71.2	4.1	1134	8	US-11-217-529-166160	Sequence 166160
	23	69.6	4.0	2501	6	US-10-517-441-562	Sequence 562, App





QY 61 AATAACCAATATTAATAAAGAGAAACGAATACTACGATGGCATAGAAAAACGCTCA 120  
DB 378 GATAACCAATATTAATAAAGAGAAACGAATAGCAACGATGCCATAGAAAAATCGCTCT 434  
QY 121 GAAGATAGAAACAGAGTCAACAAACAATGTAGATGAAACCAACCAACATTTTACAAAG 180  
DB 435 AAAGATATAACAGTCAACAAACAATGTAGATGAAACCAACCAACATTTTACAAAG 494  
QY 181 ACCCTCAAGATATATCTCTTTACAGAAAGAGAGGTAAAGAACTCTCATCAGTCGAA 240  
DB 495 ACCCTCAAGATATATCTCTTTACAGAAAGAGAGGTAAAGAACTCTCATCAGTCGAA 554  
QY 241 TCCTCAAAATTCATCAATTTGATCTGCCCCAACACCTCTCACAAACAATAATAGAGAA 300  
DB 555 TCCTCAAAATTCATCAATTTGATCTGCCCCAACACCTCTCACAAACAATAATAGAGAA 614  
QY 301 GAATCTGTTCAAAACAAGTGAATATGTAGAGATTCACAGTATCAGATTTTGGTAACTCT 360  
DB 615 GCATCTATTCAAAACAAGTGAATATGTAGAGATTTCCCGGTATCAGATTTTGGTAACTCT 674  
QY 361 AATAAAGAGAGATTAACACTGAACTCTGGTAAAGAGAGAAATCTATAGAGCAACCTAAT 420  
DB 675 AATAAAGAGAGATTAACACTGAACTCTGGTAAAGAGAGAAATCTATAGAGCAACCTAAT 734  
QY 421 AAGTAAAGAGATTCACAAACAAGTCAAGCTCGCTGGCTATCAAAATATAGATGAAAAA 480  
DB 735 AAGTAAAGAGATTCACAAACAAGTCAAGCTCGCTGGCTATCAAAATATAGATGAAAAA 794  
QY 481 ATTTCAAAATCAGATCAGTATTAATAATTTACCAATTAATGAAATATGAAATAGGCTAGA 540  
DB 795 ATTTCAAAATCAGATCAGTATTAATAATTTACCAATTAATGAAATATGAAATAGGCTAGA 854  
QY 541 CCAATTACTACAACTCTGCCCAACCATCGATTAAACGTTGTAACCGCTAAATCAATTAGCG 600  
DB 855 CCGTTATCTACAACTCTGCCCAACCATCGAGTAAAGCGTGTAAACCGCTAAATCAATTAGCG 914  
QY 601 GCGGAACAAGGTTGCAATGTTTAACTTTAAATTTAAAGTTACTGATCAAAATTTACTGAA 660  
DB 915 GCAGAAACAAGGTTGCAATGTTTAACTTTAAATTTAAAGTTACTGATCAAAATTTACTGAA 974  
QY 661 GCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
DB 975 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1034  
QY 721 GTAACCTTTTGAAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
DB 1035 GTAACCTTTTGAAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1094  
QY 781 AAGAATACAGTTCCATCAGATTTAACCGATAGCTTTTCAATACCAAAATAAAAGATAAT 840  
DB 1095 AAGAATACAGTTCCATCAGATTTAACCGATAGCTTTTCAATACCAAAATAAAAGATAAT 1154  
QY 841 TCTGGGAATCATCGCTACAGTACTTATGATATCAAAATAAAACAAATACCTATATCT 900  
DB 1155 TCTGGGAATCATCGCTACAGTACTTATGATATCAAAATAAAACAAATACCTATATCT 1214  
QY 901 TTTTACAGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
DB 1215 TTTTACAGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1274  
QY 961 ATTGATAATCAAGGTTCCAAATATATATACCAAGTTAGATGTAGAAATATAAAGCGCC 1020  
DB 1275 ATTGATAATCAAGGTTCCAAATATATATACCAAGTTAGATGTAGAAATATAAAGCGCC 1334  
QY 1021 CTTTTCATAGTAAATAAACAATTTACGTTGATATCAAGACCTTAAACGAAATCGGACT 1080  
DB 1335 CTTTTCATAGTAAATAAACAATTTACGTTGATATCAAGACCTTAAACGAAATCGGACT 1394  
QY 1081 GCTAACCTTTCAAGTATGTTTCAAAATATAGATACGAAATAATCATACGTTGAGCAACG 1140  
DB 1395 GCTAACCTTTCAAGTATGTTTCAAAATATAGATACGAAATAATCATACGTTGAGCAACG 1454  
QY 1141 ATTTATATTAACCTCTCTCGTTTATTCAGCAAGGAAACAAATGTAAATATTTTTCAGGGAAT 1200

DB 1455 ATTATATTAATTAACCTCTCTCGTTTATTCAGCAAGGAAACAAATCTTAAATATTTTCAGGGAAT 1514  
QY 1201 GGTGATGAAGGTTTCAACAATTTATAGACGATAGACAAATTAATTAAGTTTATTAAGTTTGA 1260  
DB 1515 GCGGATGAAGGTTTCAACAATTTATCGACGATAGTACAAATCATTAAGTTTATTAAGTTTGA 1574  
QY 1261 GATAATCAAAATTTTACAGATAGTAAAGAAATTTATGATTTACAGTCAATATGAAGATGTC 1320  
DB 1575 GATAATCAAAATTTTACAGATAGTAAAGAAATTTATGATTTACAGTCAATATGAAGATGTC 1634  
QY 1321 ACAATGATGATTTATCCCAATTTAGGAAATTAATGAATGATGTAATTAATTTTGGTAAAT 1380  
DB 1635 ACAATGATGATTTATCCCAATTTAGGAAATTAATGAATGATGTAATTAATTTTGGTAAAT 1694  
QY 1381 ATAGATTTCCCAATTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTTAT 1440  
DB 1695 ATAGATTTCCCAATTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTTAT 1754  
QY 1441 ACAGCTATACAGCAAACTGTGCAATGCGAGAGCTATATAAGTATGAGTATCTGCTGAGTTT 1500  
DB 1755 AGACGATACAGCAAACTGTGCAATGCGAGAGCTATATAAGTATGAGTATCTGCTGAGTTT 1814  
QY 1501 AGACGATACAGCAAACTGTGCAATGCGAGAGCTATATAAGTATGAGTATCTGCTGAGTTT 1560  
DB 1815 AGACGATACAGCAAACTGTGCAATGCGAGAGCTATATAAGTATGAGTATCTGCTGAGTTT 1874  
QY 1561 GACTTGCCTCTGCAAACTTTATAAATCGGAGATTAAGTATGAGTATCTGCTGAGTTT 1620  
DB 1875 GACTTGCCTCTGCAAACTTTATAAATCGGAGATTAAGTATGAGTATCTGCTGAGTTT 1934  
QY 1621 GATGTTTCAAAATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
DB 1935 GATGTTTCAAAATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1994  
QY 1681 ACATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
DB 1995 ACATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2054  
QY 1741 GATGG 1745  
DB 2055 GATGG 2059

## RESULT 3

US-11-348-413-14134

; Sequence 14134, Application US/11348413

; Publication No. US20060160121A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; APPLICANT: Murphy, Ellen

; APPLICANT: Olmsted, Stephen

; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES

; FILE REFERENCE: 031896-084100 (AM 101724)

; CURRENT APPLICATION NUMBER: US/11/348,413

; CURRENT FILING DATE: 2006-02-07

; PRIOR APPLICATION NUMBER: PCI/US05/035471

; PRIOR FILING DATE: 2005-10-05

; PRIOR APPLICATION NUMBER: US 11/243,445

; PRIOR FILING DATE: 2005-10-05

; PRIOR APPLICATION NUMBER: US 60/615,573

; PRIOR FILING DATE: 2004-10-05

; NUMBER OF SEQ ID NOS: 1276209

; SEQ ID NO 14134

; LENGTH: 834

; TYPE: DNA

; ORGANISM: Staphylococcus epidermidis

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)..(834)

; OTHER INFORMATION: "WAN01UQ6V; ORF: 00000000000001; SingletonSubcluster conta

; OTHER INFORMATION: ins WAN01UBTX:SRI\_3861\_Glim2.02::similar to SE0331, Ser-As



Db 1186 MAARCAGTWC---WAATGARACWAGTTTGAATTTAACTRTTTCGACAGCAGGTAAGAA 1242  
QY 1030 GTAATAAATAAATAATTCAGTGGTGAATATCAAGACCTAAACGAAATCGGACTGTAACCTT 1089  
Db 1243 ACWAGCCAAAGTYGCTGTTGATTAATCAAGAYCCAAATGCTGATGATTCACAACTT 1302  
QY 1090 CAAAGTATGTTTACAAATATAGATACGAAATAATCATACAGTTGAGCAGAAACGATTTATAT 1149  
Db 1303 CAATCTATCTTACAAATTTAGATGAARYAARCAAACTATTGAAACAACTTTATGTT 1362  
QY 1150 AACCTCTCTGTTATTCAGCCAAAGGAAACAAATGTAATAATTTTTCAGGGAATGCTGATG-- 1207  
Db 1363 AATCCWTTGAAATAAAMWCAAGCAACVACACCTAAAGTTTGTATAGCTGCTAGTAGAT 1422  
QY 1208 -----AAGTTTCAACAATTTATAGACGATAGACCAATAAT 1242  
Db 1423 GATTATGGAATATTAAACTPAGGAATGGTAGVACCATTTATGACCAAAATAACAGAAATA 1482  
QY 1243 AAGTTTATAAGTTGGAGATTAATCAAAATTTACAGATAGTAAACAGAAATTTATGATTAC 1302  
Db 1483 AARGTTTATAAGTTTAACTATCAACCAATTCGCTCAAGTAAATAGAAATCTATGATTTT 1542  
QY 1303 AGTGAATATGAACTGTCACAAATGA---TGATTATGCCCAATTTAGGAATATAATGAT 1359  
Db 1543 AGTCAATACGAAGATGTAACAAGTCAATTTGATTAATAAATAATCAATTTAGTAAATGTA 1602  
QY 1360 GTGAATATTAATTTTGGTAAATATAGATTTACCATATATTTAAAGTTTATAGTAAATAT 1419  
Db 1603 GCAACATTGGATTTTGGTGNATTAATTCAGCCTATTTATCAAGTTGTTAGTAAATAT 1662  
QY 1420 GACCTTAATAAGATGATTACACGACTATACAGCAACTGTGTGAACAATGACAGCACTATA 1479  
Db 1663 ACACCTACATCAGATGCGCAACTAGATATGTCYCAAGGTACTAGTAGAGAACCACTGAT 1722  
QY 1480 AATGATATACTGGTGAATTTAGAACAGCATCTCTATGATTAATAACAATGCTTTCTCTACA 1539  
Db 1723 AATATGTTTATTAATTAATATGACGATATTTCAAACTTCATCTGTAACCTTCTAATGACWCT 1782  
QY 1540 AGTTTCAAGGTCAAGCAAGTGTACTTTCCTCTGAAATAAATTTATAAAATCGGAGATTAC 1599  
Db 1783 GYGGTGGCGACGGTACTGTAA---ACCTGAAGAAAGTTTATCAAAATTTGGTGAATAT 1839  
QY 1600 GTATGGGAAGATGTAGATAAAGATGGTATTTCAAAATACAAATGATTAATGAAACCGCTT 1659  
Db 1840 GTATGGGAAGACGTTGATTAAGACGGTGTGCAAGGTACAGATTCRAAAGAAARCCAATG 1899  
QY 1660 AGTAAATGTTTGTAACTTTGACGTATCTGATGGAACTTCAAAATCAGTCAGAACAGAT 1719  
Db 1900 GCAAACTGTTTATGTTTACATTAACCTTACCGGACGGTACTACAAATCAGTAAGAACAGAT 1959  
QY 1720 GAAGATGGGAATATCAATTTGATGG 1745  
Db 1960 GCTAAHGGTCATTAAGATTCGGTGG 1985

## RESULT 5

US-10-471-571A-3351  
; Sequence 3351, Application US/10471571A  
; Publication No. US20060115490A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
; CURRENT APPLICATION NUMBER: US/10/471,571A  
; FILE REFERENCE: P026927WO  
; CURRENT FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: GB-0107661.1  
; NUMBER OF SEQ ID NOS: 5642  
; SOFTWARE: SeqWin99, version 1.03  
; SEQ ID NO 3351  
; LENGTH: 4047  
; TYPE: DNA  
; ORGANISM: Staphylococcus aureus

US-10-471-571A-3351

Query Match 7.2%; Score 126; DB 6; Length 4047;

Best Local Similarity 44.0%; Pred. No. 1.6e-16;

Matches 727; Conservative 0; Mismatches 915; Indels 12; Gaps 4;

QY 86 AAACGTAATACTACGATGGCATTAGAAAAACGGTTCAGAGATAGAACAGAGTCAACACAA 145  
Db 212 ATTCGAGTGATAAAGTTGATATGCAGCAACTAAATCAGAGAGACAATCTATAAAATGATA 271  
QY 146 ATGTAGATGAAACGAGCAACATTTTTCACAAAGACCCCTCAAGATAATATCATCTTTA 205  
Db 272 ATCAAAAGAAATGCTATCATCTCAAGGTAATGAAACGACTTCAATGGGAATAAATAA 331  
QY 206 CAGAACAGAGGTAAAGAAATCTCATCAGTCGAATCCTCAATCTCAATTCATCAATTTGAT 265  
Db 332 TAGAAAAGAAAGTGTACAATCTACCACTGGAAATAAAGTTGAAGTTTCACTGCGCAAT 391  
QY 266 CCCAACCAACCATCTCACACAAATAAATAGAGAAATCTGTTCAAAACAAGTGAATAATG 325  
Db 392 CAGATGAGCAAGCT---TCACCAAAATCTACGAATGAAGATTTAAACACTAAACAACTA 448  
QY 326 TAGAAGATTCACACGATCAGATTTTGTCTAACTCTTAAATAAAGAGAGTAAACACTGAAT 385  
Db 449 TAAGTAATCAAGAAGCGTTTACCACTGATTTGCAAGAGAAATAATCAGTGGTAAATGTT 508  
QY 386 CTGGTAAAGAGAGATCTATAGAGCAACCTAATAAGTAAAGAGAGATTCAACACAA 445  
Db 509 AACCAACTAATGAGGAAAAACAAAAGGTAGTGCCTCAAACTGAATCAACTACATTAATG 568  
QY 446 GTCAAGCGCTCTGGCTATACAAATATAGATGAAAAAATTTCAATCAAGATGAGTTATTA 505  
Db 569 TTAAAGTGTATGCTATCAGAGATTAATGATGAAACTCTTGTGATAACAATAGTAATCAA 628  
QY 506 ATTTACCAATAATGAATATGAAATTAAGGCTAGACCAATTAATCTACAAACATTCGCCAAC 565  
Db 629 ATAATGAAAAATTAATGACAGATATCATTTTGCCTCAAAAGTACAGCACCTAAACGTTG 688  
QY 566 CATCGATTAAGCGTGTAAACGTTAAATCAATTAAGCGCGGGAACAGAGTTGAAATGTTAAC 625  
Db 689 CA---AGAATGCTGTAGCAGCAGTACAGCCATCATCAACAGAGGCTTAAATAATGTTA 745  
QY 626 ATTTAATTAAGGTACTGATCAAGTATTAATTAATGATGATGATGATGATGATGATGATG 685  
Db 746 ATTTAATCACAATAATCAACATTAATTAATGATGATGATGATGATGATGATGATGATG 805  
QY 686 TTAAGACCATGATGCTGAAAACTTAACTATGATGATGATGATGATGATGATGATGATGAT 745  
Db 806 TACCAGCCCAAGATTATTTATCAATTAATAATTAATTAATTAATTAATTAATTAATTAAT 865  
QY 746 TGAATCTGGTGTAGTACGATGAGTGGATATAGATAAGAAATACAGTTCCATCAGATTTAA 805  
Db 866 CAGGTGATTAATTTCAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 925  
QY 806 CCGATAGCTTTTACAATACCAAAATAAAGAT---AATTTCTCGAGAAATCATCGCTACAG 862  
Db 926 AAGATATTAATAATTAATTTGGTGTATTAATTAATTAATTAATTAATTAATTAATTAAT 985  
QY 863 GTACTTATGATAACAAAAATAAACAATCACTATACCTTTTACAGATATGATGATGATGAT 922  
Db 986 CAAAACATGATACGCAAAATAATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1045  
QY 923 ATGAAAAATTAAGCACACCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 982  
Db 1046 TTAATTTCTGTACAAATGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1105  
QY 983 ATAATAATACCAAGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1042  
Db 1106 TTAGTAAACACGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1165  
QY 1043 TTACCGTTTGAATATCAAGACCTAAACGAAATTCGAGCTGCTAACCTTCAAGTATGTT 1102  
Db 1166 CTAAACATTCATCCAGATTATGTTGTAATGAGAAAAATTAATTAATTAATTAATTAAT 1225

```
QY 1103 CAATATATAGATACGAAAT---CATACAGTTGACCAACGATTTATATTAAACCTCTTC 1159
Db 1226 CTGAACAGTTTTCATCATGTTGAAATTAAGAAATCCAGGGTACTATATAACAAACGATTT 1285
QY 1160 GTTATTTCAGCAAGCAAAATGTAATATTTTCAGGGAATGGTGATGAAGTTTCAACAA 1219
Db 1286 ATGTAAATCCATCGGAAATTTCTTAAACAAATGCCAACTAAAGTTTCAAGCTTACCCT 1345
QY 1220 TTATAGACGATAGCAATATAATTAAGTTTATAAGTTTGGAGATTAATCAAAATTTACAG 1279
Db 1346 CAAATTATCTTAATAATCGGGCAATAAATAAAGATGTACACATATAAAATATATC 1405
QY 1280 ATAGTAAACAGATTTATGATTTACAGTGAATATGAAGATGTCAAAATGATGATATGCC 1339
Db 1406 AAGTTCTTAAAGTTTATACATTTAAATNAAGGATACGATGTGAATCTAAGAGCTTACAG 1465
QY 1340 AATTAGGAAATAAATGATGTGAATATTTAATTTGGTAAATATAGATTTCAACATATATTA 1399
Db 1466 ATGTAACAAATCNAATCTTGCNGAAATTTACATATGGGACAAACATAGCGCTGTATTG 1525
QY 1400 TTAAGATTATTAGTAAATATGACCCATAAAGGATGATTACACGACTATACAGCAAACTG 1459
Db 1526 ATTTTGGAAATGACAGATTCGCTTATGTTGTAATGTTTAATAGAAAATTCCAATATACA 1585
QY 1460 TGCAATGCAGACGACTAATAATGATGATATCTGGTGAGTTTGAACACATCCTATGATA 1519
Db 1586 ATAGCGAAGCCCAACACTTGTTCAAATGGCTACTTTATCTTCAACAGGTAATAAATCCG 1645
QY 1520 ATACAAATGCTTCTCTACAGTTTCAGGTCAAGGACAAAGGTGACTTGCCTCTCGAAAAA 1579
Db 1646 TTTCTACTGGCNAATCTTTAGGATTTACTAATAACAAAGTGGCGGAGCTGGTCAAGAG 1705
QY 1580 CTTATAAAATCGGAGATTACGATATGGGAAGATGTAGATAAAGATGGTATTCAAAATACAA 1639
Db 1706 TATATAAAATTTGGTAACATCGTATCGGAAGATATAATAAATAACGGTGTCAAGAAATTAG 1765
QY 1640 ATGATAATGAAMACCGCTTAGTATGATTTGGTAACTTTGACGTATCCTGATGAACTT 1699
Db 1766 GAGAAAAAGCGGTGGCAATGTAACGTGTAATTTGATAATAAATAACAAATACAAAG 1825
QY 1700 CAAATCAGTCAGAACAGATGAAGATGGAAATA 1733
Db 1826 TAGGAGAGCAGTTACTTAAGNAGATGGTCATA 1859
```

## RESULT 6

```
US-11-348-413-18343
; Sequence 18343, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIORITY APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 18343
; LENGTH: 2202
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2202)
```

```
; OTHER INFORMATION: WAN01UQ76; ORF: 0000000000000000; Cluster contains WAN014IPQ
; OTHER INFORMATION: :COL-SA0608:sdrc protein:COL:WAN01BP8A
US-11-348-413-18343
```

```
Query Match 6.5%; Score 113.6; DB 9; Length 2202;
Best Local Similarity 44.0%; Pred. No. 4.7e-14;
Matches 652; Conservative 75; Mismatches 683; Indels 72; Gaps 10;

QY 292 AATGAGAGAGATCTGTTCAACAAAGTGATGATGATGAGATTTACACGATATCAGATTTT 351
Db 214 AAAACAACTRAAAAGTTGATGTCGTCACACTAAAGAGCAATACGCAAACTGCACTGCA 273
QY 352 GCTAACTCTAAATAAAGAGAGTAACACTGAACTCTGTTAAAGAGAGAACTACTATAGAG 411
Db 274 GATCAGCTTAAGTGACAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 333
QY 412 CAACCTTAATTAAGTAAAGAGATTTCAACAAACAAAGTCAGCCGCTCTGGCTATACAAATATA 471
Db 334 CAATCACCACAAACGCTACAGCTARTCAATCTACTACAMAAACTAGCAATGTAAACAACA 393
QY 472 GATGAAAAATTTCAAAATCAAGATGAGTTATTAATTTTACCAATAATGATATGAAAAAT 531
Db 394 AATGATAAATCATCAACTACATATAGTAATGAAACTGATAAAAGTAATTTTAACACARGC 453
QY 532 AAG-----GCTAGACCAATTATCTACACATCTGCCCAACCATCGATTAAACGCTGTA 582
Db 454 AARAYGTTTCARCTCAWCCTTAAACAAACGACTATTAAACWAGARCTTTAAAYCGYATG 513
QY 583 ACCGTAATCAATTAGCGGGG---AAACAAGGTTTCAATGTTTAAACCAATTTTAATTAAGTT 639
Db 514 GCMGTGAAYACGWTGCGAGCWCACCAACAGGWAACAAATGTTAATGATAAAGTWCATTTT 573
QY 640 AC-----TGATCAAAGTATTACTGAAGGATATGATGATGATGATGATGATGATGATGAT 693
Db 574 WCRAYATGAYATTGCKATTGATAAAGGACAYCTWAATWAARRMWACGSHAAACWAGAA 633
QY 694 CATGATCG-----TGAAACCTTAATCTATCATGTAACTTTTGAAGTAGATGATGAAG 744
Db 634 TTTTGGGCAACTTCAAGTGATGTTTAAATTAAGGCAATTTACACNATCGATGATCT 693
QY 745 GTGAAATCTGTGATACGATGACAGTGGATATAGATAAGAAATACAGTTTCCATCAGATTTA 804
Db 694 GTTAAAGAGGCGGATACATTTACTTTTAAATATGTCATATTTTCCGTCAGGTCWGTGTA 753
QY 805 ACCGATAGCTTACATACCAAAATAAAGATAATTTCTGGAGAAATCATCGCTACAGGT 864
Db 754 AGATTACCTTCAACAACTCAAAATTTATATATGCCCAAGGTAATATTATTGCAAAAGGT 813
QY 865 ACTTATGATAACAAAAATAACAAATCACTATATCTTTTACAGATTTATGTAGATAAGTAT 924
Db 814 ATTTAYGAYAGTAAACAAAYACAAACRTATATCTTTTACGAATATGTAGATCAATAY 873
QY 925 GAAATATTTAAAGCACACCTTTAAATTAACGTCATACATTTGATTAATCAAAGGTTCCAAAT 984
Db 874 ACAATGTTAGMGGTAGCTTTTGAACAAAGTGYCATTTGCGAAACGTTAAATGCAACAACT 933
QY 985 AATTAATCAACAGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1044
Db 934 GATAAAAAC-----WGCTTATAAATGAAGTAAATTTTAGGTAATGATACATAT 981
QY 1045 ACGGTTGAATATCAAGACCTTAACGAAATCGGACTGCTAACCTTTCAAGATGATGTTTACA 1104
Db 982 AGYR-----AGAWRTCAATTCGNTATGTTATGTTAATTAAGAAAGSWCAACMCTTATTCR 1035
QY 1105 AATATAGATACGAAAAATCATACAGTTGAGCAAAACGATTTTATATTAACCCCTCTCTGTTAT 1164
Db 1036 AGTACAAATATATTAAYAAATGAAGATTTTTCRCGTAAATATGACTGYWTATGATTAATCAA 1095
QY 1165 TCAGCCCAAGGAAACAAATGTAATTTTCAGGGAATGATGATGATGATGATGATGATGATGAT 1224
Db 1096 CCTAAAAACACMTATACWAAASAAACRTTTGTWACWAAATTTTAACCTGGWTATAAATTAAT 1155
QY 1225 GACGATAGCAATAATAATTAAGTTTATAAGGTTTGGAGATTAATCAAAATTTTACCAGATAGT 1284
```

```
Db 1156 CCRATGCTWAAAACCTTCAAAATTTACGAAGTGACAGATCAAAATCAATTTGSGAYAGT 1215
QY 1285 AACAGAATTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTAATGATGCCAATTA 1344
Db 1216 TTCACCCGCGACTACTTCAAACTTAAAGATGTTACTTTCCTCAATTAATTAATTAATTAATTA 1275
QY 1345 GGAATAATTAATGATGTAATTAATTTTGGTAAATATAGATTACCATATATATTATTA 1404
Db 1276 AATGATAATAAARACDGCDAACAGTHGATTTAATGAAGGYCAAWCMWAGYAGYATATAACAR 1335
QY 1405 GTTATTAGTAATAATGACCTTAATAGGATGATTAACGAC-TATACAGCAAACTGTGAC 1463
Db 1336 TACATCAATCAACAAGTTGCTATCCAGATAATASWTCAACAGATAATGGRAAAATTGAT 1395
QY 1464 AATGACAGACCTATATAATGAGTATATCTGGTGAGTTTAGAACAGCATCTTATGATAATAC 1523
Db 1396 TATACITTAGMACTGAC-----AAATSKAAWAGTAGTTGGTCAAAVAGTTATTCAAA 1450
QY 1524 AATGCTTTCTCTACAAAGTTCAAGTTCAGGTCAAGGACAAGGTGACTTGGCTCTCTGAAAAAACTTA 1583
Db 1451 TGTGAATGGCTCATCACTGCAATGCWAATGGCGACC-----AAAAAGAAATA 1492
QY 1584 TAAATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGTTATTCAAAATACAAATGA 1643
Db 1493 TAATCTAGTGACTATGTATGGGAAGATACAAATAAAGATGGTAAACAAGATGCCAATGA 1552
QY 1644 TAATGAAAAACCGCTTAGTAATGTAATGTTGTAATCTTTGACGTATCTCTGATGGAACTTCAA 1703
Db 1553 AAAAGGATTAAGGTGTTTATGTCATCTTAAGATAGTACGGTAAAGAA---TTAGA 1609
QY 1704 ATCAGTCAGAACAGATGAAGATGGGAATATATCAATTTGATGG 1745
Db 1610 TCGTACGACACAGATGAAATGGTAAATATCATCAGTTCACTGG 1651
```

## RESULT 7

```
US-11-348-413-14142
; Sequence 1, Application US/11348413
; Publication No. US2006016012A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounchs, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 14142
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3300)
; OTHER INFORMATION: "WAN01U079: ORF: 00000000010100; Cluster contains WAN01OSM
; OTHER INFORMATION: G:SE2395:adrF:Ser-Asp rich fibrinogen-binding,bone sialop
; OTHER INFORMATION: otein-binding protein:ATCC12228:NC_004461.1"
US-11-348-413-14142
```

```
Query Match 6.3%; Score 110.6; DB 9; Length 3300;
Best Local Similarity 46.1%; Pred. No. 2.1e-13;
Matches 359; Conservative 3; Mismatches 417; Indels 0; Gaps 0;
```

```
QY 608 AAGGTTCCGAATGTTAAACCAATTTAAAGTTACTGATCAAAAGTATTACTGAAGGATATG 667
```

```
Db 1094 AAAATGTAATGATAAGTTAAAAATCAAAACCTTACGCTTTCACTTAATAAGAGTAATA 1153
QY 668 ATGATAGTGAAGGTGTTATTAAGACCATGATGCTGAAAACCTTAATCTATGATGTTAATCT 727
Db 1154 ATCACGCTAATTAACGTAATATGGCCCAACGAAGTAACGAACAAATTTAATTTAAAAAGCAA 1213
QY 728 TTGAAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAGTGGGATATAGATAAGAAATA 787
Db 1214 ATGAATTAGATGACAGCATAAAGAGGGAGATACCTTTTACTATTATAGTATGGTCAGTATA 1273
QY 788 CAGTTCCATCAGATTTAACCGATAGCTTTCAATACCAAAAAATAAAAGATAAATTTCTGGAG 847
Db 1274 TTAGACCGGGTGTGTTAGAACTTCTCGCAATAAAAACTCAACTACGCTAGTAGAGGTGCT 1333
QY 848 AAATCATCTCAGCTACGCTACTTATGATAACAAAAATAAACAATCACTACTACTTTTACAG 907
Db 1334 CTATTGTAGCTAATGGTGTTATGATATAAAAACTACAANAATACGACGACTTTATACATTTACTA 1393
QY 908 ATTATGTAGATAAGTATGAAAAATATTAAGACACACCTTAAATTTAACGTCATACATTTGATA 967
Db 1394 ACTATGTTGATCAATATCAAAATATTTACAGGTAGTTTGTGATTTTATTTGACGCCCTAAGA 1453
QY 968 AATCAAAAGTTCCAAATATAATACCAAGTTAGATGTAGAATATAAAGCGGCCCTTTTCAT 1027
Db 1454 GGGAAACAGCAATTAAGGATAATCAGAAATTTATCTCTATGGAAGTGACGATTTGCTAACGAAG 1513
QY 1028 CAGTAATAATAAACAATTAACGTTGTAATATCAAGACCTTAACGAANAATCGAGCTGCTAAC 1087
Db 1514 TAGTCAAAAAAGACCTTCATTTGTTGGATTTATGGTAATAAAAAAGGACAAATACAACCTACAG 1573
QY 1088 TTCAAAAGTATGTTTCAAAATATAGATACGAAAAATCATACAGTTGAGCAAAACGATTTATA 1147
Db 1574 CGGTAGCAATGCTGGATATGTAATATAAATCAACGAAGTTGTTTATCTTAACCAAA 1633
QY 1148 TTAAACCTCTTCGTTATTACGCCAAGGAAACAAATGTAAATATTTTCAGGGAATGGTGATG 1207
Db 1634 ATAACCAAAAYCCTAAATATGCTAAATATTTCTCAACAGTAAAAAATGGTAAATTTATAC 1693
QY 1208 AAGGTTCAACATTTATAGACGATAGCAACAATTAATTAAGTTTATTAAGTTGGAGATAATC 1267
Db 1694 CAGGTGAAGTGAAGTTTACGGAAGTGACGAGATACCAATGCGATGGTAGATGCTTCAATC 1753
QY 1268 AAAATTTACCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGTCACAAAATG 1327
Db 1754 CTGATTTAAATAGTTCTAATGTAAAGATGTGCAAGTCAATTTTCACCTAAAGTAAAGTG 1813
QY 1328 ATGATTATGCCCAATTAGGAAATAATATGATGTGAATATTAATTTTGGTAAATATAGAT 1386
Db 1814 CAGATGGTACTAGAGTTGATATCAATTTTGTGTAAGATATGCAAAATGCTAAAAAGTAT 1872
```

## RESULT 8

```
US-11-396-565-1
; Sequence 1, Application US/11396565
; Publication No. US20060171964A1
; GENERAL INFORMATION:
; APPLICANT: FOSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCI
; FILE REFERENCE: P0633502/BAS
; CURRENT APPLICATION NUMBER: US/11/396,565
; CURRENT FILING DATE: 2006-04-04
; PRIOR APPLICATION NUMBER: US/09/386,962
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5406
; TYPE: DNA
```



```
QY 806 CCGATAGCTTTACAAATACCAAAATAAAGAT---AATTCTGGAGAAATCATCGCTACAG 862
Db |||||
QY 926 AAGATATTAAAAATATTGGTGATATTAAAGATCCAAATTAATGTGTAACAAATGGCGACTG 985
Db |||||
QY 863 GTACTTATGATACAAAATTAACAAATCACTATCTTTTACAGATTAATGTAGATAAGT 922
Db |||||
QY 986 CAACAATGATCTGCAAAATTAATTAATACATATACATTTACAGATTAATGTGTGATCGAT 1045
QY 923 ATGAAATATTAAAGCACACCTTTAAATTAACGCTACATCATTTGATAATCAAGGTTCCAA 982
Db |||||
QY 1046 TTAATTCAGTAAATATGGGTATTAACTCAATTTATATGATGATGATGATCAATTCCTG 1105
QY 983 ATAATTAATACCAAGTTAGATGTAGATAATAAAGCGCCCTTTTCATCAGTAAATATAACAA 1042
Db |||||
QY 1106 TTGACAAGAAGATGTCTCTTTTAGTGTAACTATTGGAATCAAAATTAACACTACAAAG 1165
QY 1043 TTACGGTTGAATATCAAGACCTTAACGAAATCGGACTGCTTAACCTTCAAGATGTGTTA 1102
Db |||||
QY 1166 CAGATATCACTTATCCGGCTTATAAAGAAGCTGACAAATAATTCATAGGATCAGCTTTTA 1225
QY 1103 CAAATATAGATACGAAAAATCATACAGTTGAGCAACGATTTATATTAAACCTCTTCGTT 1162
Db |||||
QY 1226 CAGAGACAGTTCTCATGTAGGAATGTTGAAGACCTCGTTACTATTAACCAAGTAGTAT 1285
QY 1163 A---TTCAGCCAGGAAACAAATGTAAATATTTCAGGGAATGGTGATGAAGGTTCAACAA 1219
Db |||||
QY 1286 ATGTTAATCTTATGGATAAGGATTTAAAGGCTTAAGTTAAAGGTTGAAGCGTACCATC 1345
QY 1220 TTATAGACATAGCACAAATAATTAAGTTTATAAGTTGGAGATTAATCAAAATTTACCAG 1279
Db |||||
QY 1346 CGAAATATCCAACTAATATTGGTCAAAATTAATCAAAATGTTACAAATATAAAATATATC 1405
QY 1280 ATAGTAACAGAAATTTATGATTACAGTGAATATCGAGATGTCACAAATGATGATATGCC 1339
Db |||||
QY 1406 GTGTTCTCGAGGATATACITGGAATAAGGATATGACGTTAATACTAATGATTTGGTAG 1465
QY 1340 AATTAGGAATAAATATGATGTGAATTAATTTTGGTAAATATAGATTCCACCATATATTA 1399
Db |||||
QY 1466 ACGTAACTGATGAATTTAAABATATAAATGACGATGGATCAATCAAGTGTTAATCTTG 1525
QY 1400 TTAAGTTATTATAGTAAATATGACCTTAATAAGGATGATTAACGACTATACAGCAAACTG 1459
Db |||||
QY 1526 ATTTTGGTGATATTACATCAGCATATGTTGTAATGTTAATCAAAATTTCCAATATACAA 1585
QY 1460 TGACATGCAGACGACTAATATAGTATATCTGTTGAGTTTGAACAGCATCCTATGATA 1519
Db |||||
QY 1586 ATAGCAAGGCCAACACTTGTTCAAAATGGCTACTTTATCTTCAACAGGTAATAAATCGG 1645
QY 1520 ATACAATATGCTTTCTCTACAAGTTCAAGGTCAGGTCAGGTCAGTTGCTCTCGAAAAA 1579
Db |||||
QY 1646 TTTCTACTGGCAATGCTTTAGATTTACTAATAACCAAGTGGCGAGCTGGTCAAGAG 1705
QY 1580 CTTATAAATCGGAGATACGATGATGGAGATGTAGATAAAGATGGTATTCAAAATACAA 1639
Db |||||
QY 1706 TATATAAATTTGGTAACTACGATGCGAAGATACTAATAAAGGCTGTTTCAAGAATTAG 1765
QY 1640 ATGATAATGAAAAACCGCTTAGTATGATGTTGTTGACCTTTGACGATCTCTGATGAACTT 1699
Db |||||
QY 1766 GAGAAAAAGGCGTTGGCAATGPACTGTAACCTGTTATTTGATAATAATAACAAATACAAAG 1825
QY 1700 CAAATTCAGTCAGACAGATGAAGATGGGAATA 1733
Db |||||
QY 1826 TAGGAGAGCAGTTACTAAGAAGATGGGTCA 1859
```

## RESULT 10

```
US-10-471-571A-3353
; Sequence 3353, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
```

```
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3353
; LENGTH: 2985
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; US-10-471-571A-3353
```

```
Query Match 5.6%; Score 98.4; DB 6; Length 2985;
Best Local Similarity 45.7%; Pred. No. 6.4e-11;
Matches 655; Conservative 0; Mismatches 731; Indels 48; Gaps 7;

QY 315 AAGTGATTAATGTAGAAGATTCACAGTATCAGATTTTGCTAACTCTTAAATAAAGAGAG 374
Db |||||
QY 261 AACTGCAACTGCAGATCAGCCTAAAGTGACAATGAGTGATAGTGCAACAGTTTAAAGAAAC 320
Db |||||
QY 375 TAACTGTAATCTGGTAAAGAGAGAGTACTATAG---AGCAACCTTAATAAAGTAAAGA 431
Db |||||
QY 321 TAGTAGTAACATGCAATCACCACAAACGCTACAGCTAATCAATCTCTACTACAAAACTAG 380
QY 432 AGATTCAACCAACAGTCAAGCGCTCTGGCTATACAAATATAGATGAAAAATTTTCAATCA 491
Db |||||
QY 381 CAATGTACACAAATGATTAATCATCACTATATAGTAAAGAACTGTATAAAGTAA 440
QY 492 AGATGAGTTATTAAATTTTACCAATAATGAATATGAAAAATAAGGCTAGACCTATATCTAC 551
Db |||||
QY 441 TTTTACACAAAGCAAAAGATGTTTCACTACACTTAAACCAACGACTATTAAACCAAGAAC 500
QY 552 ACATCTGCCCAACCATCGATTAAACGGTGAACCGTAAATCAATTTAGCGCGCGAAACAAAG 611
Db |||||
QY 501 TTTAAATCGCATGGCAGTGAATACTGTTGCGAGCTCCACAAACAAAGCAAAATGTTAATGA 560
QY 612 TTCGAATGTTAAACCACTTTTAAATTTAAAGTTACTGATCAAAAGTATTACTGAAGGATATGATGA 671
Db |||||
QY 561 TAAAGTACATTTTCCAAATTTTGACATTTGCGGATGATGAAGGACATGTTAATCAGACTAC 620
QY 672 TAGTGAAGGTTGTTATTAAAGCACATGATGCTGAAAACTTTAATCTATGATGTAACCTTTTGA 731
Db |||||
QY 621 TGGTAAACTGAATTTTGGGCACTTCAAGTGATGTTTAAATTTAAAGCAATTTACAC 680
QY 732 AGTATGATTAAGTGGAATCTGGTGATACGATGACAGTGACAGTGGATATAGATAAAGATACAGT 791
Db |||||
QY 681 AATCGATGATCTGTTAAAGAGGCGCATACATTTACTTTTAAATATGGTCAATATTTCGG 740
QY 792 TCCATCAGATTTTAAACCGATAGCTTTTACAAATACCAAAATTAAGATTAATCTGGAGAAAT 851
Db |||||
QY 741 TCCAGATCAGTAGATTAACCTTCAAAATTCAAAATTTTATAATAATGCCAAGGTAATAT 800
QY 852 CATCGCTACAGGTACTTATGATAACAAAATAAACAATCACCTATACCTTTTACAGATTA 911
Db |||||
QY 801 TATTGCAAAAGGTTATTATGATAGTACACAAACACACACATATATCTTTTACGAACTA 860
QY 912 TGTAGATTAAGTATGAAAATATATAAGCACACCTTAAATTAACGTCATACATTTGATAAATC 971
Db |||||
QY 861 TGTAGATCAATATATACAAATGTTAGAGGTAGCTTTGAAACAAGTTGCTTTGCGAAACGTA 920
QY 972 AAAGGTTCCAAATTAATATACCAAGTTAGATGTAGATATATAAAGCGCCCTTTTCAATCAGT 1031
Db |||||
QY 921 AAATGCAACAACTGATATAAAC-----AGCTTATAAATGGAAGTAACTTTAGG 968
QY 1032 AAATAAAAACAATTAACGTTTGAATATCAAGACCTTAAACGAAATCGGACTGCTAACCTTCA 1091
Db |||||
QY 969 TAATGATACATATAGCGAAG-----AAATCATTTGTCGATTTATGGTATAAAGACACA 1022
QY 1092 AAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAAAACGATTTTATATTA 1151
Db |||||
QY 1023 ACCGCTTATTTCAAGTACAAACTATATTAACAATGAAGATTTTATCGCGTAAATATGACTGC 1082
```



```
QY 1152 CCCTCTTGTTATTTCAGCCAGGAAACAAATGCTAAATATTTTCAGGGAATGGTGATGAAGG 1211
Db 1083 ATATGTAATACACCTTAAATATACATATATCTAAACAAACGGTTTGTTACTAATTTAACTGG 1142
QY 1212 TTCAACAATTTAGACGATAGCACAAATTAATTAAGGTTTATAGGTTGGAGATAATCAAAA 1271
Db 1143 ATATAAATTTAATCCAAATGCAAAAACCTTCAAAATTTACGAAGTGACAGATCAAAATCA 1202
QY 1272 TTTACCAAGATAGTAACAGAAATTTATGATTAACGATGATGATGATGATGATGATGATGATG 1331
Db 1203 ATTTGTGATAGTTTTCACCCCTGATACCTTCAAAAC-----TTAAAGATGT 1247
QY 1332 TTATGCCCAATTTAGGAATATAATGATGATGATGATGATGATGATGATGATGATGATGATG 1391
Db 1248 TACTGATCAATTCGATGTTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1307
QY 1392 ATATATTTAATTAAGTTTATAGTAATATGACCCCTAATAGGATGATTAACGACGATATACA 1451
Db 1308 GAAAGGCCAAACACGACGCAATTAACAAATACATCATTCACAAGTT-----GCTTATCC 1361
QY 1452 GCAAACTGTGCAATGCGACGACTATATAATGAGTATATCTGGTGGTTTAGAACAGCATC 1511
Db 1362 AGATAATAGTTTCAACAGATATATGGAATAATTTGATTTATCTTTAGACACTGACAAAAC 1421
QY 1512 CTATGATAATACAATGCTTTCTCTACAAGTTTCAGTCAAGGACGACGACTTGCCTCC 1571
Db 1422 ATATAGTTGGTCAAAATAGTTTATCAATGTGATGATGATGATGATGATGATGATGATGATG 1480
QY 1572 TGAAAAAACTTTATAAAATCGGAGATTAACGATGATGATGATGATGATGATGATGATGATGAT 1631
Db 1481 --AAAAGAAATATAATCTAGTGACTATGATGATGATGATGATGATGATGATGATGATGATG 1538
QY 1632 AAATACAATGATTAATGAAAAACCGCTTAGTATGATGATGATGATGATGATGATGATGATGAT 1691
Db 1539 AGATGCCAATGAAAAAGGATTTAAAGGTGTTTATGTCATCTCTTAAAGATAGTAACGGTAA 1598
QY 1692 TGGAACTTCAAAATCAGTCAGAACAGATGCAAGTGGGAATATCAATTTGATGG 1745
Db 1599 AGAA---TTAGATCGTACGACCAAGATGAAATGGTAAATATCAGTTCACCTGG 1649
```

```
RESULT 11
US-10-471-571A-3551
; Sequence 3551, Application US/10471571A
; Publication NO. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P036927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3551
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-3551
```

```
Query Match 5.2%; Score 90.6; DB 6; Length 2844;
Best Local Similarity 44.0%; Pred. No. 2.5e-09;
Matches 571; Conservative 0; Mismatches 714; Indels 12; Gaps 4;

QY 208 GAAGAAGAGGTTAAAGAACTCTCATCAGTCGAATCCTCAAAATTCATCAATTCATCTGCC 267
Db 112 GGACAGAAAGAGAGCTCAGCATCGGAACAAACAACTACTACAGTAGAGAAAGTGGG 171
QY 268 CAACACCACTCTCACACAACTAATAGAGAGAAATCTGTTTCAACAGATGATGATGATGATG 327
Db 172 AGTTACGCTACTGAAAGTAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 231
```

```
QY 328 GAAGATTTCACACGCTATCATGAGATTTTCTAACTCTAAAAATAAAAGAGAGTAAACACTGAATCT 387
Db 232 ATAGATGAAACACAAATCATACAGCGGCACATCACTGAGCAACCCATCACATCAACACAA 291
QY 388 GGTAAAGAAGAGAAATCTATATAGACCAACCTTAATTAAGAGTAAAGAGATTTCAACAAAGT 447
Db 292 GTAAACAACAGAAAGACACCGAAAACCTGTGCAAGCACCAAAAGTAGAAAATCTTCGCGAGTT 351
QY 448 CAGCGCTCTGGCTATACAAATATAGATGAAAAAATTTCAAAATCAAGATGAGTATTAAAT 507
Db 352 GATTTGCCATCGGAAAAAGTTGCTGATAAGAAAATCTACAGGAATCAAGATGACATAGCT 411
QY 508 TTACCAATTAATTAATATGAAAAATAAGCTAGACCACTTATCTACAACATCTGCCCAACCA 567
Db 412 CAACCAAGTAACGCTCTAGAAATTTAACCAGAATGAAA---AGATCAACTGACGCTTACA 468
QY 568 TCGATTAAACCGTGAACCGTAAATCAATTAAGCGGGGAAACAAAGTTTCGAAATGTTAAACCAT 627
Db 469 GCAGTTGCAGAGAAGAAAGTAGTGGAGAAAATAAGCGCAAGGTACAGATGTTAAACAAT 528
QY 628 TTAATTAAGTTACTGATCAAAAGTATTACTGAAGGATATGATGATGATGATGATGATGATGAT 687
Db 529 AAAGTGGAAAGTAGAAGAGAGTAACTTGAATATATAATGGAATTTGGAGAGAGAAAT 588
QY 688 AAAGCAGATGATGCTGAAAACTTAATCTATGATGTAACCTTTTGAAGTAGATGATAAGGTG 747
Db 589 AATCTCTAATACGAGAAAGAGTAACTTGAATATATAATGGAATTTGGAGAGAGAAAT 648
QY 748 AAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
Db 649 AAGCGGGAGATTTATTTGATTTTCACTTAAGCGGATTAATGTTGAACCTCATGATGATGAT 708
QY 808 GATAGCTTTCAATACCAAAATTAAGAGATAATTTCTGGAGAAATCATCGCTACAGGTACT 867
Db 709 ACATCGCGTAAAGTTCCGGAGATAAAAGTACAGATGTCAGTTCAGTTATGCGGACAGG---A 765
QY 868 TATGATAACAAAAATAAACAAATCACCTATATCTTTTACAGATTTATGATAGATAAGTATGAA 927
Db 766 GAAATATTTGGAGAAAGAAAGTTAGATATACGTTTAAAGAAATATGTAACAGAAAAAGAA 825
QY 928 AATATTAAGCACACCTTTAAATTAACGTCATATGATTAATCAAGTTCAGATGATGATGATGAT 987
Db 826 GATTTAACTGCTGAATTTATCTTTAAATCTATTTATTTGATCTCTACAAACAGTGCAGCAAAA 885
QY 988 AATACCAAGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1047
Db 886 GGTAAACCA---AAATGTTGAAGTTAAATTTGGGTGAGACTACGTTAGCAAAATATTTAAT 942
QY 1048 GTTGAATATCAA---AGACCTAAACGAAAATCGGACTGCTAAACCTTCAAAGTATGTTTACA 1104
Db 943 ATTCATATTTAGGTGGAGTTAGAGATAATTTGGGGAGTAAACAGCTAATGTTGCAATTTGAT 1002
QY 1105 AATATAGATACGAAAAATCATACAGTTGAGCAAAAGATTTATTTAAACCTCTTCGTTAT 1164
Db 1003 ACTTTAAATAAAGTAGATGAGTGGGAAAATTTAGTCAVTTTGGGTATCATGAAACCTTAAAC 1062
QY 1165 TCAGCCAAGGAAACAAATGTAATATTTTCAGGGAATGTTGATGAAAGTTTCAACAATTTATA 1224
Db 1063 TCGTTAAGCTCTGTGACAGTAACTGGTCAAGTAACTAAAGGAAATTAACACGAGGTTAAT 1122
QY 1225 GACGATACCAATAATTTAAAGTTTATTAAGGTTGGAGATAATCAAAATTTTACCAGATAGT 1284
Db 1123 AATCCACAGTTTAAAGTTATATAACACATTTGGTTCCAGACGATTTAGCTGAAAGCGTATAT 1182
QY 1285 AACAGAAATTTATGATTAACAGTGAATATGAAGATGTCACAAATGATGATGATGATGATGATG 1344
Db 1183 GCAAAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1242
QY 1345 GGAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1404
Db 1243 GATACAAATGTTGGTGTATTTCTTTAAACTTTTAATATTTTAGACCAAGTAAGAAATATGTA 1302
QY 1405 GTTATTAGTAAATATGACCCCTAATAAGGATGATTAACAGACTATACAGCAAACTGTGACA 1464
```



Db 1303 ATAAATATGAGGGTATTATGATTCATGCTAGCACTTAGAATTTCAACACACCTT 1362  
QY 1465 ATGCAGCAGCTATAAATAGTAGTACTACTGGTGGAGTTTA 1501  
Db 1363 TTGGATATTAATACTATTATTATATACAGTAATTTAA 1399

## RESULT 12

US-10-517-441-691/c  
; Sequence 691, Application US/10517441  
; Publication No. US20060121467A1  
; GENERAL INFORMATION:  
; APPLICANT: FOKENS, John  
; APPLICANT: HARBECK, Nadia  
; APPLICANT: KOENIG, Thomas  
; APPLICANT: MAIER, Sabine  
; APPLICANT: MARTENS, John  
; APPLICANT: MODEL, Fabian  
; APPLICANT: NIMMICH, Inko  
; APPLICANT: RUJAN, Tamas  
; APPLICANT: SCHMITT, Armin  
; APPLICANT: SCHMITT, Manfred  
; APPLICANT: LOOK, Maxine P.  
; APPLICANT: MARK, Almuth  
; APPLICANT: HOFELER, Heinz  
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel  
; FILE REFERENCE: 47675-93  
; CURRENT APPLICATION NUMBER: US/10/517,441  
; CURRENT FILING DATE: 2004-12-11  
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: DE 10317955.0  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: DE 10300096.8  
; PRIOR FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: DE 10245779.4  
; PRIOR FILING DATE: 2002-10-01  
; NUMBER OF SEQ ID NOS: 2147  
; SEQ ID NO 691  
; LENGTH: 5493  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-517-441-691

Query Match 5.1%; Score 89.2; DB 6; Length 5493;  
Best Local Similarity 43.7%; Pred. No. 5.7e-09;  
Matches 439; Conservative 0; Mismatches 563; Indels 2; Gaps 1;  
QY 14 AAAGATGATGTGATCATATATATCATGCTAATAACACCGACGAGTATACCAATTA 73  
Db 5476 AAAAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 5417  
QY 74 TTAATAAAGACGAATACTACGATGGATGAAAAACGCTCAGAGATAGAACAG 133  
Db 5416 AAAAAACACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5357  
QY 134 AGTCAACAAATGTAGTGAAGAGCAACATTTTACAAAGACCCCTCAAGATA 193  
Db 5356 AACATCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5297  
QY 194 ATACTCATCTTACAGAGAGAGGTAAAGATTCCTCATCGATCGATCCTCAATTCAT 253  
Db 5296 AAAAAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5237  
QY 254 CAATTGATCTGCCAACACCATCTCACACACATTAATAATAGAGAGATCTGTTCAA 313  
Db 5236 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5177  
QY 314 CAAGTGATAATGTAGAAGATTACACAGTATCAGATTTTGTAACTCTA-AAATAAAGA 371

Db 5176 AAAAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5117  
QY 372 GAGTAACTGATCTGGTAAAGAGAGAAATCTATAGAGCACTTAATAAAGTAAAGA 431  
Db 5116 CACCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5057  
QY 432 AGATTCAACACACAGTCAAGCGCTGGCTATACAAATATAGATGAAAAATTTTCAATCA 491  
Db 5056 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4997  
QY 492 AGATGAGTTTAAATTTTACCAATTAATGAATATGAATAAAGCTAGACCATATCTAC 551  
Db 4996 AAATACAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4937  
QY 552 AACATCTGCCCAACCATCGATTAAAGCTGTAAACCGTAAATCAATTAGCGCGGACAGG 611  
Db 4936 CAAAAATAAATCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4877  
QY 612 TTCGAATGTTAAACCATTTTAAATTTAAAGTTTACTGATCAAAAGTATTACTGAAGGATATGATGA 671  
Db 4876 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4817  
QY 672 TAGTGAAGTGTATTAAAGCAGATGCTGCTGAAATCTTAAATCTATGATGATCTTTGA 731  
Db 4816 CAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4757  
QY 732 AGTAGATGATAGGTGAAATCTGGTGATGATGATGATGATGATGATGATGATGAT 791  
Db 4756 ATACAAAAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4697  
QY 792 TCCATCAGATTTAACCGGATAGCTTTTACAAATACCAAAATAAAGATTAATCTTGAGAAAT 851  
Db 4696 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4637  
QY 852 CATCGCTACAGTACTTATGATTAACAAAAATAAATAAATAAATAAATAAATAAATA 911  
Db 4636 AAAAAACCAATTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4577  
QY 912 TGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 971  
Db 4576 AAAAAACAAAAACCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCA 4517  
QY 972 AAAGTTCCAAATAATAATACCAAGTTAGATGATGATGATGATGATGATGATGAT 1015  
Db 4516 TAAAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4473

RESULT 13  
US-11-218-305-12130  
; Sequence 12130, Application US/11218305  
; Publication No. US20060141495A1  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO TECHNOLOGY, LLC  
; APPLICANT: McLaird, Paul L.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
; FILE REFERENCE: 38-21 (53660)B  
; CURRENT APPLICATION NUMBER: US/11/218,305  
; CURRENT FILING DATE: 2005-09-01  
; PRIOR APPLICATION NUMBER: US 60/606,880  
; PRIOR FILING DATE: 2004-09-01  
; NUMBER OF SEQ ID NOS: 25043  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12130  
; LENGTH: 2596  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-11-218-305-12130

Query Match 5.1%; Score 88.2; DB 9; Length 2596;



Qy	1342	TTAGGAATAATAATGATGCGAATATTAAATTTTCGTAAATAGATATCACCATATATTATT	1401
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	1366	AAAGAGTACGWSGYSARTTTAAARRATARAATYMMWTAYRARYATCSAAAYGTAGCWAG	1425
Qy	1402	AAAGTTTATTAGTAAATATGACCCTTAA	1427
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	1426	TATTAAATTTTCGTGATATWATMAAAA	1451

```

RESULT 15
US-11-348-413-18588
; Sequence 18588, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 18588
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1651)
; OTHER INFORMATION: WAN01UQ2X; ORF: 000000000000000; Cluster contains WAN014GQJ
; OTHER INFORMATION: ::::
US-11-348-413-18588

```

Query Match	4.6%;	Score 80.6;	DB 9;	Length 1651;
Best Local Similarity	44.9%;	Pred. No. 2.4e-07;		
Matches 310;	Conservative 37;	Mismatches 331;	Indels 13;	Gaps 4;
QY	890	TCACCTATACGTTTACAGATTATCTAGATTAAGTATGAATATATAAAGCACACCTTAAAT	949	
DB	944	TTATTATACATTTACAGACTATGTWRATCTAAAGAWRATGTWAWGCGWMTWTTCACYA	1003	
QY	950	TAAACGTCATACATTTGATPAAAATCAAAGGTTCCAAATATATAACCAAGTTAGATGTAGAAT	1009	
DB	1004	TGCGMGCTTATATTGACCCCTGAAAAATGTTANAAAGACAGGT--AATGTRACATTGRCWA	1060	
QY	1010	ATAAAACGGCCCTTTCATCAGTAAATAAAACAATACCGTTTGAATATCAAGACCTTAAACG	1069	
DB	1061	CTGCGATAGTGTATACAAACAGCAACAAAACAGTATTAGTAGATATTGAAAAATATGGTA	1120	
QY	1070	AAAATCGGACTGCTAACCTTTCAAAGTATGTTTACAAATATAGATACGAAAAATCATACAG	1129	
DB	1121	AGTTTTATACTTATCTATTAAAGGTACAAATTCGACCAAAATCGATAAAAACAAATAATACGT	1180	
QY	1130	TTGAGCAACAGATTATATTAAACCTCTTCGTTA-----TTCAGCCACGAAACAAATG	1183	
DB	1181	ATCGTCAGACAAATTTATGTCAATCCAAGTGGAGATAAAGTTATTGGCCGCGTTTTTAAACAG	1240	
QY	1184	TAAATATTTTCAGGGAATGGTGATGAAGGGTTCAACAAT--TATAGACGATACGACAAATAAT	1242	
DB	1241	GTAATTTAAACCAAAATCGGATAGTAAATGCAATTAATAGATGCAGCAAAATACWAGTATT	1300	
QY	1243	AAAGTTTAAAGGTTGGAGATAATCAAAAATTTCCAGATAGTAAACGAAATTTATGATTAAC	1302	
DB	1301	AAAGTATATAAAGTGWGATAATGCAKCGWATTTTCTGAAAAGTTATYTTGTGTGAATCCAGAW	1360	

Qy	1303	AGTGAATATCAAGATGTCACAAATGATGATTATGCCCAATTAGGAATAATAATGATGTCG	1362
Db	1361	A---ACCTTGARGATGTCACCTAGTGTGAAATATTACATTCCTCCNAATCCAAATCAATAT	1417
Qy	1363	AATATTAAATTTTCGTAAATAGAGATTCCACCATATATTATTAAAGGTATTAGTAAATATGAC	1422
Db	1418	AAAGTAGAGTTAAATACGCCCTGATGATCAAAATWACAACACCPATATATGCTAGTTGTTAAT	1477
Qy	1423	CCTAATAAGAGTGAATTACAGCATCTATACAGCAAACTGTGCACAATGCAGACGACTATAAT	1482
Db	1478	GGKCATATTGATCCCAATAGYAAAGGTGATTTTAGCTTTTACGTTTCAACTTTATATGGRTAT	1537
Qy	1483	GAGTATACTGGTGAGTTTATGAACAGCATCCTATGATAATAACAATTCGTTTCTCTACAAAGT	1542
Db	1538	RAYTCRAKWTWTGWTGGMGMTCAWTGTCATGGGAYAYGAAGTAGCATTTAATTAACGGA	1597
Qy	1543	TCAGGTCGAAGGAACAAGGTGACTTTGGCTCCCTG	1573
Db	1598	TCAGGTTCTGGTGACGGTATCGATAAAACCTG	1628

Search completed: August 14, 2006, 05:58:03  
Job time : 425 secs

**This Page Blank (uspto)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2006, 03:46:35 ; Search time 8720 Seconds  
(without alignments)

11196.692 Million cell updates/sec

Title: US-10-806-288-12

Perfect score: 1746

Sequence: 1 tctagtgtatgaagaaagaa.....ggaatatcatattgatgga 1746

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_estc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gsa1:*
12: gb_gsa2:*
13: gb_gsa3:*
14: gb_gsa4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query	ID	Description
C 1	153.6	8.8	1811	12	CG753732
C 2	151.8	8.7	1690	10	DV791571
C 3	150.2	8.6	1721	9	DR145459
4	148	8.5	1446	10	DT961541
5	147.6	8.5	1784	12	CL081992
6	146.8	8.4	1576	10	DT951966
7	146	8.4	1896	10	DV780693
8	145.6	8.3	1578	10	DV791374
C 9	145.2	8.3	1453	14	AJ591978
C 10	144.2	8.3	1407	14	AJ592026
C 11	143.8	8.2	1491	12	CG753221
12	143.6	8.2	1594	12	CL078613
13	143.4	8.2	1531	12	CG748014
14	142.8	8.2	2001	12	CL118787
15	140.8	8.1	1335	10	DT967478
16	140.8	8.1	1459	9	DN726869
17	140.6	8.1	1425	10	DT954130
C 18	140.6	8.1	1981	12	CL082000
19	140.4	8.0	1409	10	DV791907

```
20 140.4 8.0 1447 10 DT991756
21 140.2 8.0 1421 10 DT967391
22 140.2 8.0 1434 12 CL187638
C 23 139.8 8.0 1507 14 AG346189
24 139.8 8.0 1536 12 CL078538
25 139.6 8.0 1367 10 DT961562
26 139.6 8.0 1663 10 DT954172
27 139.4 8.0 1599 12 CL083840
C 28 139.2 8.0 1434 14 AJ592058
29 139.2 8.0 1632 12 CL082569
30 138.8 7.9 1256 12 CL119201
31 138.8 7.9 1594 12 CL038406
32 138.8 7.9 1654 12 CL118709
33 138.6 7.9 1938 9 DR142277
C 34 138.4 7.9 1566 12 CG757757
35 138.2 7.9 1616 12 CL081995
36 138 7.9 1687 1 AM090701
37 137.6 7.9 1447 9 DN698671
C 38 137.2 7.9 1482 14 AG332292
39 137.2 7.9 1498 10 DT953051
C 40 136.6 7.8 1519 14 AG386893
41 136 7.8 1373 10 DT965616
42 136 7.8 1727 12 CL114085
43 135 7.7 1340 10 DT970091
44 134.8 7.7 1403 10 DT961588
45 134.2 7.7 1377 10 DV795941
```

#### ALIGNMENTS

```
RESULT 1
CG753732/c
LOCUS
DEFINITION
P048-4-G03-ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
ACCESSION
CG753732
VERSION
CG753732.1 GI:37978509
KEYWORDS
GSS.
SOURCE
Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
1 (bases 1 to 1811)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
JOURNAL
Mol. Genet. Genomics 269 (5), 715-722 (2003)
PUBMED
12884007
COMMENT
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
```

FEATURES  
source

```
1..1811
Location/Qualifiers
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."
```

ORIGIN

Query Match 8.8%; Score 153.6; DB 12; Length 1811;  
Best Local Similarity 37.3%; Pred. No. 8.2e-20;  
Matches 539; Conservative 0; Mismatches 904; Indels 1; Gaps 1;

```
DT991756 CNB157-D0
DT967391 CLJ110-D0
CC187638 CH261-98P
AG346189 Mus muscu
CL078538 CH216-151
DT961562 CFW175-F0
DT954172 CFW131-F0
CL083840 ISB1-2H14
AJ592058 Arabidops
CL082569 CH216-167
CL119201 ISB1-76J1
CL038406 CH216-46A
CL118709 ISB1-72I1
DR142277 49191190
CG757757 P053-1-D0
CL081995 CH216-165
AM090701 AM090701
DN698671 CLJ18-H11
AG332292 Mus muscu
DT953051 CFW124-H0
AG386893 Mus muscu
DT965616 CFW159-H0
CL114085 ISB1-59J1
DT970091 CLJ126-D1
DT961588 CFW175-G0
DV795941 Hw_Loin_1
```





/note="Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; oligo  
dt priming from poly A+ RNA, directionally cloned"

ORIGIN

Query Match 8.6%; Score 150.2; DB 9; Length 1721;  
Best Local Similarity 42.2%; Pred. No. 3.8e-19;  
Matches 641; Conservative 0; Mismatches 877; Indels 0; Gaps 0;

QY 8 ATGAGAAAAGATGATGTGATCAATAATAATCACTCAATAAACCACCGACGATTAATACC 67  
DB 142 AAAAAAAAAAAGAAAAAAGAAAAAANNNNAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 201

QY 68 AAATAATTTAAAAAAGAAAGAAAGAACTACTACGATGGCATAGAAAAACGCTCAGAGATA 127  
DB 202 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 261

QY 128 GAACAGAGTCAACAAATGTAGATGAAACGAAAGCAACATTTTTCACAAAGACCCCTC 187  
DB 262 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 321

QY 188 AAGATAATCTCATCTTACAGAGAGAGAGGTAAAGAAATCCTCATCGTCAATCTCTCAA 247  
DB 322 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 381

QY 248 ATTCAATCAATTCATCTGCCCAACCAACCATCTCACACAACTAATAATAGAGAACTCG 307  
DB 382 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 441

QY 308 TTCAACCAAGTGATATGTAGAAGATTCCACAGTATCAGATTTTTCGCTAACTCTAAAA 367  
DB 442 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 501

QY 368 AAGAGAGTAACTGTAATCTGTGAAGAGAGAGATCTATAGAGCAACCTTAATAGTAA 427  
DB 502 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 561

QY 428 AAGAGATTCAACCAAGTCAAGCTGCGCTGTGCTATACAAATATAGATGAAAAATTTCAA 487  
DB 562 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 621

QY 488 ATCAAGATGAGTTATTAATTTACCAATTAATGAATATGAAANTAAAGCTTAGACCTTAT 547  
DB 622 NAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 681

QY 548 CTACACATCTGCCCAACCATCGATTAAACGTGTAACTGTAACCTTAATCAATTACGGCG 607  
DB 682 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 741

QY 608 AAGGTTCCGATGTTAACCATTTTAATTAAGTTTACTGATCAAGTATTTACTGAAGGATATG 667  
DB 742 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 801

QY 668 ATGATAGTGAAGGTGTTATTAAAGCACATGATGCTGAAACCTTAATCTATGATGTAAC 727  
DB 802 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 861

QY 728 TTGAAGTAGATGATAGGTGAATCTGTGTATACGATCAGATGATAGATAGATAGATA 787  
DB 862 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 921

QY 788 CAGTTCCATCAGATTTTAAACCGATAGCTTTCAATACCAAAATAAAGATTAATCTCGAG 847  
DB 922 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 981

QY 848 AAATCATCGCTACAGGTCTTTATGATAACAAAAATAAACAAATCACTTATCTTTTACAG 907  
DB 982 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1041

QY 908 ATTATGTAGATAGTATGATAATTAAGACACACCTTTAAATTAACGTCATACATGATA 967  
DB 1042 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1101

QY 968 AATCAAGGTTCCAAATAATAACCAAGTTAGATGTAGATAATAAAGCGCCCTTTCAT 1027

DB 1102 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1161

QY 1028 CAGTAAATAAACAATTACGGTTGAATATCAAGACCTCAAGAAAAATCGGCTCTCAACC 1087

DB 1162 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1221

QY 1088 TTCAAAGTATGTTTACAAATATAGATACGAAATCATACAGTTTGAGCAACGATTTATA 1147

DB 1222 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1281

QY 1148 TTAAACCTCTTCGTTATTTCAGCCAAGGAAACAAATGTAATATTTTCAGGGAATCGTGATG 1207

DB 1282 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1341

QY 1208 AAGTTTCAACAATATATAGACGATAGCAACAATAATTAAGTTTATAAGGTTGGAGATATC 1267

DB 1342 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1401

QY 1268 AAAATTTTACCAGATAGTAACAGAAATTTTATGATTACAGTGAATATGAGATGTCACAAATG 1327

DB 1402 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1461

QY 1328 ATGATTATGCCCAATTTAGGAAATAATAATGATGTGAATATTTAATTTTCGTAATATAGATT 1387

DB 1462 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1521

QY 1388 CACATATATTTAAAGTTTATTAGTAAATATGACCCCTAATAAGGATGATTACACGACTA 1447

DB 1522 AAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1581

QY 1448 TAGAGCAAACTGTGCACAAATCGACGACTAATAATGAGTATCTGCTGAGTTTAGACAG 1507

DB 1582 NAAAAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 1641

QY 1508 CATCCTATGATAATAACAA 1525

DB 1642 AAAAAAAAAAAGAAAAAAGAAAA 1659

RESULT 4  
DT961541  
LOCUS CFW175-E07 1446 bp mRNA linear EST 21-SEP-2005  
DEFINITION CFW175-E07 3', mRNA sequence.  
ACCESSION DT961541  
VERSION DT961541.1 GI:76034365  
KEYWORDS EST.  
SOURCE Gasterosteus aculeatus (three spined stickleback)  
ORGANISM Gasterosteus aculeatus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;  
Gasterosteidae; Gasterosteus.  
REFERENCE 1 (bases 1 to 1446)  
AUTHORS Kingaley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,  
Schmutz,J. and Myers,R.M.  
TITL Expresed sequence tags from Gasterosteus aculeatus  
JOURN Unpublished (2003)  
COMMENT Contact: Grimwood, Jane  
Stanford Human Genome Center  
Stanford University School of Medicine  
975 S California Ave, Palo Alto, CA 94304, USA  
Tel: 650 320 5917  
Fax: 650 320 5801  
Email: Jane@shgc.stanford.edu  
Plate: 175  
High quality sequence start: 97  
High quality sequence stop: 320.  
Location/Qualifiers  
FEATURES  
source 1. 1446  
/organism="Gasterosteus aculeatus"  
/mol\_type="mRNA"



/strain="Conner Creek sticklebacks, WA USA"

/db\_xref="taxon:69293"

/clone="CFW175-E07"

/sex="mixed male and female"

/tissue type="gills"

/dev stage="adult"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="SHGC-CFW"

/notes="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTTCAGTCGAGCGGCCCTT25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5' prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: [http://www.openbiosystems.com/cdna\\_library\\_construction\\_fa\\_q.php#8](http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8) The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: <http://www.openbiosystems.com/stickleback>"

# ORIGIN

Query Match 8.5%; Score 148; DB 10; Length 1446;  
Best Local Similarity 41.3%; Pred. No. 1e-18;  
Matches 556; Conservative 0; Mismatches 790; Indels 0; Gaps 0;

```

QY 7 GATGAAGAAAGATGATGTCATATATATCATCTCAATTAACACCGACGATATATAC 66
DB 84 GATAATGATGATCGTTCGTGCTAGTAAATATATATATATATATATATATATAT 143

QY 67 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 126
DB 144 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 203

QY 127 AGAACHGAGTCAACAAATGTAGTAAAGAGAGCAACATTTTACAAAGCCCTT 186
DB 204 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 263

QY 187 CAAGATAATCTCATCTTACAGAGAGAGGTAAGAGATCTCATCTGCGAATCTCA 246
DB 264 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 323

QY 247 AATTTCATCAATTGATCTGCCCAACACCATCTCACACCAATTAATAGAGAATCT 306
DB 324 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 383

QY 307 GTTCAACCAAGTGATATGTAGAGATTCACAGTATCAGATTTTGCTTAATCTTAAATA 366
DB 384 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 443

QY 367 AAGAGAGTAACTCACTGAATCTGGTAAAGAGAGATCTATAGAGCACTTAATAGTA 426
DB 444 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 503

QY 427 AAGAGAGATTCACCAACAGTCAGCGCTCGGTCTATACAAATATAGATCAAAAAATTTCA 486
DB 504 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 563

QY 487 AATCAAGATGAGTTATTAATTTACCAATTAATGAATATGAATAAGGCTAGACCATTA 546
DB 564 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 623

QY 547 TCTACACATCTGCCCAACCATCGATTAACCGTGTAAACCGTAAATCAATTACGGCGGNA 606
DB 624 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 683

```

```

QY 607 CAAGGTTCCGAATGTTAAACCAATTTAAATTAAGTTTACTGATCAAAAGTATTACTGAAGGATAT 666
DB 684 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 743

QY 667 GATGATAGTGAAGGTTTATTAAAGCAGCATGATGCTGGAACCTTAATCTATGATGTAAT 726
DB 744 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 803

QY 727 TTGGAAGTAGATGATAAGGTTGCTGCTGATACGATCAGTGGATAGTATAGTATAGTAT 786
DB 804 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 863

QY 787 ACAGTTTCCATCAGATTTTACCCGATAGCTTTTACAATACCAAAATATAAAGATATTTCTGGA 846
DB 864 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 923

QY 847 GAAATCATCGCTACAGGTTACTTATGATTAACAAATAAACAATCACTATATCTTTTACA 906
DB 924 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 983

QY 907 GATTATGTAGATAGTATGAAATATTAAGGCACACCTTTAAATTTACGTCATACATTTGAT 966
DB 984 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1043

QY 967 AATCAAGGTTTCCAAATTAATATACCAAGTTTAGATGTAGAATATATAAACGGCCCTTTTCA 1026
DB 1044 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1103

QY 1027 TCAGTAAATAAACAATTCAGGTTGAATATCAAGACCTTAACGAAATCGGACTGCTAAC 1086
DB 1104 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1163

QY 1087 CTTCAAGTATGTTTACAAATATAGTACGAAATATCATACAGTTGAGCAACGATTTAT 1146
DB 1164 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1223

QY 1147 ATTAACCTCTCTCGTTATTTCAGCCCAAGGAAACAAATGTAATATTTTCAGGGAATGCTGAT 1206
DB 1224 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1283

QY 1207 GAAGTTCAACAAATTTATGACGATAGCACAATAATTAAGTTTAAAGTTGAGGATAAT 1266
DB 1284 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1343

QY 1267 CAABATTTTACAGATAGTAAACAGATTTTATGATTACGTTGATATGAGATGTCACAAAT 1326
DB 1344 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1403

QY 1327 GATGATTATGCCCAATTAGGAATAA 1352
DB 1404 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1429

```

## RESULT 5

LOCUS

CL081992 CH216-165M9 1784 bp DNA linear GSS 31-DEC-2003

DEFINITION CH216-165M9, RM4.1 CH216 Xenopus tropicalis genomic clone

ACCESSION CH216-165M9, genomic survey sequence.

VERSION CL081992

KEYWORDS CL081992.1 GI:40537905

SOURCE GSS.

ORGANISM Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 1784)

AUTHORS Krenitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)

COMMENT Contact: Richard K Wilson

Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@watson.wustl.edu  
Insert Length: 175000 Std Error: 0.00  
Seq primer: RM4 ctcaaggcgatcggtcgagc  
Class: BAC end  
High quality sequence start: 409  
High quality sequence stop: 503.

## FEATURES

Location/Qualifiers

source

1..1784  
/organism="Xenopus tropicalis"  
/mol\_type="genomic DNA"  
/strain="Nigerian frog"  
/db\_xref="taxon:8364"  
/clone="CH216-16SM9"  
/sex="male"  
/cell\_line="Stock 248 F7A2, inbred N7"  
/clone\_lib="CH216"  
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis BAC library"

## ORIGIN

Query Match 8.5%; Score 147.6; DB 12; Length 1784;  
Best Local Similarity 44.4%; Pred. No. 1.2e-18;  
Matches 636; Conservative 0; Mismatches 795; Indels 2; Gaps 1;  
QY 11 AAGAAAAGATGATGTGATCAATAATTAATCAGTCAATTAACACCGACGATTAATACCAA 70  
DB 309 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAG 368  
QY 71 TAAATTAAGAAAAAGAACGATTAACGATGCGATAGAAAAAGCGCTCAGAGATAGAA 130  
DB 369 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 428  
QY 131 CAGAGTCAACAAATAGATGAAAAAGCAACATTTTACAAAGACCCCTCAAG 190  
DB 429 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 488  
QY 191 ATATACATCTTTACAGAGAGGGTTAAAGAACTCTCATGCTGATGCAATCTCAAT 250  
DB 489 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 548  
QY 251 CATCAATTTGATCTGCCCAACACCATCTCACAAACAATAAATAGAGAAATCTGTT 310  
DB 549 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 608  
QY 311 AAACAAGTGAATGTAGAGATTACACGCTATCAGATTTTGTCACTCTAAAAATAAAG 370  
DB 609 ATAAAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 668  
QY 371 AGAGTAACTGAATCTGTAAAGAGAGATCTATAGACCAACCTTAATTAAGTAAAG 430  
DB 669 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 728  
QY 431 AAGATTCAACCAAGTCAAGCGCTGCGCTATACAAATATAGATGAAAAATTTTCAAT 490  
DB 729 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 788  
QY 491 AAGATGAGTTTAAATTTACCAATAAATGAATATGAAAAATAAGCTAGACCAATTTCTA 550  
DB 789 ATAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 848  
QY 551 CAACATCTGCCCAACCATCGATTAAACGTTAAACGTTAAATCAATTAAGCGGCGGAACAG 610  
DB 849 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 908  
QY 611 GTTCGATGTTTAAACCATTTTAAAGTTACTGATCAAGATTAATTAAGAGATATGATG 670  
DB 909 GAAAAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 968  
QY 671 ATAGTGAAGGTGTTTATTAAAGCACATGATCTGAAAACTTTAATCTATGATGAATTTTG 730  
DB 969 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1028

QY 731 AAGTAGATGATAGGTGAATCTGGTATACGATGACAGTGGATATAGATAGATACAG 790  
DB 1029 ATAAAGAAATAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1089  
QY 791 TTCATCAGATTTTAAACCGATAGCTTTTACAATACCAAAATAAAGATAAATCTCGAGAAA 850  
DB 1089 AAAGAAAAATTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1148  
QY 851 TCATCGCTACAGTACTTATGATAACAAATAAACAATCACTATATCTTTTACAGATT 910  
DB 1149 ATAAAAATAAATAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGATA 1208  
QY 911 ATGTAGATAGTATGAATAATTTAAAGCACACCTTTAAATTAACGTCATACATTTGATTAAT 970  
DB 1209 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1268  
QY 971 CAAAGGTTTCCAAATAAT - AATACCAAGTTAGATGTAGAATATAAAGCGGCCCTTTTCATC 1028  
DB 1269 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1328  
QY 1029 AGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1388  
DB 1329 AAGATATAGAAAGAAAAATAATATAAATAAAGAAAAAATAAATAAATAAATAAATAA 1388  
QY 1089 TCAAGTATCTTTTACAATAATATAGATAGAAAAATCATACAGTTGAGCAACGATTTATAT 1148  
DB 1389 AAAAAATGATAAAGAAAAAATAAATAAATAAAGAAAAAATAAATAAATAAATAAATAA 1448  
QY 1149 TAACCCCTCTTCTGTTATTTCAGCAGGAAAAACAATGTAAATATTTTCAGGGAATGCTGATGA 1208  
DB 1449 AATGAAAAAGAAAAAATAAATAAATAAAGAAAAAATAAATAAATAAATAAATAAATAA 1508  
QY 1209 AGGTTTCAACAATATAGACGATAGCACAAATAATTAAGTTTATTAAGTTGAGAGATAATCA 1268  
DB 1509 AAAGAAGAAAAAATAAATAAATAAATAAAGATAGTATAAATAAATAAATAAATAAATAA 1568  
QY 1269 AATTTTACCAGATAGTAAAGAAATTTATGATTCAGTGAATATGAAGATGTCACAAATGA 1328  
DB 1569 AGAAAGAAATAATAGAAAAAATAAATAAATAAAGTAAAGATAGAAATAGTAGGAAAAA 1628  
QY 1329 TGATTATGCCCAATTTAGGAAATAATATGATGTGAATATTAATTTTGGTAAATATAGATTC 1388  
DB 1629 TAATAATATAAATAAAGATGAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1688  
QY 1389 ACCATATATTATTAAGTTTATAGTAAATATGACCCCTTAATAAGGATGATTACA 1441  
DB 1689 ATAATAATAATAATAAAGAAAAAGAAAAAAGAAAAAAGAAAAAATAAAGAGATA 1741

## RESULT 6

DT951966

LOCUS

DEFINITION

CFW118-D11.x1d-t SHGC-CFW Gasterosteus aculeatus cdna clone

CFW118-D11 3', mRNA sequence.

DT951966.1 GI:76024790

EST.

Gasterosteus aculeatus (three spined stickleback)

Gasterosteus aculeatus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;

Gasterosteidae; Gasterosteus.

1 (bases 1 to 1576)

Schultz, J. and Myers, R. M.

Expressed sequence tags from Gasterosteus aculeatus

Unpublished (2003)

Contact: Grimwood, Jane

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Ave, Palo Alto, CA 94304, USA

Tel: 650 320 5917  
 Fax: 650 320 5801  
 Email: jane@shgc.stanford.edu  
 Plate: 118  
 High quality sequence start: 133  
 High quality sequence stop: 453.  
 Location/Qualifiers

# FEATURES

## source

1. 1576  
 /organism="Gasterosteus aculeatus"  
 /mol\_type="mRNA"  
 /strain="Conner Creek sticklebacks, WA USA"  
 /db\_xref="taxon:69293"  
 /clone="CFW18-D11"  
 /sex="mixed male and female"  
 /tissue\_type="gills"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="SHGC-CFW"  
 /notes="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTTCTAGATCGGAGCGGCCCTT25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:  
<http://www.openbiosystems.com/cdna.library.constructionfaq.php#8>  
 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems:  
<http://www.openbiosystems.com/stickleback>"

## ORIGIN

Query Match 8.4%; Score 146.8; DB 10; Length 1576;  
 Best Local Similarity 39.1%; Pred. No. 1.8e-18;  
 Matches 532; Conservative 0; Mismatches 828; Indels 0; Gaps 0;

QY 11 AAGAAAAGAAATGATGTGATCAATAATAATCACTCAATAAACCCGACGATATAACCAA 70  
 |||||  
 Db 203 AA 262

QY 71 TAAATTAAGAAAGAAACGAATAACTACGATGGCAGAAACCGCTCAGAAAGATAGAA 130  
 |||||  
 Db 263 AA 322

QY 131 CAGAGTCACACAAATGTAGATGAACGAGACACATTTTACAAAGACCCCTCAAG 190  
 |||||  
 Db 323 AA 382

QY 191 ATAATACCTCATCTTACAGAAAGAGGTAAAGAAATCCTCATCGATCCTCAAAAT 250  
 |||||  
 Db 383 AA 442

QY 251 CATCAATTGATACCTGCCCAACCACTCTCACACAACTAATAATAGAGAAATCTGTT 310  
 |||||  
 Db 443 AA 502

QY 311 AAACAGTGATTAATGTAGAGATTACACGATATCAGATTTTCTTAATTAAG 370  
 |||||  
 Db 503 AA 562

QY 371 AGAGTAACACTGAATCTGTGTAAGAGAGAAATCTATAGAGCACTTAATAAGTAAAG 430  
 |||||  
 Db 563 AA 622

QY 431 AAGATTCAACAAAGTCAGCGCTCTGGCTATACAAATATAGATGAAATTTTCAATC 490

Db 623 AA 682

QY 491 AAGATCAGTTATTAATTTTACCAATAAATGAATATGAAATATAGGCTAGACCTTATCT 550  
 |||||

Db 683 AA 742

QY 551 CAACATCTGCCCAACCATCGATTTAAACGTGTACCGTAAATCAATTTAGCGGCGAACAAG 610  
 |||||

Db 743 AA 802

QY 611 GTTCGAATGTTAACCATTTTAAAGTTACTGATCAAAAGTATTACTGAAGGATATGATG 670  
 |||||

Db 803 AA 862

QY 671 ATAGTAGAGGTGTTATTAAAGCACATGATGCTGGAACCTTAATCTATGATGTAACCTTT 730  
 |||||

Db 863 AA 922

QY 731 AAGTAGATGATAAGGTGAAATCTGGTGATACCATGACAGTGGATATAGATATAGAAATACAG 790  
 |||||

Db 923 AA 982

QY 791 TTCCATCAGATTTAACCGATAGCTTTTCAATACCAATAATAAAAGATAATTTCTGGAGAA 850  
 |||||

Db 983 NNNAAA 1042

QY 851 TCATCGCTCAGGTACTTATGATACAAAAATAAACAATCACCTATCTTTTACAGATT 910  
 |||||

Db 1043 AA 1102

QY 911 ATGTAGATAAGTATCAAAATATTAAGGCACACCTTTAAATTTACGTCATACATTGATAAT 970  
 |||||

Db 1103 AA 1162

QY 971 CAAAGTTTCCAAATATAATCAAGTTTAGATGTAGAATATATAAAGCGCCCTTTTCATCAG 1030  
 |||||

Db 1163 NNAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1222

QY 1031 TAAATAAACAATTAACGTTGGATATCAAGACCTTACGAAATCGGATCGCTTAACCTTC 1090  
 |||||

Db 1223 ANNAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1282

QY 1091 AAGTATGTTTCAAAATATAGATACGAAAAATCATACAGTTTCAGCAACGATTTATTTA 1150  
 |||||

Db 1283 AA 1342

QY 1151 ACCCTCTTCTGTTATTCAGCCAAAGGAAACAAATGTAAATATTTTCAGGGAATGCTGATGAAG 1210  
 |||||

Db 1343 AA 1402

QY 1211 GTTCAACAAATTTAGACGATGACACAAATAATTAAGTTTATTAAGTTGGAGATATCAAA 1270  
 |||||

Db 1403 AANNAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1462

QY 1271 ATTTACCAGATAGTAACAGAAATTTATGATACAGTGAATATGAAGTGTCAAAATGATG 1330  
 |||||

Db 1463 NANNNAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1522

QY 1331 ATTATGCCCAATTAGGAAATTAATGATGATGAATATTTAA 1370  
 |||||

Db 1523 NNNAAA 1562

RESULT 7  
 DV780693  
 LOCUS  
 DEFINITION Hw\_FAT\_11\_A12 Bos taurus CF-24-HW fat cDNA library Bos taurus cdna,  
 mRNA sequence.  
 DV780693  
 ACCESSION  
 VERSION DV780693.1 GI:82633569  
 KEYWORDS EST.  
 SOURCE Bos taurus (cattle)



Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

## REFERENCE

1 (bases 1 to 1578)  
Yoon,D.H., Lee,S.H., Park,S.H., Cho,Y.M., Lee,J.H., Kim,H.,  
Kim,H.Y., Park,J.H. and Oh,S.J.

## AUTHORS

Gene Expression Profiling of the Bovine liver, adipose, and  
skeletal muscle

## TITLE

Unpublished (2005)

## JOURNAL

Contact: Dr. Du-Hak Yoon

## COMMENT

National Livestock Research Institute, RDA

564 Omoekchun-dong, Suwon, 441-350, Korea

Tel: 82 31 290 1593

Fax: 82 31 290 1792

Email: dhyoon@rda.go.kr.

Location/Qualifiers

1. .1578

/organism="Bos taurus"

/mol\_type="mRNA"

/db\_xref="taxon:9913"

/sex="Four males mixed"

/cell\_type="myocyte"

/dev\_stage="24 months old"

/lab\_host="XL1-BlueMRF' strain"

/clone\_lib="Bos taurus CP-24-HW loin cDNA library"

/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site\_1:

ECORI; Site\_2: Xho I"

Query Match 8.3%; Score 145.6; DB 10; Length 1578;

Best Local Similarity 39.4%; Pred. No. 3.1e-18;

Matches 535; Conservative 0; Mismatches 824; Indels 0; Gaps 0;

QY 11 AAGAAAAGAAATGATGTGATCAATAATAATCAGTCAATAAACCCGACGATATAACCAA 70

DB 214 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 273

QY 71 TAAATTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 130

DB 274 NAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 333

QY 131 CAGAGTCAACAAATGTAGATGAACGAGCAGACATTTTACAAAGACCCCTCAG 190

DB 334 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 393

QY 191 ATAATACTCATCTTACAGAAAGAGGTAAGAAAGATCCCTCATCGTCAATCTCAA 250

DB 394 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 453

QY 251 CATCAATTTGATCTGCCCAACCAACCATCTCACACAAATAATAGAGAGAAATCTG 310

DB 454 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 513

QY 311 AAACAGTGTATGTAGAGATTCACAGGTATCAGATTTTCTAACTTAAATTAAG 370

DB 514 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 573

QY 371 AGAGTAAACACTGAATCTGGTGAAGAGAAATCTATAGAGCAACTTAATAAGTAAAG 430

DB 574 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 633

QY 431 AAGATTCAACAAAGTCAGCGCTCTGGCTATACAAATATAGATGAAATTTCAATC 490

DB 634 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 693

QY 491 AGATGAGTTATTAATTTACCAATAATGAATGTGAATTAAGGTAGACCATTTATCT 550

DB 694 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 753

QY 551 CAACATCTGCCCAACCATCGATTAAACCGTGAACCGTCAATCAATTTAGCGGGAAC 610

DB 754 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 813

QY 611 GTTCGAATGTTAAACCATTTTAAAGTTTACTGATCAAGTATTACTGAAGGATGATG 670

814 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 873

QY 671 ATAGTGAAGGTCTTATTAAAGCACATGATGCTGAAACCTTAATCTATGATGTAAC 730

DB 874 NNANANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 933

QY 731 AAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAGTCAGATATAGATAAGAA 790

DB 934 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 993

QY 791 TTCCATCAGATTTAAACCGATAGCTTTTCAATACCAAAATAAAGATTAATTTCTG 850

DB 994 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1053

QY 851 TCATCGTCTACAGGTACTTATGATAACAAAAATAAACAATCACTTACTCTTACAG 910

DB 1054 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1113

QY 911 ATGTAGATAAGTATGAAATATTAAGACACACCTTTAAATTAACGTCATACATTTG 970

DB 1114 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1173

QY 971 CAAAGGTTCCAAATTAATATCAAGTTAGATGTAGATATATAAAGCGCCCTTTCT 1030

DB 1174 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1233

QY 1031 TAAATTAACAATTAACGTTGATATCAAGACCTTAACGAAATCGGACTGCTTAAC 1090

DB 1234 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1293

QY 1091 AAGATGATGTTTCAAAATATAGATACGAAAAATCATACAGTTCAGCAACGATTT 1150

DB 1294 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1353

QY 1151 ACCCTCTTCTGTTTATTCAGCCAGGAAACAAATGTTAAATTTTCAAGGATGTTG 1210

DB 1354 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1413

QY 1211 GTTCAACATTTATACAGCTAGCACAATAATTAAGTTTATAGGTTGGAGATATCA 1270

DB 1414 NNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1473

QY 1271 ATTTACCAAGTAGTAACAGAAATTTATGATTACAGTGAATATCAAGATGTCA 1330

DB 1474 NAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1533

QY 1331 ATTATGCCCAATTAGGAAATTAATATGATGTAATTTA 1369

DB 1534 AAAAAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 1572

## RESULT 9

AJ591978/c

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence, right border, clone

59BD01, genomic survey sequence.

ACCESSION

AJ591978.1 GI:37941602

VERSION

GSS; right border; T-DNA flanking sequence.

KEYWORDS

Arabidopsis thaliana (thale cress)

SOURCE

Arabidopsis thaliana

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1

REFERENCE

AUTHORS

Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,

Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,

Lepintec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences

of pre-insertion sites

JOURNAL

EMBO Rep. 3 (12), 1152-1157 (2002)

PUBMED

12446565

```

REFERENCE 2 (bases 1 to 1453)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.inbioigen.fr).
FEATURES
source
1..1453
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="598D01"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
misc_feature
1..1453
/note="T-DNA flanking sequence
right border"
ORIGIN
Query Match 8.3%; Score 145.2; DB 14; Length 1453;
Beat Local Similarity 40.5%; Pred No. 3.7e-18;
Matches 543; Conservative 0; Mismatches 792; Indels 5; Gaps 1;
Qy 14 AAAAGAATGATGTGATCAATAATATACGTCAATAAACCACGACGATAATACCAATAA 73
Db 1344 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1285
Qy 74 TTAATAAGAGAAACGAATTAACGTACGTGCGTAGAAGAAACGCTCAGAGATAGACAG 133
Db 1284 ANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1225
Qy 134 AGTCAACAACAAATGTAGATGAAACGAACGACACATTTTCAAAAGACCCCTCAAGATA 193
Db 1224 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1165
Qy 194 ATACTCATCTTACAGAAGAGAGGTAAAGAAATCCTCATCATGTCGAATCTCAATTCAT 253
Db 1164 ANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1105
Qy 254 CAATTGTATCGCCCAACACATCTCACACACATTAATAGAGAGATCTGTTCAA 313
Db 1104 NAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1045
Qy 314 CAAGTGAATGTAGAAGATTACACAGTATCAGATTTTGCTAACTCTTAAATAAAGAGA 373
Db 1044 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 985
Qy 374 GTAACACTGAATCTGGTAAAGAAGAGATACTATAGAGCAACCTAATAAGTAAAGAAG 433
Db 984 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 925
Qy 434 ATTCAACAACAGTCAGCCGCTGCTGTATACAAATATGATGAAATAATTCAAATCAG 493
Db 924 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 865
Qy 494 ATGAGTTATTAAATTTTACCAATTAATGAATATGAAATAAGCTAGACCATTTCTCAA 553
Db 864 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 805
Qy 554 CATCTGCCCAACCATCGATTAAACGCTGAACCGTAAATCAATTAGCGCGCAACAGTT 613
Db 804 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 745

```

```

Qy 614 CGBATGTTAACCATTTTAATTTAAAGTTACTGATCAAGTATTTACTGAAGGATATGATGATA 673
Db 744 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 685
Qy 674 GTGAAGGTGTTATTAAAGCACATGATGCTGAAAACTTTAATCTATGATGTTAACTTTTGAG 733
Db 684 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 625
Qy 734 TAGATGATTAAGGTGAATCTGGTGATACGATGACAGTGGATATAGATAAGAAATACAGTTC 793
Db 624 ANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 565
Qy 794 CATCAGATTTAACCGATAGCTTTACATACCAAAATATAAGATAATCTCGGAGAAATCA 853
Db 564 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 505
Qy 854 TCGTACAGGTACTTATGATAACAAAAATAACAAATCACTATATCTTTTACAGATATATG 913
Db 504 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 445
Qy 914 TAGATAAGTATGAAAAATTTAAAGCACACCTTTAAATTAACGTCTATACATTGATTAATCAA 973
Db 444 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 385
Qy 974 AGTTCCCAATTAATATACCAAGTTAGATGCTAGATATATAAACGCGCCCTTTTCATCAGTAA 1033
Db 384 ANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 325
Qy 1034 ATAAACAATTTACGGTTGAATATCAAAAGACCTTAAAGAAATCGGACTGTCAACCTTCAA 1093
Db 324 AAAAAAAAAAAAAA-----AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 270
Qy 1094 GTATGTTTACAATATATAGATACGAAATATCATCAGTTGAGCAACCGATTATATTATTAACC 1153
Db 269 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 210
Qy 1154 CTCTTCGTTTTCAGCCCAAGCAACCAATCTAAATATTTTCAGGGAATGGTATCAAGTT 1213
Db 209 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 150
Qy 1214 CAACAATTTATAGCGATAGCACCAATTAATTAAGTTTATAAGTTTGGAGATTAATCAAAATT 1273
Db 149 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 90
Qy 1274 TACCAAGTAGTACAGAAATTTTATGATTTACAGTGAATGATGATGTCACAAATGATGATT 1333
Db 89 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
Qy 1334 ATGCCCAATTAGGAATAAT 1353
Db 29 NNANNNNNAAAAAAAAAANT 10
RESULT 10
AJ592026/c
LOCUS AJ592026
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone
600D05, genomic survey sequence.
ACCESSION AJ592026
VERSION AJ592026.1 GI:37941650
KEYWORDS GSS; right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Brunau,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,P.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)

```

PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
12446565	2 (bases 1 to 1407)	Balzergue, S.	Direct Submission		
		Submitted (23-OCT-2003)	Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE		
		PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <a href="http://dbgap.versailles.inra.fr/publiclines/">http://dbgap.versailles.inra.fr/publiclines/</a> . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' ( <a href="http://www.genoplante.com">http://www.genoplante.com</a> and <a href="http://genoplante-info.infobiogen.fr">http://genoplante-info.infobiogen.fr</a> ).			
FEATURES	Location/Qualifiers				
source	1..1407	/organism="Arabidopsis thaliana"			
		/mol_type="genomic DNA"			
		/db_xref="taxon:3702"			
		/clone="60D05"			
		/clone_lib="Arabidopsis thaliana T-DNA insertion lines"			
		/ecotype="Wassilewskija"			
misc_feature	1..1407	/note="T-DNA flanking sequence right border"			
ORIGIN					
	Query Match	8.3%;	Score 144.2;	DB 14;	Length 1407;
	Best Local Similarity	40.1%;	Pred. No. 5.7e-18;		
	Matches 539;	Conservative 0;	Mismatches 806;	Indels 0;	Gaps 0;
QY	11	AAGAAAGATGATGTCATCAATAATATCAGTCATAAACAACGACGAGATAATACCAAA	70		
Db	1396	AA	1337		
QY	71	TAAATTAAGAGAAACGAATTAATACGATGGCATAGAAAAACGCTCAGAAGATAGAA	130		
Db	1336	AA	1277		
QY	131	CAGAGTCACAACAATATGTAGATGAACAACGAAGCAACATTTTTCACAAAGACCCCTCAAG	190		
Db	1276	AA	1217		
QY	191	ATAATCTCATCTTACAGAGAGAGAGTAAAGATCCTCATCGTCGAATCTCCTCAAT	250		
Db	1216	AA	1157		
QY	251	CATCAATGGATCTGCGCCCAACACCATCTCACACAACATAAATAGAGAGAATCTGTT	310		
Db	1156	AA	1097		
QY	311	AAACAAGTGATAATGTAGAAGATTCAACGCTATCAGATTTTGTCTAACTCTAAATATAAG	370		
Db	1096	AA	1037		
QY	371	AGAGTAACACTGAATCTGGTAAGAAGAGAGATCTATAGAGCAACCTTAATAAGTAAAG	430		
Db	1036	AA	977		
QY	431	AAGATTCAACAACAGTCAGCGCTCTGGCTATACAAATATAGATGAAAAATTTCAATC	490		
Db	976	AA	917		
QY	491	AAGATGAGTTATTAATTTTACCAATAATGAATATGAAAAATAAGGCTAGACCATTTATCTA	550		
Db	916	AA	857		
QY	551	CAACATCTGCCCAACCATTCGATTAAACGCTGTACCGTAAATCAATTAGCGCGGACAAG	610		
Db	856	AA	797		



COMMENT	CONTACT: SOMMER RJ EVOLUTIONARY BIOLOGY MAX-PLANCK-INSTITUTE FOR DEVELOPMENTAL BIOLOGY SPEMANNSTR. 37-39, TUEBINGEN D-72076, GERMANY TEL: 00497071601371 FAX: 00497071601498 EMAIL: RAIF.SOMMER@TUEBINGEN.MPG.DE CLASS: BAC ENDS.
FEATURES	Location/Qualifiers
source	1. .1491
	/organism="Pristionchus pacificus"
	/mol_type="genomic DNA"
	/strain="California"
	/db_xref="taxon:54126"
	/clone_lib="Ppa EcoRI BAC Library"
	/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."
ORIGIN	
	Query Match 8.2%; Score 143.8; DB 12; Length 1491;
	Best Local Similarity 38.9%; Pred. No. 6.9e-18;
	Matches 544; Conservative 0; Mismatches 856; Indels 0; Gaps 0;
Qy	11 AAGAAAAGATGATGTGATCAATAATATCATGTCAATAAACCACGACGATATAACCAA 70
Db	1453 AANNAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1394
Qy	71 TAATTAAAAAGAGAAACGAAATAACTACGATGGCATAGAAAAACGCTCAGACATAGA 130
Db	1393 NNAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1334
Qy	131 CAGAGTCACCAACCAATGTAGATGAACCAAGCAACACTTTTTCACAAAGACCCCTCAAG 190
Db	1333 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1274
Qy	191 ATAATACTCATCTTACAGAAGAGGTAAGAATCCTCATCAGTCGAATCCTCAAT 250
Db	1273 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1214
Qy	251 CATCAATTGATCTGCCCAACACCATCTCACACACATATAATAGAGAAGAACTGTTC 310
Db	1213 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1154
Qy	311 AACCAAGTGATAATGTGAAGATTACACAGTATCAGATTTTGTCTAACTCTAAAA 370
Db	1153 NANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1094
Qy	371 AGAGTAAACACTGAATCTGTGTAAGAAGAGAAATCTATATAGACCACTTAATAAG 430
Db	1093 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 1034
Qy	431 AAGATTCAACCAAGTCAGCGCTGTGGCTATACAAATATAGATGAAGAAATTTCAAT 490
Db	1033 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 974
Qy	491 AAGATGAGTTAATTAATTTTCCCAATTAATGAATATGAAAAATAAGCTAGACCTAT 550
Db	973 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 914
Qy	551 CAACATCTGCCCAACCTCGATTAAACCGTGTAAACCGTAAATCAATTTAGCGCGGA 610
Db	913 ANANANNAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 854
Qy	611 GTTCGAATGTTAACATTTAATTTAAAGTTACTGTATCAAGGTATTACTGAAGGATAT 670
Db	853 ANAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 794
Qy	671 ATAGTGAGGTGTTATTATAAGCACATGATGCTGAAAACTTAATCTATGATGTAACT 730
Db	793 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 734
Qy	731 AAGTAGATGATAAGGTGAAATCTGTGTGATACGATGACAGTGGATATAGATAAGAA 790



[illegible][illegible]







GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 12, 2006, 07:41:21 ; Search time 58.4 Seconds  
(without alignments)

4100.856 Million cell updates/sec

Title: US-10-806-288-12

Perfect score: 3026

Sequence: 1 tctagtatgaagaaga.....ggaaatatcaattgtatgga 1746

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 5179358

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/abs/ABSSWEB spool/US10806288/runat\_11082006\_163403\_21030/app query.fasta\_1  
-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0 1 -LOOPECL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=Blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02p  
-USER=US10806288 @CGN 1 1 440 @runat\_11082006\_163403\_21030 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A Geneseq 8:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3013	99.6	1092	2 AAW41602	AAW41602 Staphyloc
2	3013	99.6	1092	7 ABM79019	ABM79019 Staphyloc
3	2810.5	92.9	892	6 ABU42557	ABU42557 Protein e
4	2810.5	92.9	892	8 ADO84849	ADO84849 S epiderm
5	2810.5	92.9	892	8 ADS20651	ADS20651 S. epider
6	2810.5	92.9	930	5 ABP40469	ABP40469 Staphyloc
7	2810.5	92.9	930	8 ADS06014	ADS06014 Staphyloc
8	2810.5	92.9	991	3 AAY83171	AAY83171 Cell wall

9	2810.5	92.9	991	3 AAY70120	AAY70120 Staph. ep
10	2670	88.2	549	7 ABM79020	ABM79020 Staphyloc
11	2510.5	83.0	560	7 ABM79015	ABM79015 Staphyloc
12	1702	56.2	331	9 AEB23146	AEB23146 Ligand bi
13	1672	55.3	343	7 ABM79016	ABM79016 Staphyloc
14	1562	51.6	316	7 ABM79017	ABM79017 Staphyloc
15	1144.5	37.8	1166	2 AAY08643	AAY08643 S. aureus
16	1142.5	37.8	1166	6 ABJ18982	ABJ18982 Pathogen
17	1137.5	37.6	1141	6 ABU42327	ABU42327 Protein e
18	1116.5	36.9	670	6 ABU42520	ABU42520 Protein e
19	857	28.3	278	4 AAG82803	AAG82803 S. epider
20	795.5	26.3	338	9 AEB23147	AEB23147 Ligand bi
21	576	19.0	1315	2 AAY08642	AAY08642 S. aureus
22	576	19.0	1315	6 ABJ18969	ABJ18969 Pathogen
23	576	19.0	1349	4 AAU37544	AAU37544 Staphyloc
24	576	19.0	1349	4 AAU34402	AAU34402 Staphyloc
25	576	19.0	1349	6 ABM72436	ABM72436 Staphyloc
26	559	18.5	1385	6 ABU16400	ABU16400 Protein e
27	499.5	16.5	932	4 AAU36845	AAU36845 Staphyloc
28	499.5	16.5	932	4 AAU34082	AAU34082 Staphyloc
29	499	16.5	1802	3 AAY83170	AAY83170 Cell wall
30	499	16.5	1802	3 AAY70119	AAY70119 Staph. ep
31	497	16.4	1155	4 AAG82343	AAG82343 S. epider
32	493	16.3	1633	6 ABU42513	ABU42513 Protein e
33	489	16.2	953	6 ABU16533	ABU16533 Protein e
34	486.5	16.1	1920	6 ABU43489	ABU43489 Protein e
35	476	15.7	408	9 AEB23148	AEB23148 Ligand bi
36	455	15.0	841	4 AAU37158	AAU37158 Staphyloc
37	455	15.0	841	4 AAU34283	AAU34283 Staphyloc
38	455	15.0	930	2 AAY08641	AAY08641 S. aureus
39	455	15.0	933	6 ABJ18947	ABJ18947 Pathogen
40	455	15.0	947	6 ABJ18940	ABJ18940 Pathogen
41	455	15.0	995	6 ABM72437	ABM72437 Staphyloc
42	454	15.0	927	6 ABM72221	ABM72221 Staphyloc
43	454	15.0	936	2 AAW89801	AAW89801 Staphyloc
44	452	14.9	933	3 AAY58435	AAY58435 Staphyloc
45	452	14.9	933	4 AAB69508	AAB69508 Staphyloc

ALIGNMENTS

RESULT 1  
AAW41602

ID AAW41602 standard; protein; 1092 AA.

XX AC AAW41602;

XX AC AAW41602;

DT 17-OCT-2003 (revised)

DT 22-JUN-1998 (first entry)

XX Staphylococcus epidermidis fibrinogen binding protein FIG.

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

XX Fibrinogen binding protein; FIG; aggregation; infection;

PD 24-DEC-1997.  
 XX 18-JUN-1997; 97WO-SE001091.  
 XX 20-JUN-1996; 96SE-00002496.  
 XX (GUSS/) GUSS B.  
 PA (NILS/) NILSSON M.  
 PA (FRYK/) FRYKBERG L.  
 PA (FLOC/) FLOCK J.  
 PA (LIND/) LINDBERG M.  
 XX GUSS B, Nilsson M, Frykberg L, Flock J, Lindberg M;  
 XX WPI; 1998-063079/06.  
 DR N-PSDB; AAV04279.  
 XX Fibrinogen-binding protein from coagulase-negative Staphylococcus - used  
 PT for prevention, treatment and diagnosis of Staphylococcus infection.  
 XX Example 3; Fig 6; 45pp; English.  
 XX The protein comprises the fibrinogen binding protein (FIG) of coagulase-  
 CC negative Staphylococcus epidermidis HB. Its amino acid sequence was  
 CC deduced from the isolated fig gene (see AAV04279). The closest known  
 CC analogue of FIG is the clumping factor of *S. aureus* which also binds  
 CC fibrinogen and promotes bacterial aggregation in serum. Recombinant FIG  
 CC polypeptides can be expressed in host cells. They are used as immunogens,  
 CC particularly in vaccines (which may be expressed in vivo) to protect  
 CC humans and animals against coagulase-negative Staphylococcus infection.  
 CC Antibodies raised against FIG can be used for passive immunisation. They  
 CC block the adherence of bacteria) and for diagnosis. (Updated on 17-OCT-  
 CC 2003 to standardise OS field)  
 XX SQ Sequence 1092 AA;  
 Alignment Scores:  
 Pred. No.: 7.5e-222 Length: 1092  
 Score: 3013.00 Matches: 582  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 99.6% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-806-288-12 (1-1746) x AAW41602 (1-1092)  
 QY 1 TCTAGTGATGAGAAAGAAATGATGTGATCAATAATAATCAGTCAATAAACCACGACGAT 60  
 DB 75 SerSerAspGluGluLysAsnAspValIleAsnAsnAsnGlnSerIleAsnThrAspAsp 94  
 QY 61 ANTAACCAATATTAATAAAGAAAGAAACGAATAACTACGATGGCATAGAAAAACGCTCA 120  
 DB 95 AsnAsnGlnIleIleLysLysGluGluThrAsnAsnTyrAspGlyIleGluLysArgSer 114  
 QY 121 GAAGATAGACAGAGTCAACCAAAATGTAGATGAAACCAAGCAACATTTTACAAAAG 180  
 DB 115 GluAspArgThrGluSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 134  
 QY 181 ACCCTCAAGATAATCTCATCTTTACAGAAAGAGAGTAAAGAATCTCTCATCGTCGAA 240  
 DB 135 ThrProGlnAspAsnThrHisLeuThrGluGluValLysGluSerSerValGlu 154  
 QY 241 TCCTCAAAATTCATATGATGATGCTGCCCCAACCAACCATCTCACACAATAAATAGAGAA 300  
 DB 155 SerSerAsnSerSerIleAspThrAlaGlnProSerHisThrThrIleAsnArgGlu 174  
 QY 301 GAATCTGTTCAACAAGTGTATGTAGAGAGTTACACCTATCAGATTTTGTCTAACTCT 360  
 DB 175 GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer 194  
 QY 361 AAAATAAAGAGAGTAACTGATCTGTTAAAGAGAGAGAAATCTATAGAGCAACCTAAT 420  
 DB 195 LysIleLysGluSerAsnThrGluSerGlyLysGluAsnThrIleGluGlnProAsn 214

QY 421 AAGTAAAGAAAGATTCAACAACAAGTCAAGCCTCTGGCTATACAAATATAGATGAAAAA 480  
 DB 215 LysValLysGluAspSerThrThrSerGlnProSerGlyTyrThrAsnIleAspGluLys 234  
 QY 481 ATTTCAAATCAAGATCAGTTATTAAATTTACCAATAAATGAATATGAAAAAAGGCTAGA 540  
 DB 235 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysAlaArg 254  
 QY 541 CCATTATCTACAACATCTGCCCAACCATCGATTAAACCGTGAACCGTAAATCAATAGCG 600  
 DB 255 ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla 274  
 QY 601 GCGGAACAAGGTTGGAATGTTAACCATTTAAATTTAAAGTTACTGATCAAGTATTACTGAA 660  
 DB 275 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 294  
 QY 661 GGATATGATGATGATGCAAGGTGTTATTAAAGCACATGATGCTGAAAACTTTAACTCTATGAT 720  
 DB 295 GlyTyrAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 314  
 QY 721 GTAACCTTTTGAAGTAGATGATGAAGTGAATCTGGTGATACGATGACAGTGGATATAGAT 780  
 DB 315 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAspIleAsp 334  
 QY 781 AAGAATACAGTTCCATCAGATTAAACCGATAGCTTTTACATACCAAAAATAAAGATAAT 840  
 DB 335 LysAsnThrValProSerAspLeuThrAspSerPheThrIleProLysIleLysAspAsn 354  
 QY 841 TCTGGAGAAATCATCGCTCAGGTACTTATGATAACAAAAATAAACAATACACCTATACT 900  
 DB 355 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnLysAsnLysGlnIleThrTyrThr 374  
 QY 901 TTTACAGATTATGTAGATAAGTAAATATTTAAAGCACACCTTTAAATTTAAGCTCATAC 960  
 DB 375 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 394  
 QY 961 ATGTATAATCAAGGTTCCAAATAATAATACCAAGTTAGATGATAGATAATAAAGCGCC 1020  
 DB 395 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 414  
 QY 1021 CTTTCATCAGTAAATAAAACAATTACGGTTGTAATATCAAGACCTAACGAAAAATCGGACT 1080  
 DB 415 LeuSerSerValAsnLysThrIleThrValGluTyrGlnArgProAsnGluAsnArgThr 434  
 QY 1081 GCTAACCTTTCAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAACG 1140  
 DB 435 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 454  
 QY 1141 ATTTATATTAAACCTCTCTGTTATTCAGCCCAAGGAACAATACTTAATAATTTTCAGGGAAT 1200  
 DB 455 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 474  
 QY 1201 GGTGATGAAGGTTCAACAATATTAGACGATAGCACAAATAATTTAAAGTTTATAGGTTGGA 1260  
 DB 475 GlyAspGluGlySerThrIleIleAspAspSerThrIleLysValTyrLysValGly 494  
 QY 1261 GATAATCAAAATTTACCATAGTAGTAACAGATTTTATGATTACAGTGAATATGAAGATGTC 1320  
 DB 495 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 514  
 QY 1321 ACAAAATGATGATTATGCCCAATTAGGAATAATAATGATGTGAATATTATTTTGGTAAAT 1380  
 DB 515 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn 534  
 QY 1381 ATAGATTCCCATATATTAAAGTTATTAGTAAATATGACCTAATTAAGGATGATTAC 1440  
 DB 535 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 554  
 QY 1441 AGCATATATCAGCAAACTGTGCAATTCGACAGACGACTATTAATGAGTATACTTGTGAGTTT 1500  
 DB 555 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 574







Db	454	AspAsnGlnAsnLeuProAspSerAsnArgGileTyrAspTyrSerGluTyrGluAspVal	473
QY	1321	ACAAATGATGATTATGCCCAATTAGGAAATAATAATGATGATGATTAATTAATTTTGGTAAT	1380
Db	474	ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn	493
QY	1381	ATAGATTACACCATATATTATTAAAGTTATTAGTAAATATATCACCTTAATAAGGATGATTAC	1440
Db	494	IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr	513
QY	1441	ACGACTATACAGCAACTGTGACAAATGCAGACGACTATAAATGAGTATATCTGTTGAGTTT	1500
Db	514	ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe	533
QY	1501	AGAACAGACCTCATGATATACAAATTCCTCTCTACAGTTTCAGTCAAGCACRAGGT	1560
Db	534	ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly	553
QY	1561	GACTTGGCTCTCGAAAAAATTTATAAATCCGAGATTCACCTATGCGGAAGATGTAGATATAA	1620
Db	554	AspLeuProProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys	573
QY	1621	GATGGTATTCAAATATACAAATGATATGAAAAACCGCTTAGTAAATGATTTGGTAACTTTG	1680
Db	574	AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu	593
QY	1681	ACGTATCCTGATCGAACTTCAAAATCAGTCAGACACAGATGAAGATGGGAATATCAATTT	1740
Db	594	ThrTyrProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyrGlnPhe	613
QY	1741	GATGGA 1746	
Db	614	AspGly 615	
RESULT 4			
ID	ADO84849		
XX	ADO84849	standard; protein; 892 AA.	
XX	ADO84849;		
XX			
DT	29-JUL-2004	(first entry)	
DE		S epidermidis surface anchored LPXTG protein SeqID21.	
KW		LPXTG; cell wall-anchored surface protein; Gram positive bacterium;	
KW		extracellular matrix molecule; sequence database; C-terminal;	
KW		immunoglobulin-like fold region; Ig-like fold region; antibacterial;	
KW		vaccine; gene therapy; infection; medical device; prosthesis;	
KW		premature newborn; AIDS; debilitated cancer; bone marrow transplantation.	
XX			
OS		Staphylococcus epidermidis.	
XX			
FN	WO2004025416-A2.		
XX			
PD	25-MAR-2004.		
PF	15-SEP-2003; 2003WO-US028789.		
XX			
PR	13-SEP-2002; 2002US-0410303P.		
XX			
PA	(TEXA ) UNIV TEXAS A & M SYSTEM.		
PA	(INH1-) INHIBITEX INC.		
PA	(UNBR-) UAB RES FOUND.		
XX			
PI	Hook M, Xu Y, Sillanpaa JV, Sthanam N, Ponnuraj K, Patti JM;		
PI	Hutchins JT, Hall A;		
XX			
DR	WPI; 2004-315684/29.		
XX			
PT		Identifying LPXTG-containing cell wall-anchored surface proteins from	
PT		Gram positive bacteria, for treating infection caused by the bacteria,	
PT		comprises searching sequence information database for the sequence having	
PT		LPXTG-motif.	

XX PS Claim 16; SEQ ID NO 21; 96pp; English.

CC This invention relates to a novel method of identifying LPXTG-containing

CC cell wall-anchored surface proteins from Gram positive bacteria that bind

CC to an extracellular matrix molecule which comprises searching a database

CC of sequence information for a putative protein sequence having the LPXTG-

CC motif in its C-terminal region and analysing the sequence for the

CC presence of one or more immunoglobulin (Ig)-like fold regions. The

CC invention may be useful for the production of compounds with an

CC antibacterial activity or for production of a vaccine. In addition the

CC disclosed sequences may be useful for gene therapy. The antibody is

CC useful for treating or preventing an infection of Gram-positive bacteria

CC in a human or animal patient. The method and the proteins are useful in

CC generating antibodies for treating and preventing the spread of

CC infections of Gram positive bacteria, for interfering with, or inhibiting

CC binding interactions by Gram positive bacteria, for monitoring the level

CC of gram positive bacterial antigens, or antibodies recognising the

CC antigens in a human or animal patients suspected of containing the

CC devices or antibodies, in preventing or reducing infection of medical

CC preventing infections caused by such organisms, and in treating or

CC newborns, AIDS and debilitated cancer patients, and bone marrow

CC transplantation. The present sequence is that of a surface anchored LPXTG

CC protein identified using the method of the invention.

XX SQ Sequence 892 AA;

Alignment Scores:

Pred. No.:	2,246-206	Length:	892
Score:	2810.50	Matches:	545
Percent Similarity:	96.2%	Conservative:	15
Best Local Similarity:	93.6%	Mismatches:	21
Query Match:	92.9%	Indels:	1
DB:	8	Gaps:	1

US-10-806-288-12 (1-1746) x ADO84849 (1-892)

QY	1	TCGTAGTGAAGAAAGAAATGATGATCAATAATAATCAAGTCAATAAACACCGACGAT	60
DB	35	SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp	54
QY	61	AATACCAATAATTAATAAAGAGAACCAATTAACATGATGGCATAGAAAAACGCTCA	120
DB	55	AspAsnGln---IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer	73
QY	121	GAAGATAGACAGAGTCAACAAATGTAGATGAAACGAACCAACATTTTACAAAAG	180
DB	74	LysAspIleThrGlnSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys	93
QY	181	ACCCCTCAAGATAATCTCATCTTACAGAGAAGAGGTAAAGAATCCCTCATCGTCGAA	240
DB	94	ThrProGlnAspAsnThrGlnLeuLysGluGluValLysGluProSerSerValGlu	113
QY	241	TCCTCAAAATTCATCAATGATCTGCCCAACACCATCTCACACAACTAATAATAGGAA	300
DB	114	SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu	133
QY	301	GAATCTGTTCAAAAGTGTATAATGTAGAAAGATTACACGATTCAGATTTTGTAACTCT	360
DB	134	AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer	153
QY	361	AAATAAAGAGATGAACCTGAATCTGGTAAAGAGAGAAATCTATAGAGCAACCTAAT	420
DB	154	LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn	173
QY	421	AAAGTAAAGACAGATTCAACACAGTCACGCGCTGCTGGCTATACAAATATAGATGAARA	480
DB	174	LysValArgGluAspSerIleThrSerGlnProSerSerTyrLysAsnIleAspGluLys	193
QY	481	ATTTCAAAATCAAGATGAGTATTAAATTTACCAATAAATCAATATGAAATAAGGCTAGA	540
DB	194	IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysValArg	213

QY	541	CCATTATCTACAAACATCTGCCCAACCATCGATTAACACGTGTAAACCTGAATCAATTAGCG	600
DB	214	ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla	233
QY	601	GGGGAACAGGTTCCGAATCTTAACCAATTTAAAGTTTACTGATCAAAAGTATTACTGAA	660
DB	234	AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu	253
QY	661	GGATATGATGATGAGGAGGTTTATTAAGCACATGATGCTGGAACCTTAATCTATGAT	720
DB	254	GlyTyrAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp	273
QY	721	GTAACCTTTGAAGTAGATGATGAAGTGAATCTGGTGATACGATGACAGTGGATATAGAT	780
DB	274	ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp	293
QY	781	AAGAATACAGTTCACATGATTAACCGATAGCTTTACAAATACCAAAAATAAAAAGATAAT	840
DB	294	LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn	313
QY	841	TCTGGAGAAATCATCGCTACAGTACTTATGATAACAAAAATAAACAAATCACCTATACT	900
DB	314	SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr	333
QY	901	TTTACAGATTATGATGAATAGTATGAAATATTAAGACACACCTTAAATTAAGCTATAC	960
DB	334	PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr	353
QY	961	ATTGATAAATCAAGGTTCCAAATATAATACCAAGTTAGATGTAGAAATATAAACCGCC	1020
DB	354	IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla	373
QY	1021	CTTTCATCAGTAAATAAAAACAATTAACGGTTGAATATCAAGACCTTAACGAAATTCGGACT	1080
DB	374	LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr	393
QY	1081	GCTAACCTTCAAGATGATGTTTCAATATAGATACGAAAAATCATACAGTTGAGCAACG	1140
DB	394	AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr	413
QY	1141	ATTATATTAAACCTCTTCCTGTTATTTCAGCAAGGAAACAAATGTAATATTTTCAGGGAAT	1200
DB	414	IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn	433
QY	1201	GGTGATGAAGGTTCAACAAATATAGACGATAGCACAAATTAATAAGTTTATAAGTTGGA	1260
DB	434	GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly	453
QY	1261	GATATCAAAATTTACCAGATAGTAACAGATTTTATGATTCAGTCAATATAGAGATGTC	1320
DB	454	AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal	473
QY	1321	ACAAATGATGATTATGCCCAATTTAGGAAATAATAATGATGTGAATATTAATTTGGTAAAT	1380
DB	474	ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn	493
QY	1381	ATAGATTCACCATATATTAAGATTATAGTAATATATGACCCCTAATAAGGATGATTAC	1440
DB	494	IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr	513
QY	1441	ACGACTATACACCACTGTCACATGACAGACGCTATATAATGAGTATACTGCTGAGTTT	1500
DB	514	ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe	533
QY	1501	AGAACAGCATCTTATGATAATAATCAATGCTTCTCAAGTTTCAGGTCAGGCAAGGT	1560
DB	534	ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly	553
QY	1561	GACTTGCCTCCTGAAAAAATCTTATAAAAAATCGGAGATTAGCTATGGGAAGATGTAGATAA	1620
DB	554	AspLeuProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys	573



```
QY 1021 CTTTCATCAGTAATAAAACAATTTACGGTTGAAATATCAAAGACCTAACGAAATCGGACT 1080
DB |||||||
QY 374 LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr 393
DB |||||||
QY 1081 GCTAACCTTCAAAGTATGTTTACAAATATATAGATACGAAATAATCATACAGTTGACAAACG 1140
DB |||||||
QY 394 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 413
DB |||||||
QY 1141 ATTATATATTAACCTCTTCCTGTTATTCAGCCAGGNAACAATGTAATATTTTTCAGGGAAT 1200
DB |||||||
QY 414 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 493
QY 1201 GGTGATGAAGGTTCAACAAATATATAGACGATAGCACATAATAATAAGTTTATAAGGTTGGA 1260
DB |||||||
QY 434 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 453
QY 1261 GATAATCAAAATTTACAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGTC 1320
DB |||||||
QY 454 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 473
QY 1321 ACAATGATGATTTATGCCCCAATTAGGNAATAATAATGATGCTGAATATTAATTTTGGTAAT 1380
DB |||||||
QY 474 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn 493
QY 1381 ATAGATTACCATATATTTATTAAGTTATTAGTAAATATGACCTTAATAGGATGATTAC 1440
DB |||||||
QY 494 IleAspSerProTyrIleIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 513
QY 1441 ACAGCTATACAGCAAACTGTGACAACTGACAGCACTATAATCAGTATATCTGCTGAGTTT 1500
DB |||||||
QY 514 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 533
QY 1501 AGAACAGCATCCTATGATATACATGCTTCTCTACAGTTTCAGGTCAAGCAGCAGGT 1560
DB |||||||
QY 534 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 553
QY 1561 GACTTGCTCTCGAATAAACTTATAAATCGAGATTACGTATGGGAAGATGAGATAAA 1620
DB |||||||
QY 554 AspLeuProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys 573
QY 1621 GATGGTATTCAAATACAAATGATATAATGAAAAACCCGCTTAGTAAATGATGTTGGTAACCTTG 1680
DB |||||||
QY 574 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 593
QY 1681 ACATATCTCATCGAATTCAAATCAGTCAGACAGATGCGAAGATGCGAATATCAATTT 1740
DB |||||||
QY 594 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluGlyLysTyrGlnPhe 613
QY 1741 GATGGA 1746
DB |||||||
QY 614 AspGly 615
RESULT 6
ABP40469
ID ABP40469 standard; protein; 930 AA.
XX
XX
AC ABP40469;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5314.
XX
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX
KW antibacterial; gene therapy.
XX
OS Staphylococcus epidermidis.
XX
XX US6380370-B1.
XX
XX 30-APR-2002.
PD
XX
XX 13-AUG-1998; 98US-00134001.
PF
XX
```

```
PR 14-AUG-1997; 97US-0055779P.
PR 08-NOV-1997; 97US-0064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
XX WPI: 2002-381255/41.
DR N-PSDB; ABN93014.
XX
PT Novel isolated nucleic acid encoding a Staphylococcus epidermis
PS polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS Disclosure; SEQ ID NO 5314; 267pp; English.
XX
CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC antibacterial activity and can be used in gene therapy. The sequences can
CC also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life cycle
CC or inhibit S. epidermidis infection. N.B. The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site
XX
SQ Sequence 930 AA;
Alignment Scores:
Pred. No.: 2,25e-206 Length: 930
Score: 2810.50 Matches: 545
Percent Similarity: 96.2% Conservative: 15
Best Local Similarity: 93.6% Mismatches: 21
Query Match: 92.9% Indels: 1
DB: 5 Gaps: 1
US-10-806-288-12 (1-1746) x ABP40469 (1-930)
QY 1 TCTAGTGATGAGAAAGAAATGATGATGATCAATATAATACGTCAATTAACACCGAGAT 60
DB |||||||
QY 73 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 92
DB |||||||
QY 61 AATAACCAATTAATTAATAAAGAAAGAAACGAATACTACGATGGCATAGAAAACCGCTCA 120
DB |||||||
QY 93 AspAsnGln---IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer 111
QY 121 GAAGATAGAACAGAGTCAACAAATGATGATGATGAAACGAAACCAACATTTTACAAAG 180
DB |||||||
QY 112 LysAspIleThrGlnSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 131
QY 181 ACCCTCAGATTAATCTCATCTTACAGAGAGAGAGGTAAGAATCCTCATCAGTCGAA 240
DB |||||||
QY 132 ThrProGlnAspAsnThrGlnLeuLysGluGluValValLysGluProSerSerValGlu 151
QY 241 TCCTCAAATTCATCAATTCATGATCTGCCCAACCAACCATCTCACACAAACAATAATAGAGAA 300
DB |||||||
QY 152 SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu 171
QY 301 GAATCTGTTCAAACAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB |||||||
QY 172 AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer 191
QY 361 AAAATAAAGAGAGTAAACACTGAATCTGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB |||||||
QY 192 LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn 211
QY 421 AAAGTAAAAGAGATTCAACCAACCAACCTCAGCGCTCTGGCTATATACAAATATAGATGAAAA 480
DB |||||||
QY 212 LysValArgGluAspSerIleThrSerGlnProSerSerTyrLysAsnIleAspGluLys 231
QY 481 ATTTCAAATCAAGATGAGTATTAAATTTACCAATAAATGAATATATGAAATAAGCGTAGA 540
DB |||||||
QY 232 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysValArg 251
```

QY 541 CCATTATCTACAACTCTGCCCAACCATCGATTAAACCTGTAAACCGTAAATCAATTAGCG 600  
Db |||||||  
252 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 271  
QY 601 GCGGAACAAGGTTCCGAATGTTAAACCATTTAAATTAAGTTACTGTCAAGTATTACTGAA 660  
Db |||||||  
272 AlaGluGlnGlySerAsnValAsnHisLeuLeuLysValThrAspGlnSerIleThrGlu 291  
QY 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Db |||||||  
292 GlyTyrAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 311  
QY 721 GTAACCTTTTGAAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
Db |||||||  
312 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 331  
QY 781 AAGATACAGTCCATCAGATTACCGATGATGATGATGATGATGATGATGATGATGATGAT 840  
Db |||||||  
332 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 351  
QY 841 TCTGGAGAAATCATCGCTACAGGTACTTATGATACAAATAAATAAACAATCACCTACT 900  
Db |||||||  
352 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr 371  
QY 901 TTTACAGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
Db |||||||  
372 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 391  
QY 961 ATTGATAAATCAAGGTTCCAAATTAATTAACCAAGTTAGATGATGATGATGATGATGAT 1020  
Db |||||||  
392 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 411  
QY 1021 CTTTCATCAGTAATAAACAATTAACGTTCAATATCAACAGCACCTAACGAAATCGGACT 1080  
Db |||||||  
412 LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr 431  
QY 1081 GCTAACCTTCAAAGTATGTTTACAAATATATAGATACGAAATAATCATACAGTTTGCAACG 1140  
Db |||||||  
432 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 451  
QY 1141 ATTTATATTAACCTCTCTCGTTATTCAGCCAGGAACAATGTAATATTTACGGGAAT 1200  
Db |||||||  
452 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 471  
QY 1201 GGTGATGAAGTTTCAACAATATAGACGATAGCAACAATAATTAAGTTTAAAGTTTGA 1260  
Db |||||||  
472 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 491  
QY 1261 GATAATCAAAATTTTACCAGATAGTAAACAGAAATTTATGATACAGTGAATATGAAGATGTC 1320  
Db |||||||  
492 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 511  
QY 1321 ACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
Db |||||||  
512 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 531  
QY 1381 ATAGATTACCATATATTTAAAGTTTATTAAGTTTATGATGATGATGATGATGATGATGAT 1440  
Db |||||||  
532 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 551  
QY 1441 ACAGTATACAGCAAACTGTGACAACTGACAGCACTATAATGATGATGATGATGATGATGAT 1500  
Db |||||||  
552 ThrThrIleGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 571  
QY 1501 AGAACAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
Db |||||||  
572 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 591  
QY 1561 GACTTGCTCTGAAAACCTTATAAATCGAGATTACGTTACGTTACGTTACGTTACGTTACGTT 1620  
Db |||||||  
592 AspLeuProProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys 611

QY 1621 GATGGTATTCAAAATACAAATGATAATCAAAACCGCTAGTAATGTATTGTTGTTGTTG 1680  
Db |||||||  
612 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 631  
QY 1681 ACGTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
Db |||||||  
632 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyrGlnPhe 651  
QY 1741 GATGGA 1746  
Db |||||||  
652 AspGly 653  
RESULT 7  
ADS06014  
ID ADS06014 standard; protein; 930 AA.  
XX  
AC ADS06014;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Staphylococcus epidermis polypeptide seqid 5309.  
XX  
KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;  
KW recombinant expression vector; infection; computer readable medium;  
KW computer based system.  
XX  
OS Staphylococcus epidermidis.  
XX  
PN US2004147734-A1.  
XX  
PD 29-JUL-2004.  
XX  
PF 01-DEC-2003; 2003US-00724972.  
PR 08-NOV-1997; 97US-0064964P.  
PR 13-AUG-1998; 98US-00134001.  
PR 29-NOV-1999; 99US-00450969.  
XX  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
XX  
PI Doucette-Stamm L, Bush D;  
XX WPI; 2004-580138/56.  
XX N-PSDB; ADS02242.  
XX  
PT New isolated polypeptide and encoding nucleic acid derived from  
PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or  
PT treating an S. epidermidis bacterial infection.  
XX  
PS Claim 17; SEQ ID NO 5309; 741pp; English.  
XX  
CC The invention describes an isolated nucleic acid comprising a nucleotide  
CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:  
CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any  
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as  
CC given in the specification. Also described are: a recombinant expression  
CC vector; a cell comprising a recombinant expression vector of (1);  
CC producing an S. epidermidis polypeptide; an isolated nucleic acid  
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a  
CC vaccine composition for prevention or treatment of an S. epidermidis  
CC infection, comprising a nucleic acid cited above and a carrier; treating  
CC a subject for S. epidermidis infection; a recombinant or substantially  
CC pure preparation of an S. epidermidis polypeptide or its fragment; a  
CC vaccine composition for prevention or treatment of an S. epidermidis  
CC infection; detecting the presence of a Staphylococcus nucleic acid in a  
CC sample; a computer readable medium having recorded in it the nucleotide  
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based  
CC system for identifying fragments of the Staphylococcus genome of  
CC commercial importance; a computer based system for identifying fragments  
CC of the Staphylococcus plasmids of commercial importance; identifying  
CC commercially important nucleic acid fragments of the Staphylococcus  
CC genome and/or plasmids; and identifying an expression modulating fragment



Cell wall protein SdrG.

SdrF; SdrG; SdrH; coagulase negative; staphylococcus; scepticemia;  
osteomyelitis; endocarditis; immune response; vaccine; graft; stent;  
intravenous catheter; heart valve; cardiac.

Staphylococcus sp.

Key Location/Qualifiers

Misc-difference 14 /note= "Position encoded by TAG stop codon"

Misc-difference 33 /note= "Position encoded by TGA stop codon"

Misc-difference 964 /note= "Position encoded by TAA stop codon"

Misc-difference 980 /note= "Position encoded by TAG stop codon"

Misc-difference 989 /note= "Position encoded by TAA stop codon"

WO200012689-A1.

09-MAR-2000.

31-AUG-1999; 99WO-US019728.

31-AUG-1998; 98US-0098443P.

25-JAN-1999; 99US-0117119P.

(QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.

(TEXA ) UNIV TEXAS A & M SYSTEM.

Foster TJ, Hook M, Davis S, Hartford O, McCreia K, Ni Bidhin D;

WPI: 2000-256637/22.

N-PSDB; AA293534.

Recombinant or synthetic proteins from coagulase-negative staphylococci

useful for prevention, treatment and diagnosis of staphylococcal

infections bind soluble and immobilized fibrinogen.

Claim 8; Fig 3; 104pp; English.

Isolated Staphylococcus Sdr cell wall proteins which bind both soluble

and immobilized fibrinogen are useful for treating or preventing

coagulase-negative staphylococcal infection such as scepticemia,

osteomyelitis or endocarditis, and for inducing immune responses in

patients. The cell wall proteins are also useful for reducing coagulase-

negative staphylococci infection of indwelling medical devices such as

vascular grafts, vascular stents, intravenous catheters, artificial heart

valves and cardiac assist devices. The cell wall associated proteins are

able to inhibit staphylococcal adhesion to immobilised extracellular

matrix or host cells present on the surface of implanted biomaterials

SQ Sequence 991 AA;

Alignment Scores:

Pred. No.: 2,28e-206 Length: 991

Score: 2810.50 Matches: 545

Percent Similarity: 96.2% Conservative: 15

Best Local Similarity: 93.6% Mismatches: 21

Query Match: 92.9% Indels: 1

DB: 3 Gaps: 1

US-10-806-288-12 (1-1746) x AAY83171 (1-991)

Qy 1 TCTAGTGAAGAAAAGAAATGATGTGATCAATAATATCAATCAATAAACCACCGCAT 60

Db 106 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 125

Qy 61 AATAACCAATAATTAATAAGAAAGAAACGAAATCACTACGATGCGATGAGAAAACGCTCA 120

Db 126 AspAsnGln----IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer 144

Qy 121 GAAGATAGAACAGAGTCAACAAACAAATGTAGATGAAACCAAGCAACAAATTTTACAAAG 180  
Db 145 LysAspIleThrGlnSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 164  
Qy 181 ACCCTCAAGATAATCTCATCTTACAGAGAAGAGGTAAAGAATCTCATAGTCGAA 240  
Db 165 ThrProGlnAspAsnThrGlnLeuLysGluGluValValLysGluProSerSerValGlu 184  
Qy 241 TCCTCAAAATTCATCAATTTGATCTGCCCAACCAACATCTCACAAACAATAAATAGAGAA 300  
Db 185 SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu 204  
Qy 301 GAATCTGTCTCAACCAAGTGAATAATGTAGAAAGATTCACACGATATCAGATTTTGTAACTCT 360  
Db 205 AlaSerIleGlnThrSerAspAsnGluAsnSerArgValSerAspPheAlaAsnSer 224  
Qy 361 AAAATAAAGAGAGTAACACTGAATCTCGTGAAGAAGAAATCTATATAGAGCAACTAAT 420  
Db 225 LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn 244  
Qy 421 AAAGTAAAGAAGATTCAACCAACCAAGTCAGCGCTGCTATACAAATATAGATGAAAA 480  
Db 245 LysValArgGluAspSerIleThrSerGlnProSerSerIleLysAsnIleAspGlnLys 264  
Qy 481 ATTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAAAAATAGCGTAGA 540  
Db 265 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluThrGluAsnLysValArg 284  
Qy 541 CCATTATCTACACATCTGCCCAACCATCGATTAAACGTGTAACCGTAATAATCAATTAGCG 600  
Db 285 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 304  
Qy 601 GCGGAACAAGGTCGAATGTTAACCATTAACTTAAGTTACTGTAGTCAAGTTACTTCTGAA 660  
Db 305 AlaGlnGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 324  
Qy 661 GGATATGATGATGTAAGGTGTTATTAAAGCACATCATGCTGAAAACTTAATCTATGAT 720  
Db 325 GlyThrAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleThrAsp 344  
Qy 721 GTAACTTTTGAAGTAGATGATAAGGTGAATCTGGTGTATGATGACGATGATGATATAGAT 780  
Db 345 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 364  
Qy 781 AAGATACACTTCATCCAGATTAAACCGATAGCTTTACATAATCCAAAATAAAGATTAAT 840  
Db 365 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 384  
Qy 841 TCTGGAGAAATCATCGCTACAGGTACTTTATGATAACAAAAATAAACAATCACCTATATCT 900  
Db 385 SerGlyGluIleIleAlaThrGlyThrThrAspAsnThrAsnLysGlnIleThrThr 404  
Qy 901 TTACAGATTATGTAGATAAGTATGAAAATATTAAAGCACACCTTTAAATTAACGTCATAC 960  
Db 405 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 424  
Qy 961 ATTGATAAATCAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATAATAAACCAGCC 1020  
Db 425 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 444  
Qy 1021 CTTTTCATCAGTAAATAAACAATTTACGGTTGAATATCAAGAGCCTTAACGAAAAATCGGACT 1080  
Db 445 LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr 464  
Qy 1081 GCTAACCTTCAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAACG 1140  
Db 465 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 484  
Qy 1141 ATTTATATTAAACCTCTTCGTTATTTCGCCCAAGAAACAATGTAATATTATTCAGGGAAT 1200  
Db 485 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 504



```

QY 1201 GGTGATGAAGGTTCAACAATTATAGACGATAGCACAAATTAATAAGCTTTATAGGTGGA 1260
Db |||||||
QY 505 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleValTyrLysValGly 524
Db |||||||
QY 1261 GATAATCAAAATTTACCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGTC 1320
Db |||||||
QY 525 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 544
QY 1321 ACAAATGATGATTCGCCAATTAGGAAATAATAATGATGTAATATTAATTTTGGTAAT 1380
Db |||||||
QY 545 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn 564
QY 1381 ATAGATTCACCATATATTATTAAAGTTATTAGTAATATGACCTTAATAGGATGATTAC 1440
Db |||||||
QY 565 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 584
QY 1441 ACGACTATACAGCAAACTGTGACAATGCAGACGACTATAATGAGTATACCTGCTGAGTTT 1500
Db |||||||
QY 585 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 604
QY 1501 AGAACAGCATCTATGATAATACAAATGCTTCTCTACAAAGTTCAGGTCAAGCAAGGT 1560
Db |||||||
QY 605 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 624
QY 1561 GACTTGCTCTCGAAAACTTATAAATCGGAGATTACGTATGGGAGAGTGTAGATAAA 1620
Db |||||||
QY 625 AspLeuProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys 644
QY 1621 GATGGTATTCAAAATGATAATGATAATGAAACCGCTTAGTAAATGATTGGTAACTTTG 1680
Db |||||||
QY 645 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 664
QY 1681 ACGTATCTCATGAACTTCAAAATCAGTCAGAACAGATGAAGATGGGAAATCAATTT 1740
Db |||||||
QY 665 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyrGlnPhe 684
QY 1741 GATGGA 1746
Db |||||||
QY 685 AspGly 686

RESULT 9
AAV70120
ID AAV70120 standard; protein; 991 AA.
XX
AC AAV70120;
XX
DT 06-JUN-2000 (first entry)
XX
DE Staph. epidermidis serine-aspartate repeat region protein SdrG.
XX
KW Multicomponent vaccine; immunostimulatory; antibacterial; MSCRAMM;
KW microbial surface components recognising adhesive matrix molecules;
KW collagen binding protein; CBP; CNA; fibrinogen binding protein;
KW Clumping factor A; ClfA; Clumping factor B; ClfB; FnBP;
KW fibronectin binding protein; Staphylococcus infection;
KW serine-aspartate repeat region protein; SDR protein; SdrG.
XX
OS Staphylococcus epidermidis.
XX
PH Key Location/Qualifiers
FT Misc-difference 14 /note= "Encoded by in-frame stop codon TAG"
FT Misc-difference 33 /note= "Encoded by in-frame stop codon TGA"
FT Misc-difference 964 /note= "Encoded by in-frame stop codon TAA"
FT Misc-difference 980 /note= "Encoded by in-frame stop codon TAG"
FT Misc-difference 989 /note= "Encoded by in-frame stop codon TAA"
XX
PN WO200012131-A1.
XX

```

```

PD 09-MAR-2000.
XX
PF 31-AUG-1999; 99WO-US019727.
XX
PR 31-AUG-1998; 98US-0098439P.
XX
PA (INH1-) INHIBITEX INC.
PA (TEXA) UNIV TEXAS A & M SYSTEM.
PA (QUEB-) QUEEN ELIZABETH COLLEGE DUBLIN.
XX
PI Patti JM, Foster TJ, Hook M;
XX
WPI; 2000-237781/20.
DR N-PSDB; AA251202.
XX
Composition used for generating immune response or for inhibiting
PT microbial colonization in an animal comprises antibodies that bind
PT collagen binding protein, fibrinogen binding protein and, optionally,
PT fibronectin binding protein.
XX
PS Claim 8; Fig 4; 115pp; English.
XX
CC The patent discloses multicomponent vaccines containing selected
CC combinations of bacterial binding proteins termed MSCRAMM (microbial
CC surface components recognising adhesive matrix molecules) or their
CC antibodies. A vaccine composition is provided that includes collagen
CC binding protein or peptide, e.g. CNA, a fibrinogen binding protein
CC preferably Clumping factor A (ClfA) or Clumping factor B (ClfB), and
CC optionally a fibronectin binding protein e.g. FnBP-A. The vaccines are
CC useful for imparting protection against a broad spectrum of
CC Staphylococcal strains and for inhibiting microbial colonisation.
CC especially of Staphylococcus aureus, in an animal. The combinations can
CC also be used to select donor blood pools for the preparation of purified
CC blood products for passive immunisation. The present sequence is a serine
CC -aspartate repeat region protein, SdrG from Staphylococcus epidermidis.
CC The Sdr protein is useful in vaccine preparation in combination with
CC specific bacterial binding proteins. These vaccines can be used to treat
CC a broad spectrum of bacterial infections, including those arising from
CC both coagulase-positive and coagulase-negative bacteria
XX
SQ Sequence 991 AA;

Alignment Scores:
Pred. No.: 2,28e-206 Length: 991
Score: 2810.50 Matches: 545
Percent Similarity: 96.2% Conservative: 15
Best Local Similarity: 93.6% Mismatches: 21
Query Match: 92.9% Indels: 1
DB: 3 Gaps: 1

US-10-806-288-12 (1-1746) x AAV70120 (1-991)
QY 1 TCTAGTGTGAAGAAAAAGAAATGATGTGATCAATAATAATCAGTCAATAAACACCGACGAT 60
Db 106 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 125
QY 61 AATAACCAAAATAATTAAAAAGAAAGCAATATACTAGTGGCATAGAAAAACGCTCA 120
Db 126 AspAsnGln---IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer 144
QY 121 GAAGATAGAACAGAGTCAACAACAATGTAGATGAAACGAACGAACATTTTACAAAAG 180
Db 145 LysAspPileThrGlnSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 164
QY 181 ACCCTCAAGATAATACTCATCTTACAGAAAGAGAGGTAAAAAGAAATCCTCATCAGTCGAA 240
Db 165 ThrProGlnAspAsnThrGlnLeuLysGluGluValValLysGluProSerSerValGlu 184
QY 241 TCCTCAAAATTCATCAATTGATCTAGTCCCAACCAACCATCTCACACAACAATAATAGAGAA 300
Db 185 SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu 204
QY 301 GAATCTGTTCAAAACAGTGTGATAATGTAGAAGATTTCACAGTATCAGATTTTGTAACTCT 360

```



Db	205	AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer	224
Qy	361	AAAATAAAGAGAGTAACACATCGAATCTGGTAAGAAGAGAGATATCTATAGACCAACTAAT	420
Db	225	LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn	244
Qy	421	AAAGTAAAGAAGATTCAACAACAAGTCAGCGCTCGCTGCTATACAAATATAGATGAAAAA	480
Db	245	LysValArgGluAspSerIleThrSerGlnProSerSerTyrLysAsnIleAspGluLys	264
Qy	481	ATTTCAAATCAAGATGAGTATTAAATTTACCAATAAATGAATGAATAAAGCTAGA	540
Db	265	IleSerAsnGlnAspGluLeuAsnLeuProIleAsnGluTyrGluAsnLysValArg	284
Qy	541	CCATTATCTACAAATCTGCCCAACCATCTGATTAAACCGTAAACCGTAAATCAATTAGCG	600
Db	285	ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla	304
Qy	601	CGCGAACAAAGTTTCAAGTTTAAACCATTTAAATTAAGATTACTGATCAAAAGTATTACTGAA	660
Db	305	AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu	324
Qy	661	GGATATGATGATGATGAGGTGTTATTAAACCAATGATGCTGCTGAAAACCTTAATCTATGAT	720
Db	325	GlyTyrAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp	344
Qy	721	GTAACCTTTTGAAGTAGATGATAAGGTGAAATCTCGTGATACGATGACAGTCGATGATAGAT	780
Db	345	ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp	364
Qy	781	AAGAATACAGTTCATCAGATTTTAAACCGATAGCTTTACAAATACCAAAAAATAAAGATAAT	840
Db	365	LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn	384
Qy	841	TCTGGAGAAATCATCGCTACAGGTACTTATGATTAACAAATAAACAACATCACTCTACTACT	900
Db	385	SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr	404
Qy	901	TTTACAGATTATGTAGATAGATGATAAAATATTAAAGCACACACCTTTAAATTAACGTCATAC	960
Db	405	PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr	424
Qy	961	ATTGATAAATCAAAGGTTCCAAATTAATAATACCAAGTTTAGATGTAGATAATAAACCGGCC	1020
Db	425	IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla	444
Qy	1021	CTTTTCATCAGTAAATAAACAATTACGGTTGAATATCAAAGACCTAACGAAATTCGGACT	1080
Db	445	LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr	464
Qy	1081	GCTAAACCTTCAAAGTGTGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAACG	1140
Db	465	AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr	484
Qy	1141	ATTTATATTAAACCTCTTCGTTATTCAGCAAGGAAAAAAATGTAATATTTTCAGGGAAT	1200
Db	485	IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn	504
Qy	1201	GGTGATGAAGGTTCAACAATTATAGACGATAGCACAATAATTAAAGTTTATAAGTTTGA	1260
Db	505	GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly	524
Qy	1261	GATTAATCAAATTTTACCAGATAGTAAGCAATTTATGATTTACAGTGAATATGAGATGTC	1320
Db	525	AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal	544
Qy	1321	ACAAATGATGATTATGCCCCAATTAGGAAAAATAATATGATGTGAATATTAATTTTGGTAAAT	1380
Db	545	ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn	564
Qy	1381	ATGATTCCACATATATTATTAAGTTTATTAGTAAATATGACCCCTAATAAGGATGATTAC	1440

Db	565	IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr	584
QY	1441	ACGACTATACACAAACCTGTGACAAATCAGACAGACTATAAATCAGTATACCTGCTGAGTTT	1500
Db	585	ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe	604
QY	1501	AGACAGCATCCTATGATATAACAAATTCGCTTTCTCTCAAGTTTCAGTCAAGGACAAGGT	1560
Db	605	ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly	624
QY	1561	GACCTGCCTCTGAAANAACCTATAAATCGGAGATTACGTATCGGAGAAGATGATATAA	1620
Db	625	AspLeuProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys	644
QY	1621	GATGGTATTCAAAATACAAATGATAATGAAAAACCGCTTAGTAATGTATTGGTAACCTTG	1680
Db	645	AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu	664
QY	1691	ACGTATCCTGATGAACTTCAAAATCAGTCAGACAGATCAAGATCGGAAATATCAATTT	1740
Db	665	ThrTyrProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyrGlnPhe	684
QY	1741	GATCGA	1746
Db	685	AspGly	686
RESULT 10			
ABM79020			
ID	ABM79020	standard; protein; 549 AA.	
AC	ABM79020;		
XX			
DT	15-JAN-2004	(first entry)	
XX			
DE	Staphylococcus epidermidis polypeptide.		
XX			
KW	Infection; antibacterial; vaccine.		
XX			
OS	Staphylococcus epidermidis.		
XX			
FN	WO2003076470-A1.		
XX			
PD	18-SEP-2003.		
XX			
PF	05-MAR-2003; 2003WO-US006415.		
XX			
PR	05-MAR-2002; 2002US-0361324P.		
XX			
PA	(INH1-) INHIBITEK INC.		
PA	(TEXA) UNIV TEXAS A & M SYSTEM.		
XX			
PI	Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;		
PI	Robbins J, Vernachio J, Bowden MG;		
XX			
DR	WPI; 2003-722324/68.		
XX			
PT	New antibody recognizing a Staphylococcus epidermidis protein comprising		
PT	SdrG N1N2N3, SdrG N2N3 or SdrGrx2 useful for preparing a composition for		
PT	treating or preventing a coagulase-negative Staphylococcal infection.		
XX			
PS	Claim 20; Page 37; 78pp; English.		
XX			
CC	The present sequence comprises the protein sequence of a polypeptide of a		
CC	coagulase-negative Staphylococcus epidermidis. A claimed monoclonal		
CC	antibody recognises this protein and is used in a claimed method of		
CC	treating or preventing a coagulase-negative staphylococcal infection in a		
CC	human or animal, e.g. a nosocomial coagulase-negative staphylococcal		
CC	infection in low birth weight infants		
XX			
SQ	Sequence 549 AA;		
Alignment Scores:			
Pred. No.:	1-156-195	Length:	549

Score:	2670.00	Matches:	519
Percent Similarity:	99.2%	Conservative:	3
Best Local Similarity:	98.7%	Mismatches:	4
Query Match:	88.2%	Indels:	0
DB:	7	Gaps:	0
US-10-806-288-12 (1-1746) x ABM79020 (1-549)			
QY	1	TCTAGTCATCAAGAAAGATGATGTCATCAATAATATCAGTCATCAATAAACCAGCAGAT	60
Db	24	SerSerAspGluGluGluAsnAspValIleAsnAsnAsnGlnSerIleAsnSerAspAsp	43
QY	61	AATAACCAATAATTTAAAAAGAGAAACCAATAACTACGATGCGCATAGAAAAACGCTCA	120
Db	44	AsnAsnGlnIleAsnIleAsnIleGluGluThrAsnAsnAsnAspGlyIleGluIleSerSer	63
QY	121	GAAGATAGAACAGAGTCAACCAACAATGTAGATGAAACGAACCAACATTTTACAAAAG	180
Db	64	GluAspArgThrGluSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys	83
QY	181	ACCCCTCAAGATAATCTATCTCTACAGAAAGAGGTAAAGATCCCTCATCAGTCGAA	240
Db	84	ProGlnAspAsnThrHisLeuThrGluGluGluValLysGluProSerSerValGlu	103
QY	241	TCCTCAAAATTCATCAATTTGATCTGCCCAACACCATCTCACACAACAATAAATAGAGAA	300
Db	104	SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrIleAsnArgGlu	123
QY	301	GAATCTGTTCAAAACAAGTGATAATGTAGAAAGATTCAACGTATCAGATTTTGCTAACTCT	360
Db	124	GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer	143
QY	361	AAATAAAGAGAGTAACACTGAATCTGCTGTAAGAGAGAGATACTATAGAGCAACCTAAT	420
Db	144	LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn	163
QY	421	AAAGTAAAGAAAGATTCAACAACAAGTCAGCGCTCTGGCTATACAAATATAGATGAAAAA	480
Db	164	LysValLysGluAspSerThrThrSerGlnProSerGlyThrAsnIleAspGluLys	183
QY	481	ATTTCAAATCAAGATGAGTTATTAAATTTTACCAATAAATGAATATGAAATTAAGGCTAGA	540
Db	184	IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrgluAsnLysAlaArg	203
QY	541	CCATTATCTACACATCTGCCCAACCATTCGATTAACGGTGTAACCGTAATCAATTAGCG	600
Db	204	ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla	223
QY	601	GCGGAACAAGGTTGGAATGTTAAACCATTTTAAATTAAGTTACTCATCAAAAGTATTACTGAA	660
Db	224	AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu	243
QY	661	GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	720
Db	244	GlyTyrgluAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrglu	263
QY	721	GTAACCTTTCAAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	780
Db	264	ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAspIleAsp	283
QY	781	AGAATACAGTTCATCAGATTTTAAACGATAGCTTTTACAAATACCAAAATAAAGATAAT	840
Db	284	LysAsnThrValProSerAspLeuThrAspSerPheThrIleProLysIleLysAspAsn	303
QY	841	TCGGAGAAATCATCGCTACAGGTACTTATGATAACAAAAATAAACAATCACCTTACT	900
Db	304	SerGlyGluIleIleAlaThrGlyThrTyrgluAsnLysAsnLysGlnIleThrTyrglu	323
QY	901	TTTACAGATTATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	960
Db	324	PheThrAspTyrgluValAspLysTyrgluAsnIleLysAlaHisLeuLysLeuThrSerTyrglu	343
QY	961	ATTGATAAATCAAAGGTTCCAAATAATAATACCAAGTTAGATGATGATAAATAAACAAGGCC	1020
Db	344	IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrgluThrAla	363
QY	1021	CTTTTCATCAGTAAATAAACAATTCACGGTTGAATATCAAGACCTAACGAAATTCGAGCT	1080
Db	364	LeuSerSerValAsnLysThrIleThrValGluTyrgluArgProAsnGluAsnArgThr	383
QY	1081	GCTAACCTTCAAGTATGTTTCAAAATATAGATACGAAAAATCATACAGTTGACCAACG	1140
Db	384	AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr	403
QY	1141	ATTATATTAAACCTCTTCGTTATTTCAGCAAGGAAACAAATCTAAATATTTTCAGGGAAT	1200
Db	404	IleTyrgluAsnProLeuArgTyrgluSerAlaLysGluThrAsnValAsnIleSerGlyAsn	423
QY	1201	GGTATGAAGGTTCAACAATATAGACATAGACACAATAATTAAGATTTTATAAGTTGGA	1260
Db	424	GlyAspGluGlySerThrIleIleAspAspSerThrIleLysValTyrgluValGly	443
QY	1261	GATATCAAAATTTACCATAGTACAGATTAACAGATTTATGATTTACAGTCAATATGAGATGTC	1320
Db	444	AspAsnGlnAsnLeuProAspSerAsnArgIleTyrgluAspTyrgluTyrgluAspVal	463
QY	1321	ACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1380
Db	464	ThrAsnAspAspTyrgluAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn	483
QY	1381	ATAGATTCACCATATATTAAGTTATTAGTAAATATGACCTTAATAGAGATGATGAT	1440
Db	484	IleAspSerProTyrgluIleLysValIleSerLysTyrgluAspProAsnLysAspAspTyrglu	503
QY	1441	ACGACTATACACCAACTGTCACATGACAGACGACTATAAATGAGTATGATGATGATGATGAT	1500
Db	504	ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrgluGluPhe	523
QY	1501	AGAACAGCATCTCATGATAATCAATGCTTCTCTACAAAGTTTCAGGTCAAGGACAAGGT	1560
Db	524	ArgThrAlaSerTyrgluAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly	543
QY	1561	GACTTGCTCTCGAAAAA 1578	
Db	544	AspLeuProGluLys 549	
RESULT 11			
ABM79015	ID ABM79015 standard; protein; 560 AA.		
XX	AC ABM79015;		
XX	DT 15-JAN-2004 (first entry)		
XX	DE Staphylococcus epidermidis SdrG NIN2N3 domain.		
XX	KW SdrG; surface protein; infection; antibacterial; vaccine.		
XX	OS Staphylococcus epidermidis.		
XX	PN WO2003076470-A1.		
XX	PD 18-SEP-2003.		
XX	PF 05-MAR-2003; 2003WO-US006415.		
XX	PR 05-MAR-2002; 2002US-0361324P.		
XX	PA (INHI-) INHIBITEX INC.		
XX	PA (TEXA) UNIV TEXAS A & M SYSTEM.		
XX	PI Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;		
XX	PI Robbins J, Vernachio J, Bowden MG;		
XX	DR WPI; 2003-722324/68.		
XX	DR N-PSDB; ACP80624.		

QY	1	TTCTAGTGATGAAGAAAGAATGATGTGTATCAATAATAATACGTCAATAAACAACCGACGAT	60
Db	36	SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp	55
QY	61	AATAACCAATAATATAAAAAAGAAACGAAATACCTACGATGCGCATAGAAAAACGCTCA	120
Db	56	AspAsnGln---IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer	74
QY	121	GAAGATAGAACAGAGCTCAACAAATGTAGATGAAAAAGAAAGCAACATTTTTACAAAAG	180
Db	75	LysAspIleThrGlnSerThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys	94
QY	181	ACCCCTCAAGATAATACTCATCTTACAGAAGAGGTAAAAAGAAATCCTCATCGTGGAA	240
Db	95	ThrProGlnAspAsnThrGlnLysLysGluGluValLysGluProSerSerValGlu	114
QY	241	TCCTCAAAATTCATCAATGTACTACTCCCAACCAACCATCTCACACAAATAAATAGAGAA	300
Db	115	SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrIleAsnSerGlu	134
QY	301	GAATCTGTTTCAACAAAGTGATAATGTAGAAGATTACACGTTATCAGATTTTTGCTAACTCT	360
Db	135	AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer	154
QY	361	AAATATAAAGAGAGTAACTGAATCTGGTAAAGAGAGATACTATAGAGCAACCTAAT	420
Db	155	LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn	174
QY	421	AAAGTAAAAAGAGATTCAACAAACAGTCAGCGCTCTGGCTATACAAATATAGATGAAAAA	480
Db	175	LysValArgGluAspSerIleThrSerGlnProSerSerTyrLysAsnIleAspGluLys	194
QY	481	ATTTCAAAATCAAGATGAGTTATTAAATTTACAATAATGAATATGAAAAATAAGCGTAGA	540
Db	195	IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysValArg	214
QY	541	CCATTATCTACAACTCTGCCCAACCATCGATTAAACGTGTAAACCGTAATCAATTAGCG	600
Db	215	ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla	234
QY	601	GGCGCAACAGGTTCCGAATGTTAACCATTTAATTAAGTTTACTGATCAAAAGTATTACTGAA	660

DT 08-SBP-2005 (first entry)

DE Ligand binding region of bacterial adhesin, SdrG.

XX candida infection; candida albicans infection; infection;

XX antibody therapy; antigen; diagnosis; immunotherapy;

KW serine-aspartate repeat G; SdrG; adhesin; fungicide.

XX Staphylococcus epidermidis.

OS

XX WO2005060713-A2.

PN

XX 07-JUL-2005.

PD

XX 20-DEC-2004; 2004WO-US043276.

PF

XX 19-DEC-2003; 2003US-0530654P.

PR

XX 13-APR-2004; 2004US-0561540P.

PR

XX 29-APR-2004; 2004US-0566082P.

PR

XX (INH1-) INHIBITEX INC.

XX (TEXA) UNIV TEXAS A & M SYSTEM.

PA

XX Patti J, Vernachio J, Liu Y, Hook M, Bowden M, Singvall JK;

PI

XX WPI; 2005-479410/48.

DR

XX Inhibiting a Candidial infection for preventing or treating such

XX infections by administering a purified human donor immunoglobulin

PT composition having antibody titer to *S. aureus* Cifa protein and/or *S.*

PT epidermidis SdrG protein.

PT

XX Example 7; Fig 4; 42pp; English.

PS

XX The invention relates to a method of inhibiting a Candidial infection.

XX The method comprises administering to a patient a purified human donor

CC immunoglobulin composition having an antibody titer to a *Staphylococcus*

CC aureus Clumping Factor A (CfA) protein in combination with an antibody

CC titer to a *Staphylococcus epidermidis* serine-aspartate repeat G (SdrG)

CC protein where both antibody titers are higher than that found in pooled

CC intravenous immunoglobulin obtained from unselected human donors in an

CC amount effective to inhibit a Candidial infection. Also described are:

CC (1) a method of diagnosing a Candidial infection comprising introducing

CC the immunoglobulin composition to a sample suspected of containing

CC antigens from *Candida* yeast for a time sufficient to allow the *Candida*

CC antigens to bind to the antibodies in the immunoglobulin composition, and

CC diagnosing a Candidial infection by determining if *Candida* antigens in

CC the sample have bound to the antibodies in the immunoglobulin composition

CC ; (2) a method of identifying a Candidial surface antigen comprising

CC obtaining a cell wall extract from a culture of *Candida* yeast cells,

CC introducing into the extract the immunoglobulin composition, and

CC detecting *Candida* antigens that have bound to the antibodies in the

CC immunoglobulin composition; (3) a probe for identifying Candidial surface

CC antigens comprising the immunoglobulin composition, and a means for

CC detecting binding of the antibodies in the immunoglobulin composition

CC with Candidial surface antigens; and (4) a method of inhibiting an

CC infection caused by *Candida albicans* comprising administering to a

CC patient a purified human donor immunoglobulin composition as cited above

CC in an amount effective to inhibit an infection caused by *Candida*

CC albicans. The methods and compositions are useful for treating or

CC preventing infections caused by *Candida albicans*. This sequence

CC represents the ligand binding region of a bacterial adhesin.

XX

SQ Sequence 331 AA;

Alignment Scores:

Pred. No.:	1,17e-121	Length:	331
Score:	1702.00	Matches:	325
Percent Similarity:	99.4%	Conservative:	4
Best Local Similarity:	98.2%	Mismatches:	2
Query Match:	56.2%	Indels:	0
DB:	9	Gaps:	0

US-10-806-288-12 (1-1746) x AEB23146 (1-331)

QY 601 GCGGAACAAGGTTGGAATGTTAAACCAATTAATAAAGTTACTGATCAAAGTATTACTGAA 660

DB 1 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 20

QY 661 GGATATGATGATGAGTGAAGGTGTTAATAAGACACATGATGCTGAAACCTTAATCTATGAT 720

DB 21 GlyTyrAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 40

QY 721 GTAACCTTTTGAAGTAGATGATGAAGGTGAATCTGGTGATACGATGACAGTGGATATAGAT 780

DB 41 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 60

QY 781 AAGATACAGTTCCATCAGATTTAACCGATAGCTTTTACAATATACCAATAAATAAAGATAAT 840

DB 61 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 80

QY 841 TCTGGAGAAATCATCGCTACAGTACTTATGATAACAAAAATAACAAATCACCCTACTACT 900

DB 81 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr 100

QY 901 TTTACAGATTATGTAGATAAGTATGAAATATTTAAAGCACACACCTTAAATTAACGTATAC 960

DB 101 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 120

QY 961 ATTGATAAATCAAGGTTCCAAATAATAATACCAAGTTAGATGATAGATAATAAAGCGCC 1020

DB 121 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 140

QY 1021 CTTTCATCAGTAAATAAACAATACGGTTGGAATATCAAGACCTAACGAAATCCGACT 1080

DB 141 LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr 160

QY 1081 GCTAACCTTCAAAGTATGTTTACAATATAGATACGAAAAATCATACAGTTGAGCAACG 1140

DB 161 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 180

QY 1141 ATTATATTAAACCTCTCGTTATTGAGCCAGCAAGAAACAATGTAATATTTCAGGGAAT 1200

DB 181 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 200

QY 1201 GGTGATGAAGGTTCAACAATTATAGACGATAGCACAAATAATTAAGTTTATAGGTGGA 1260

DB 201 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 220

QY 1261 GATAATCAAAATTTACCAGATAGTAACAGAAATTTATGATTACAGTGAATGAAGATGTC 1320

DB 221 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 240

QY 1321 ACAATATGATGATTATGCCCAATTAGCAATATATATGATGTGATATTAATTTTGGTAAT 1380

DB 241 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 260

QY 1381 ATAGATTCCACCATATATTAAAGTTATTAGTAAATATATGACCTTAATAGAGTATTAC 1440

DB 261 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 280

QY 1441 ACGACTATACAGCAAACTGTGCAATGACAGACCACTATAAATGAGTATACTGCTGAGTTT 1500

DB 281 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 300

QY 1501 AGAACAGCATCTATGATAATCAATGCTTCTCTACAGTTTCAGGTCAGGTCAGGCAAGGT 1560

DB 301 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 320

QY 1561 GACTTGCCCTCCTGAAAAAATCTTATAAAATCGGA 1593

DB 321 AspLeuProProGluLysThrTyrIleGly 331

RESULT 13

ABM79016

ID ABM79016 standard; protein; 343 AA.

XX ABM79016;  
 AC  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Staphylococcus epidermidis SdrG N2N3 domain.  
 XX  
 KW SdrG; surface protein; infection; antibacterial; vaccine.  
 XX  
 OS Staphylococcus epidermidis.  
 XX  
 XX W02003076470-A1.  
 XX  
 XX 18-SEP-2003.  
 XX  
 XX 05-MAR-2003; 2003WO-US006415.  
 XX  
 XX 05-MAR-2002; 2002US-0361324P.  
 XX  
 XX (INH1-) INHIBITEX INC.  
 XX (TEXA) UNIV TEXAS A & M SYSTEM.  
 XX  
 XX Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;  
 XX Robbins J, Vernachio J, Bowden MG;  
 XX  
 XX WPI; 2003-722324/68.  
 XX  
 XX N-PSDB; ACF80625.  
 XX  
 XX New antibody recognizing a Staphylococcus epidermidis protein comprising  
 PT SdrG N1N2N3, SdrG N2N3 or SdrGTR2 useful for preparing a composition for  
 PT treating or preventing a coagulase-negative Staphylococcal infection.  
 XX  
 XX Claim 27; Page 25; 78pp; English.  
 XX  
 XX The present sequence comprises the protein sequence of the N2N3 region  
 CC (amino acids 273-597) of the SdrG surface protein of coagulase-negative  
 CC Staphylococcus epidermidis. A claimed antibody recognises a protein  
 CC selected from SdrG N1N2N3, N2N3 and TR2. The antibody may be a monoclonal  
 CC antibody, including a chimeric, murine, humanized, human or single chain  
 CC monoclonal antibody, which prevents a coagulase-negative staphylococcal  
 CC infection in a human or animal by inhibiting binding of staphylococcus  
 CC bacteria to fibrinogen. Such antibodies can be used to treat or prevent  
 CC staphylococcal infections including nosocomial coagulase-negative  
 CC staphylococcal infections in low birth weight infants. A claimed vaccine  
 CC comprises the isolated SdrG N1N2N3, N2N3 or TR2 protein  
 XX  
 XX Sequence 343 AA;  
 SQ  
 Alignment Scores:  
 Pred. No.: 2,32e-119 Length: 343  
 Score: 1672.00 Matches: 319  
 Percent Similarity: 99.4% Conservative: 5  
 Best Local Similarity: 97.9% Mismatches: 2  
 Query Match: 55.3% Indels: 0  
 DB: 7 Gaps: 0  
 US-10-806-288-12 (1-1746) x ABM79016 (1-343)  
 QY 601 GCGGAACAGGTCGATGTTTAAACCATTTAAAGTTACTGATCAAGTATTACTGAA 660  
 DB 18 SerGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 37  
 QY 661 GGATATGATGATAGTGAAGGTGTTATTAAAGCACATGATGCTGAAACTTAATCTATGAT 720  
 DB 38 GlyTyrAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 57  
 QY 721 GTAACATTTGAAGTAGATGATAAGGTGAATCTCGGTGATACGATGACAGTGGATATAGAT 780  
 DB 58 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 77  
 QY 781 AAGNATHACAGTTCATCAGATTTAAACCGATAGCTTTACAATACCAAAAATAAAGATAAT 840  
 DB 78 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 97

QY 841 TCTGGAGAAATCATCGCTACAGGTACTTATGATAACAAATAAAACAAATCACCCTACT 900  
 DB 98 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr 117  
 QY 901 TTTACAGATTATGATAGATAAGTATGAAATATTAAAGCACACCTTTAAATTAACCTCATAC 960  
 DB 118 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 137  
 QY 961 ATTGATAAATCAAGGTTCCAAATAATAACCAAGTTAGATGTAGATATATAAACCGCC 1020  
 DB 138 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 157  
 QY 1021 CTTTCATCAGTAAATAAAACAAATTACGGTTTCAATATCAAGACCTAACGAAAAATCGGACT 1080  
 DB 158 LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr 177  
 QY 1081 GCTAACCTTCAAGATGTTTACAATATAGATACGAAAAATCATACAGTTGACCAACG 1140  
 DB 178 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 197  
 QY 1141 ATTTATTATTAACCTCTTCGTTATTTCAGCCCAAGGAAACAAATGTAATATTTCAGGGAAT 1200  
 DB 198 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 217  
 QY 1201 GGTGATGAAGGTTCAACAATTATAGACGATAGCACATAATTAAGTTTATAAGTTTGA 1260  
 DB 218 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 237  
 QY 1261 GATAATCAAAATTTACAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGTC 1320  
 DB 238 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 257  
 QY 1321 ACAATGATGATGATGCCCAATTAGGAAATAATAATGATGCTGATATTAATTTTGGTAAT 1380  
 DB 258 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn 277  
 QY 1381 ATAGATTCCACATATATTATAAGTTATTAGTAAATATGACCCCTAATAAGGATGATTAC 1440  
 DB 278 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 297  
 QY 1441 ACAGTATACAGCAAACTGTGCAACTGACAGACGACTATAAATGAGTATCTGTTGAGTTT 1500  
 DB 298 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 317  
 QY 1501 AGAACAGCATCCTATGATATACAAATGCTTCTCTACAAGTTCAGGTCAAGGACAAAGT 1560  
 DB 318 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 337  
 QY 1561 GACTTGCTCCTCGTCAAAAA 1578  
 DB 338 AspLeuProProGluLys 343  
 RESULT 14  
 ABM79017  
 ID ABM79017 standard; protein; 316 AA.  
 XX  
 AC ABM79017;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Staphylococcus epidermidis SdrG TR2 protein.  
 XX  
 KW SdrG; surface protein; infection; antibacterial; vaccine.  
 XX  
 OS Staphylococcus epidermidis.  
 XX  
 XX W02003076470-A1.  
 XX  
 XX 18-SEP-2003.  
 XX  
 XX 05-MAR-2003; 2003WO-US006415.  
 XX  
 XX

PR	05-MAR-2002; 2002US-0361324P.	QY	1081	GCTAACCTTCAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTTGACCAACG	1140
XX	(INH1-) INHIBITEX INC.	Db	172	AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr	191
PA	(TEXA ) UNIV TEXAS A & M SYSTEM.	QY	1141	ATTATATTAAACCTCTCTCGTTATTTCAGCCAGCAAACTAAATCTAAATATTTTCAGGGAAT	1200
XX	Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M; Robbins J, Vernachio J, Bowden MG;	Db	192	IleTyrlleAsnProleuArgTySerAlaLysGluThrAsnValAsnIleSerGlyAsn	211
XX	WPI; 2003-722324/68.	QY	1201	GGTGATGAAGGTTCAACAATTATAGACGATAGCACAAATAATTAAGTTTATAAGTTTGGGA	1260
DR	N-PSDB; ACP80626.	Db	212	GlyAspGluGlySerThrIlelleAspAspSerThrIlelleLysValTyLysValGly	231
XX	New antibody recognizing a Staphylococcus epidermidis protein comprising SdrG N1N2N3, SdrG N2N3 or SdrGTR2 useful for preparing a composition for treating or preventing a coagulase-negative Staphylococcal infection.	QY	1261	GATNATCAAAATTTACAGATAGTACAGNATTTATGATTACAGTACAGTACGATGATGTC	1320
PT		Db	232	AspAsnGlnAsnLeuProAspSerAsnArgIleTyAspTySerGluTyGluAspVal	251
XX	Claim 27; Page 26; 78pp; English.	QY	1321	ACAAATGATGATTATATCCCAATTTAGGAAAATAATAATGATGTGAATATTATTTTGGTAAT	1380
CC	The present sequence comprises the protein sequence of the TR2 protein (amino acids 273-577) of the SdrG surface protein of coagulase-negative Staphylococcus epidermidis. A claimed antibody recognises a protein selected from SdrG N1N2N3, N2N3 and TR2. The antibody may be a monoclonal antibody, including a chimeric, murine, humanized, human or single chain monoclonal antibody, which prevents a coagulase-negative staphylococcal infection in a human or animal by inhibiting binding of staphylococcus bacteria to fibrinogen. Such antibodies can be used to treat or prevent staphylococcal infections including nosocomial coagulase-negative staphylococcal infections in low birth weight infants. A claimed vaccine comprises the isolated SdrG N1N2N3, N2N3 or TR2 protein	Db	252	ThrAsnAspAspTyAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn	271
XX	Sequence 316 AA;	QY	1381	ATAGATTCCACATATATTTAAAGTTATTAGTAAATATGACCTTAATAGAGATGATTAC	1440
Alignment Scores:		Db	272	IleAspSerProTyrllelleLysValIleSerLysTyAspProAsnLysAspAspTy	291
Pred. No.:	5.94e-111	QY	1441	ACGACTATACAGCAAACTGTCGACAAATGCAGACGACTATAAATGAGTATCTGCTGAGTTT	1500
Score:	1562.00	Db	292	ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyThrGlyGluPhe	311
Percent Similarity:	99.3%	QY	1501	AGAACAGCATCCTAT 1515	
Best Local Similarity:	97.7%	Db	312	ArgThrAlaSerTy 316	
Query Match:	51.6%	RESULT 15			
DB:	7	AY08643			
		ID	AY08643	standard; protein; 1166 AA.	
		AC	AY08643;		
		XX	20-MAR-2003 (revised)		
		DT	09-AUG-1999 (first entry)		
		XX	S. aureus SdrE protein.		
		XX	Fibrinogen-binding protein; alpha chain; beta chain; ClfB; SdrC; SdrD; SdrE; fibrinogen; medical device; competitive inhibitor; pharmaceutical; treatment; infection; septicemia; osteomyelitis; mastitis; endocarditis; extracellular matrix; vascular graft; vascular stent; vaccine; intravenous catheter; artificial heart valve; cardiac assist device; antibacterial.		
		XX	Staphylococcus aureus.		
		OS	WO9277109-A2.		
		XX	03-JUN-1999.		
		PD	25-NOV-1998; 98WO-US025246.		
		XX	26-NOV-1997; 97US-0066815P.		
		PR	31-AUG-1998; 98US-0098427P.		
		XX	(INH1-) INHIBITEX INC.		
		PA	(FORP-) FORPAS T/A BIORSEARCH IRELAND.		
		PA	(TEXA ) UNIV TEXAS A & M.		
		PA	(PATT/) PATTI J M.		
		PA	(POST/) FOSTER T J.		
		PA	(JOSE/) JOSEFSSON E.		
		PA	(EIDH/) EIDHIN D N.		
		PA	(HOOK/) HOOK M A O.		
		XX	(PERK/) PERKINS S E.		
		XX	Patti JM, Foster TJ, Josefsson E, Eidhin DN, Hook MAO;		
		PI	Perkins SE;		

XX

WPI; 1999-357844/30.

DR

N-PSDB; AAX77594.

XX

Staphylococcus aureus fibrinogen-binding proteins for treating septicemia, osteomyelitis, mastitis or endocarditis.

PS

Claim 8; Fig 9; 143pp; English.

XX

This invention describes novel Staphylococcus aureus fibrinogen-binding proteins that bind both the alpha and beta fibrinogen chains. The proteins (and their encoding nucleic acids) are ClfB, SdrC, and SdrE. Staphylococcus aureus is thought to utilize fibrinogen to adhere to medical devices, binding proteins that bind both the alpha and beta fibrinogen chains (ClfB, SdrC, SdrD and SdrE) can therefore be used as competitive inhibitors to block this binding. Antibodies against ClfB, SdrC, SdrD and SdrE inhibit ClfB, SdrC, SdrD and SdrE mediated binding. The proteins of the invention can be used in a pharmaceutical composition for the treatment of Staphylococcus aureus infection e.g. septicemia, osteomyelitis, mastitis or endocarditis or to inhibit the binding of S. aureus to the extracellular matrix. The proteins or their fragments may be used to coat a medical device to reduce the S. aureus infection of an indwelling medical device, especially where the medical device is selected from the group consisting of vascular grafts, vascular stents, intravenous catheters, artificial heart valves, and cardiac assist devices. ClfB, SdrC, SdrD, SdrE, or an active fragment, subdomain or encoding gene may be used as a vaccine. The DS (aspartate serine) repeat region or a gene encoding it may be used as an identifying probe for the identification of genes and encoding proteins from Staphylococcus aureus (other than ClfA), S. hemolyticus, S. lugdenensis, and S. schleriferi. The proteins of the invention have antibacterial activity. (Updated on 20 CC -MAR-2003 to correct PA field.)

XX

SQ Sequence 1166 AA;

## Alignment Scores:

Pred. No.:	6.36e-79	Length:	1166
Score:	1144.50	Matches:	263
Percent Similarity:	60.1%	Conservative:	108
Best Local Similarity:	42.6%	Mismatches:	191
Query Match:	37.8%	Indels:	55
DB:	2	Gaps:	18

US-10-806-288-12 (1-1746) x ANY08643 (1-1166)

QY	1	TCTAGTCATGAAGAAAGAAATGATGTCATCAATAATAATCAGTCATCAATAAACAACCGCAT	60
DB	66	AlaThrThrSerAspAsnLysGluValSerGluThrGluAsnAsnSerThrThrGlu	85
QY	61	ATAAACCAATA-----ATTAAAGAAAGAAACGAATACTACGATGCGCATAGAAAAA	114
DB	86	AsnAsnSerThrAsnProIleLysLysGlu-----ThrAsnThrAspSerGlnProGlu	103
QY	115	CGCTCAGAGATGAACAGAGTCACAAACAAATAGATGAAGAAACGAAGCAACATTTTA	174
DB	104	AlaLysLysGluSerThrSerSerThrGlnLysGlnAsnAsnValThrAlaThr	123
QY	175	CAAAAGACCCCTCAAGATAATCTCATCTTACAGAAAGAGGTAAAGATCC-----	228
DB	124	ThrGluThrLysProGlnAsn-----IleGluLysGluAsnValLysProSerThrAsp	141
QY	229	---TCAGTCAGTCAATCTCAAAATTCATCAATTCAGTCTGCCCAACCAACCATCTTCACACA	285
DB	142	LysThrAlaThrGluAspThrSerValIleLeuGluGluLysLysAlaProAsnAsnThr	161
QY	286	ACAATAATAGAGAAGAACTGTTTCAACAGAGTGAATGTAGAGATTCACAGTATCA	345
DB	162	-----AsnAsnAspValThrLysProSer-----ThrSer	172
QY	346	GATTTTCCTAACTCTAAATAAAGAGAGTAACACT-----GAATCTGGTAAAGAA	396
DB	173	GluProSerThrSerGluIleGlnThrLysProThrThrProGlnGluSerThrAsnIle	192

QY	397	GAGAACTACTATAGAGCAACCTTAATAAGTAAAGAGAGATTCACAAACAAGTCAGCCGCTCT	456
DB	193	GluAsnSerGlnProGlnProThrProSerLysValAsp-----AsnGlnValThr	209
QY	457	GGCTATACAAATATAGATGAAATAATTTC-----AATCAAGATGAGTTTAAATTTACCA	513
DB	210	AspAlaThrAsnProLysGluProValAsnValSerLysGluLysLysAsnAsnPro	229
QY	514	-----ATAAATGAATATGAAATAAAGAGTAAAGCTGACCATTA	546
DB	230	GluLysLysLysGluLeuValArgAsnAspSerAsnThrAspHisSerThrLysProVal	249
QY	547	TCTACACATCTGCCCAACCATCGATTAAACGTGTA-----ACCGTA	588
DB	250	AlaThrAlaProThrSerValAlaProLysArgValAsnAlaLysMetArgPheAlaVal	269
QY	589	AATCAATTAAGCGGCGGCAAGGTTTCAATGTTTAAACATTTAATTAAGTTTACTGATCAA	648
DB	270	AlaGlnProAlaAlaValAlaSerAsnAsnValAsnAspLeuIleLysValThrLysGln	289
QY	649	AGTATTACTGAAGGATATGATGATGAGTGAAGTGTATTAAAGCACATGATGCTGAAAC	708
DB	290	ThrIleLysValGly---AspGlyLysAspAsnValAlaAlaHisAspGlyLysAsp	308
QY	709	TTAATCTATCATGTPAACTTTTGAAGTAGATGATGAAGTGAATCTGTGTATACGATGACA	768
DB	309	IleGluThrAspThrGluPheThrIleAspAsnLysValLysLysGlyAspThrMetThr	328
QY	769	GTGGATATAGATAGATACAGTTCATCCATGATTTACCGATAGCTTTTACATACCAAAA	828
DB	329	IleAsnTyrAspLysAsnValIleProSerAspLeuThrAspLysAsnAspProIleAsp	348
QY	829	ATAAAGATAAATCTCGAGAAATCATCGCTACAGGTACTTATGATAACAAAAATAACAA	888
DB	349	IleThrAspProSerGlyGluValIleAlaLysGlyThrPheAspLysAlaThrLysGln	368
QY	889	ATCAGCTATCTTTACAGATTTAGTAGATGAAGTATGAAATATTAAGACACACCTTAAA	948
DB	369	IleThrThrThrPheThrAspThrValAspLysThrGluAspIleLysSerArgLeuThr	388
QY	949	TTAAGCTCATACATTTGATTAATCAAGGTTTCCAAATTAATTAACCAAGTAGATGTAGAA	1008
DB	389	LeuTyrSerTyrIleAspLysLysThrValPro---AsnGluThrSerLeuAsnLeuThr	407
QY	1009	TATAAAGCGCCCTTTTCATCAGTAAATAAACAACATACGGTTTGAATATCAAGACCTTAAC	1068
DB	408	PheAlaThrAlaGlyLysGluThrSerGlnAsnValThrValAspThrGlnAspProMet	427
QY	1069	GAAATCGGACTGCTACCTTCAAGTATGTTTACAAATATAGATACGAAATAATCATACA	1128
DB	428	ValHisGlyAspSerAsnIleGlnSerIlePheThrLysLeuAspGluAspLysGlnThr	447
QY	1129	GTTGAGCAACGATTTATATTAACCTCTTCGTTTATTCACCCAGGAACAAATGTAAAT	1188
DB	448	IleGluGlnGlnIleTyrValAsnProLeuLysSerAlaThrAsnThrLysValAsp	467
QY	1189	ATTTCAGGGAATCGT-----GATGAAGGTTTCAACAAAT	1221
DB	468	IleAlaGlySerGlnValAspAspThrGlyAsnIleLysLeuGlyAsnGlySerThrIle	487
QY	1222	ATAGACGATAGCAATAATTAAGTTTATAGGTTGGAGATTAATCAAAATTTTACAGAT	1281
DB	488	IleAspGlnAsnThrGluIleLysValThrLysValAsnSerAspGlnGlnLeuProGln	507
QY	1282	AGTAACAGATTTTATGATACAGTATGATGAGATGTCAAAATGAT---GATTATGCC	1338
DB	508	SerAsnArgIleTyrAspPheSerGlnTyrGluAspValThrSerGlnPheAspAsnLys	527
QY	1339	CAATTAGGAATAATATGATGTAATTAATTAATTTGGTAAATATAGATCCACCATATATT	1398
DB	528	LysSerPheSerAsnAsnValAlaThrLeuAspPheGlyAspIleAsnSerAlaTyrIle	547
QY	1399	ATTAAAGTTTATAGTAAATATGACCTTAATAGGATGATTACAGCACTATACAGCAAACT	1458

```

Db      548  ILeIysValSerIysTyrThrProThrSerAspGlyGluLeuAspIleAlaGInGly 567
Qy      1459 GTGCAATGCAGACGACTATAAATAGTATACCTGGTGAGTTTAGAACAGCATCCTATGAT 1518
Db      568  ThrSerMetArgThrThr---AspLysTyr---GlyTyrTyrAsnTyrAlaGlyTyrSer 585
Qy      1519 AATACAAATTGCTTCTCTACAAAGTTCAGGTCAGGACAGGCAAGTGACTTG---CCTCCTGAA 1575
Db      586  AsnPhelIleValThrSerAsnAspThrGlyGlyAspGlyThrVallysProGluGlu 605
Qy      1576 AAAAATATATAAATCGGAGATTACGTATGGGAAGATGATAGATAAGATGGTATTCAAAAT 1635
Db      606  LysLeuTyrIlysIleGlyAspTyrValTrpGluaspValAspLysAspGlyValGInGly 625
Qy      1636 ACAATGATTAATGAAACCGCTTAGTAAATGTATTGGTAACTTTGACGTATCCTGATGGA 1695
Db      626  ThrAspSerLysGluLysProMetAlaAsnValIleuValThrLeuThrTyrProAspGly 645
Qy      1696 ACTTCAAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTGATGGA 1746
Db      646  ThrThrLysSerValArgThrAspAlaAsnGlyHisTyrGluPheGlyGly 662

```

Search completed: August 12, 2006, 07:52:04  
 Job time : 333 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 12, 2006, 08:44:06 ; Search time 58.4 Seconds  
(without alignments)  
4154.657 Million cell updates/sec

Title: US-10-806-288-12  
Perfect score: 3026  
Sequence: 1 tctagtgtatgaagaaga.....ggaaatatcaattgtatgga 1746

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 4195594

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/abs/ABSSWEB.spool/US10806288/runat\_11082006\_163419\_21409/app\_query.fasta\_1  
-DB=PublishedApplications\_AA\_Main -QFMT=fastan -SUFFIX=rapbm -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blseum2  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abs02p  
-USER=US10806288 @CGN\_1\_1 446 @runat\_11082006\_163419\_21409 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA Main:

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US08\_PUBCOMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10A\_PUBCOMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10B\_PUBCOMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3013	99.6	593	4	US-10-806-288-11
2	3013	99.6	1092	4	US-10-378-674-8
3	3013	99.6	1092	4	US-10-806-288-15
4	3007	99.4	582	4	US-10-806-288-13
5	2810.5	92.9	892	4	US-10-806-288-122A-70481
6	2810.5	92.9	892	4	US-10-661-809-21
7	2810.5	92.9	930	4	US-10-615-383-10
8	2810.5	92.9	930	4	US-10-630-184-10
9	2810.5	92.9	930	4	US-10-689-082-10
10	2810.5	92.9	930	4	US-10-724-972A-5309
11	2670	88.2	549	4	US-10-378-674-9

12	2510.5	83.0	560	4	US-10-378-674-2	Sequence 2, Appli
13	1702	56.2	331	6	US-11-016-564-3	Sequence 3, Appli
14	1672	55.3	343	4	US-10-378-674-4	Sequence 4, Appli
15	1562	51.6	316	4	US-10-378-674-5	Sequence 6, Appli
16	1144.5	37.8	1166	5	US-10-744-672-7	Sequence 7, Appli
17	1144.5	37.8	1166	5	US-10-744-616-7	Sequence 7, Appli
18	1142.5	37.8	1166	5	US-10-470-048B-153	Sequence 153, App
19	1137.5	37.6	1141	4	US-10-282-122A-70251	Sequence 70251, A
20	1116.5	36.9	670	4	US-10-282-122A-70444	Sequence 70444, A
21	857	28.3	278	5	US-10-793-626-2700	Sequence 2700, Ap
22	795.5	26.3	338	6	US-11-016-564-4	Sequence 4, Appli
23	576	19.0	1315	5	US-10-744-672-5	Sequence 5, Appli
24	576	19.0	1315	5	US-10-744-616-5	Sequence 5, Appli
25	576	19.0	1315	5	US-10-470-048B-124	Sequence 124, App
26	576	19.0	1349	3	US-09-815-242-5898	Sequence 5898, Ap
27	576	19.0	1349	3	US-05-815-242-13137	Sequence 13137, A
28	559	18.5	1385	4	US-10-282-122A-44324	Sequence 44324, A
29	499.5	16.5	932	3	US-09-815-242-5578	Sequence 5578, Ap
30	499.5	16.5	932	3	US-09-815-242-12438	Sequence 12438, A
31	499	16.5	1742	4	US-10-615-383-4	Sequence 4, Appli
32	499	16.5	1742	4	US-10-690-184-4	Sequence 4, Appli
33	499	16.5	1742	4	US-10-689-082-4	Sequence 4, Appli
34	497	16.4	1155	5	US-10-793-626-1780	Sequence 1780, Ap
35	493	16.3	1633	4	US-10-282-122A-70437	Sequence 70437, A
36	489	16.2	953	4	US-10-282-122A-44457	Sequence 44457, A
37	486.5	16.1	1920	4	US-10-282-122A-71413	Sequence 71413, A
38	476	15.7	408	6	US-11-016-564-5	Sequence 5, Appli
39	455	15.0	841	3	US-09-815-242-5779	Sequence 5779, Ap
40	455	15.0	841	3	US-09-815-242-12751	Sequence 12751, A
41	455	15.0	930	5	US-10-744-672-3	Sequence 3, Appli
42	455	15.0	930	5	US-10-744-616-3	Sequence 3, Appli
43	455	15.0	933	5	US-10-470-048B-93	Sequence 93, Appli
44	455	15.0	947	5	US-10-470-048B-86	Sequence 86, Appli
45	454	15.0	936	2	US-08-781-986A-5249	Sequence 5249, Ap

#### ALIGNMENTS

RESULT 1  
US-10-806-288-11  
; Sequence 11, Application US/10806288  
; Publication No. US20040209326A1  
; GENERAL INFORMATION:  
; APPLICANT: Guss, Bengt  
; APPLICANT: Nilsson, Martin  
; APPLICANT: Frykberg, Lars  
; APPLICANT: Lindberg, Martin  
; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from  
; TITLE OF INVENTION: Coagulase-Negative Staphylococcus  
; FILE REFERENCE: guss 09/147405  
; CURRENT APPLICATION NUMBER: US/10/806,288  
; CURRENT FILING DATE: 2004-03-23  
; PRIOR APPLICATION NUMBER: US/09/147,405  
; PRIOR FILING DATE: 1999-04-11  
; PRIOR APPLICATION NUMBER: PCT/SE97/10191  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: SE 9602496-3  
; PRIOR FILING DATE: 1996-06-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
; US-10-806-288-11  
Alignment Scores:  
Pred. No.: 2.29e-193 Length: 593  
Score: 3013.00 Matches: 582  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 99.6% Indels: 0

DB:	4	Gaps:	0
US-10-806-288-12 (1-1746) x US-10-806-288-11 (1-593)			
QY	1	TCTAGTGTGATGAAGAAAAGAAATGATGTGATCAATAATAATCAGTCAATAAATACACCGACGAT	60
DB	8	SerSerAspGluGluLysAsnAspValIleAsnAsnAsnGlnSerIleAsnThrAspAsp	27
QY	61	AATAACCAATTAATAAAGAAAGAAACGAATAACTACGATGGCATAGAAAAACGCTCA	120
DB	28	AsnAsnGlnIleIleLysLysGluGluThrAsnAsnTyrAspGlyIleGluLysArgSer	47
QY	121	GAAGATAGACAGAGTCAACAACAATGTAGATCAAAACGAACCAACATTTTACAAAAG	180
DB	48	GluAspArgThrGluSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys	67
QY	181	ACCCCTCAAGATATATCTCTTACAGAAAGAGAGGTAAGAAATCCTCATCAGTCGAA	240
DB	68	ThrProGlnAspAsnThrHisLeuThrGluGluValLysGluSerSerSerValGlu	87
QY	241	TCCTCAAAATTCATCAATTGATCTACGCCCACCAACCATCTCCACAACAATAAATAGAGAA	300
DB	88	SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrThrIleAsnArgGlu	107
QY	301	GAATCTGTTCAACAAGTGAATGTAGAGATTTCACCGTATCAGATTTTGTCTACTCT	360
DB	108	GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer	127
QY	361	AAAAATAAAGAGAGTACACTGTAATCTGGTAAAGAGAGAAATACTATAGACCAACCTAAT	420
DB	128	LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn	147
QY	421	AAAGTAAAGAGATTCAACAACAGTCAGCCGCTGCGCTATACAAATATAGATGAAAAA	480
DB	148	LysValLysGluAspSerThrThrSerGlnProSerGlyTyrThrAsnIleAspGluLys	167
QY	481	ATTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATCAATATCAAAATAGAGCTAGA	540
DB	168	IleSerAsnGlnAspGluLeuLeuAsnLeuProLysGlnGluThrGluAsnLysAlaArg	187
QY	541	CCATTATCTCAACATCTGCCCAACCATCGATTAAACGTGAACCGTAAATCAATTAGCG	600
DB	188	ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla	207
QY	601	CCGGAACAAGCTTCGAATGTTACCATTTAATTAAGTTACTGATCAAGTATTACTGAA	660
DB	208	AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu	227
QY	661	GGATATGATGATGTGAAGGTGTTATTAAAGCATCATGCTGAAACCTTAATCTATGAT	720
DB	228	GlyTyrAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp	247
QY	721	GTAACCTTTGAAGTATGATAAGGTGAATCTGGTGATACGATGACAGTGGATATAGAT	780
DB	248	ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAspIleAsp	267
QY	781	AAGATACAGTTCATCAGATTTTAACCGATAGCTTTACATACCAAAAATAAAGATAAT	840
DB	268	LysAsnThrValProSerAspLeuThrAspSerPheThrIleProLysIleLysAspAsn	287
QY	841	TCTGGAGAAATCATCGCTACAGGTACTTATGATAACAAAATAAACAACATCACCTACT	900
DB	288	SerGlyGluIleAlaThrGlyThrTyrAspAsnLysAsnLysGlnIleThrTyrThr	307
QY	901	TTTACAGATTATGTAGATAAGTATGAATAATTAAGACACACCTTTAAATTAACGTCATAC	960
DB	308	PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr	327
QY	961	ATTGATAAATCAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATAATAAAGCGCC	1020
DB	328	IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla	347
QY	1021	CTTTTCATCAGTAAATAAACAATTTACGGTTTGAATATCAAGACCTCAACGAAAATCGGACT	1080

DB	348	LeuSerSerValAsnLysThrIleThrValGluTyrGlnArgProAsnGluAsnArgThr	367
QY	1081	GCTAACCTTTCAAGATATGTTTACAAATATAGATACGAAAAAATCATACAGTTGAGCAACG	1140
DB	368	AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr	387
QY	1141	ATTATATTAAACCTCTTCTGTTATTTCAGCCAGGAAACAAATGTAAATATTATTCAGGGAAT	1200
DB	388	IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn	407
QY	1201	GGTGATGAAGGTTTCAACAATATAGACGATAGCACAAATTAATAAGTTTATAAGTTGGGA	1260
DB	408	GlyAspGluGlySerThrIleIleAspAspSerThrIleLysValTyrLysValGly	427
QY	1261	GATAATCAAAATTTACAGATAGTAAACAGATTTATGATTACAGTGAATTAAGATGTC	1320
DB	428	AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal	447
QY	1321	ACAAATGATGATTATGCCCAATTAGGAAATATAATATGATGTGAATATTATTTGTTAAT	1380
DB	448	ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn	467
QY	1381	ATAGATTCCACCATATATTATTAAAGTTATTAGTAAATATGACCCCTTAATAAGGATGATTAC	1440
DB	468	IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr	487
QY	1441	ACGACTATACAGCAAACTGTGCAATGCAGACGACTATAAATGAGTATACTTGTGAGTTT	1500
DB	488	ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe	507
QY	1501	AGAACAGCATCTCATGATAATACAATGCTTCTCTCTACAGTTTCAGGTCAGGCAAGCAGGT	1560
DB	508	ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly	527
QY	1561	GACTTCCTCTCTGAAAAAATCTATAAAATCGGAGATTACGTATGGGAAGATGTAGATAAA	1620
DB	528	AspLeuProProGluLysThrTyrLysIleGlyAspTyrValTyrGluAspValAspLys	547
QY	1621	GATGGTATTCAAAATCAAAATGATAATGAAAAACCCCTTAGTAATATGTTGTTAATTTG	1680
DB	548	AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu	567
QY	1681	ACGTATCTCTGATGGAGACTTCMAAAATCAGTCAGAACAGATGAAGATCGGAAATCAATTT	1740
DB	568	ThrTyrProAspGlyThrSerLysSerValArgThrAspGluAspGlyLysTyrGlnPhe	587
QY	1741	GATGGA 1746	
DB	588	AspGly 589	

RESULT 2

US-10-378-674-8  
; Sequence 8, Application US/10378674  
; Publication No. US20040006209A1  
; GENERAL INFORMATION:  
; APPLICANT: PARTI, Joseph M.  
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATIVE  
; TITLE OF INVENTION: STAPHYLOCOCCAL PROTEINS  
; FILE REFERENCE: P07556US01/BAS  
; CURRENT APPLICATION NUMBER: US/10/378,674  
; CURRENT FILING DATE: 2003-03-05  
; PRIOR APPLICATION NUMBER: 60/361,324  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 1092  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-10-378-674-8  
Alignment Scores:

Pred. No.: 2,33e-193 Length: 1092  
 Score: 3013.00 Matches: 582  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 99.6% Indels: 0  
 DB: 4 Gaps: 0

US-10-806-288-12 (1-1746) x US-10-378-674-8 (1-1092)

Qy	1	TCTAGTGATGAAGAAAAGAAATGATGATCAATAATAATCAGTCAATAAAACACCGACGAT	60
Db	75	SerSerAspGluGluLysAsnAspValIleAsnAsnAsnGlnSerIleAsnThrAspAsp	94
Qy	61	AATAACCAATAATTAATAAAAGAGAAACGAATAACTACGATGCGCATAGAAAAACGCTCA	120
Db	95	AsnAsnGlnIleIleLysLysGluGluThrAsnAsnTyrAspGlyIleGluLysArgSer	114
Qy	121	GAAGATAGACAGATCAACACAAATCTAGATGAAGAAAGCAAGCAACATTTTTCACAAAG	180
Db	115	GluAspArgThrGluSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys	134
Qy	181	ACCCCTCAAGATAATCTCATCTTACAGAAGAGGTAAGAAAGATCCTCATCAGTCGAA	240
Db	135	ThrProGlnAspAsnThrHisLeuThrGluGluValLysGluSerSerSerValGlu	154
Qy	241	TCCTCAAAATTCATCAATGTACTGCCCAACCAACCATCTCCACACAAATAAATAGAGAA	300
Db	155	SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrThrIleAsnArgGlu	174
Qy	301	GAATCTGTTCAACAAAGTATATGTAGAGATTTCACAGTATCAGATTTTGTCACTCT	360
Db	175	GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer	194
Qy	361	AAATAAAAGAGATTAACACTGAACTCTGTTAAAGAGAGATCTATAGACCACTAAT	420
Db	195	LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn	214
Qy	421	AAAGTAAAGAGATTCAACAAACAGTCAGCCGCTCTGGCTATACAAATATAGATGAAAA	480
Db	215	LysValLysGluAspSerThrThrSerGlnProSerGlyThrAsnIleAspGluLys	234
Qy	481	ATTTCAAATCAAGATAGTATTAAATTTACCAATAAATGATATGAATAAGGCTAGA	540
Db	235	IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysAlaArg	254
Qy	541	CCATTATCTCAACATCTGCCCAACCATCGATTAAAGCTGTAAACCGTAATCAATTAGCG	600
Db	255	ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla	274
Qy	601	CGGGAACAAGTTCCGAATGTTAACCATTTAATTAAGTTACTGATCAAAAGTATTACTGAA	660
Db	275	AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu	294
Qy	661	GGATATGATGATAGTGAAGGTGTTATTAAAGCACATGATGCTGAAAACTTAATCTATGAT	720
Db	295	GlyTyrAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp	314
Qy	721	GTAATTTTCAAGTAGATGATAGCTGAATCTGCTGATACGATACGATGATATAGAT	780
Db	315	ValThrPheGluValAspAspLysValIleSerGlyAspThrMetThrValAspIleAsp	334
Qy	781	AAGAATACAGTTCCATCAGATTAAACCGATAGCTTTTACAATACCAAAATAAAGATAAT	840
Db	335	LysAsnThrValProSerAspLeuThrAspSerPheThrIleProLysIleLysAspAsn	354
Qy	841	TCTGGGAATATCATCGCTACAGTACTTATGATTAACAAAAATAAACAATCACTATACT	900
Db	355	SerGlyGluIleIleAlaThrGlyThrTyrAspAsnLysAsnLysGlnIleThrTyrThr	374
Qy	901	TTTACAGATTATGTAGATAGATGAAATATTAAGCACACACCTTAATTAACGTCATAC	960
Db	375	PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr	394

Qy	961	ATTGATAAATCAAAGGTTCCAAATTAATAATACCAAGTTAGATGTAGATATAAAACGGCC	1020
Db	395	IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla	414
Qy	1021	CTTTCATCAGTAATAAAACAATTTACGTTGCAATATCAAGACCTTAACGAAAAATCGGACT	1080
Db	415	LeuSerSerValAsnLysThrIleThrValGluTyrGlnArgProAsnGluAsnArgThr	434
Qy	1081	GCTAACCTTCAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAACG	1140
Db	435	AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr	454
Qy	1141	ATTTATATTAACCTCTCTGTTATTCAGCCCAAGAAACAAATGTAAATATTTCAGGGAAT	1200
Db	455	IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn	474
Qy	1201	GGTGATCAAGGTTCAACAATTTATAGACGATAGCACAATTAATTAAGTTTATAAGTTGGA	1260
Db	475	GlyAspGluGlySerThrIleIleAspAspSerThrIleLysValTyrLysValGly	494
Qy	1261	GATAATCAAATTTTACCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGC	1320
Db	495	AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal	514
Qy	1321	ACAAATGATGATTATGCCCAATTTAGGAAATAATAATGATGTGAATATTATTTTGGTAAT	1380
Db	515	ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn	534
Qy	1381	ATGATTTCCACATATATTATTAAGTTATTAGTAAATATATGACCCCTAATAAGGATGTAC	1440
Db	535	IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr	554
Qy	1441	ACGACTATACAGCAAACTGTGCAATGCAACAGCAGCTAATAATGATGATCTGCTGAGTTT	1500
Db	555	ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe	574
Qy	1501	AGAACAGCATCCTATGATAATAACAATTCCTTCTCAAGTTTCAGGTCAAGGCAAGGT	1560
Db	575	ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly	594
Qy	1561	GACTTGCTCTCGAAAACTTATAAATCGGAGATTACGTATGGGAAGATGTAGATAAA	1620
Db	595	AspLeuProGluLysThrTyrLysIleGlyAspTyrValTyrGluAspValAspLys	614
Qy	1621	GATGGTATTCAAAATCAAAATGATAATGAAAAACCGCTTAGTATGATTGTTGTAACCTTG	1680
Db	615	AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu	634
Qy	1681	ACGTATCCTGATGGAATTCAAAATCAGTCAGAACAGATCAAGATCGGAATATCAATTT	1740
Db	635	ThrTyrProAspGlyThrSerLysSerValArgThrAspGluAspGlyLysTyrGlnPhe	654
Qy	1741	GATGGA 1746	
Db	655	AspGly 656	

RESULT 3  
 US-10-806-288-15  
 ; Sequence 15, Application US/10806288  
 ; Publication NO. US20040209326A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guss, Bengt  
 ; APPLICANT: Nilsson, Martin  
 ; APPLICANT: Frykberg, Lars  
 ; APPLICANT: Flock, Jan-Ingmar  
 ; APPLICANT: Lindberg, Martin  
 ; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from  
 ; TITLE OF INVENTION: Coagulase-Negative Staphylococcus  
 ; FILE REFERENCE: guss 09/147405  
 ; CURRENT APPLICATION NUMBER: US/10/806,288  
 ; CURRENT FILING DATE: 2004-03-23  
 ; PRIOR APPLICATION NUMBER: US/09/147,405  
 ; PRIOR FILING DATE: 1999-04-11

; PRIOR APPLICATION NUMBER: PCT/SE97/10191  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: SE 9602496-3  
; PRIOR FILING DATE: 1996-06-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 1092  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-10-806-288-15

## Alignment Scores:

Pred. No.: 2,33e-193 Length: 1092  
Score: 303.00 Matches: 582  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 99.6% Indels: 0  
DB: 4 Gaps: 0

US-10-806-288-12 (1-1746) x US-10-806-288-15 (1-1092)

Qy	1	TCTAGTGATGAAGAAAGAAATGATGTCATCAATAATAATCAGTCAATAAACCACGACGAT	60
Db	75	SerSerAspGluGluLysAsnAspValIleAsnAsnAsnGlnSerIleAsnThrAspAsp	94
Qy	61	AAATACCAATTAATTAAGAAAGAAACGAATAACTACGATGGCATAGAAAAACGCTCA	120
Db	95	AsnAsnGlnIleIleLysGluGluThrAsnAsnTyrAspGlyIleGluLysArgSer	114
Qy	121	GAGATAGACAGAGTCACCAACAAATGTAGTGAAGAAACGAACCAATTTTACAAAAG	180
Db	115	GluAspArgThrGluSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys	134
Qy	181	ACCCCTCAAGATAACTCTCTTACAGAAAGAGGTAAGAAATCCTCATCAGTCGAA	240
Db	135	ThrProGlnAspAsnThrHisLeuThrGluGluValLysGluSerSerValGlu	154
Qy	241	TCCTCAAAATTCATATGATGATGCTGCCCAACACCATCTCACACAAATAATAGAGAA	300
Db	155	SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrThrIleAsnArgGlu	174
Qy	301	GAATCTGTTCAACCAAGTGATATGTAGAAGATTCACACGTATCAGATTTTGTAACTCT	360
Db	175	GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer	194
Qy	361	AAATAAAGAGAGTAACACTGAATCTGGTAAAGAGAGAAATACTATAGACCAACCTAAT	420
Db	195	LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn	214
Qy	421	AAAGTAAAGAGATTCACCAACAGTCACCGCTGGCTATACAAATATAGATGAAGAA	480
Db	215	LysValLysGluAspSerThrThrSerGlnProSerGlyThrAsnIleAspGluLys	234
Qy	481	ATTTCAATCAAGATGAGTTATTAAATTTACCAATAATCAATATGAAATAAGGCTAGA	540
Db	235	IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluThrGluAsnLysAlaArg	254
Qy	541	CCATTATCTAACATCTGCCCAACCATCGATTAAACGTTAAACCGTAAATCAATTAGCG	600
Db	255	ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla	274
Qy	601	CGCGAACAGGTCGAATGTTAAACCATTTAATTAAGTTACTGATCAAGTATTACTGAA	660
Db	275	AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu	294
Qy	661	GGATATGATGATGATGAGGTGTTATTAAAGCACATCATCTGAAAACCTTAATCTATGAT	720
Db	295	GlyTyrAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp	314
Qy	721	GTAACCTTTGAAGTAGATGAAGGTGAATCTGGTGATACGATGACAGTGGATATAGAT	780
Db	315	ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAspIleAsp	334

## RESULT 4

US-10-806-288-13  
; Sequence 13, Application US/10806288  
; Publication No. US20040209326A1

Qy	781	AGAATAACAGTTCCATCAGATTTAACCGATAGCTTTACATACCAAAAAATAAAGATAAT	840
Db	335	LysAsnThrValProSerAspLeuThrAspSerPheThrIleProLysIleLysAspAsn	354
Qy	841	TCTGGAGAAATCATCGCTACAGGTACTTATGATAACAAAAATAAACAATACCTACTACT	900
Db	355	SerGlyGluIleIleAlaThrGlyThrTyrAspAsnLysAsnLysGlnIleThrTyrThr	374
Qy	901	TTTACAGATTATGTAGATAAGTAAATATTAAGACACACCTTAAATTAACGTCATAC	960
Db	375	PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr	394
Qy	961	ATTGATAATCAAGGTTCCAAATATAATCAACGTTAGATCTAGATATATAAAGCGCC	1020
Db	395	IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla	414
Qy	1021	CTTTTCATCAGTAAATAAACAATACGTTGTAATATCAAGACCTAACGAAAAATCGACT	1080
Db	415	LeuSerSerValAsnLysThrIleThrValGluTyrGlnArgProAsnGluAsnArgThr	434
Qy	1081	GCTAACCTTCAAAGTATGTTTCAAAATATAGATATACGAAAAATCATACAGTTGAGCAACG	1140
Db	435	AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr	454
Qy	1141	ATTTATATTAAACCTCTCTGTTATTTCAGCCCAAGGAACAAATCTAAATATTTTCAGGGAAT	1200
Db	455	IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn	474
Qy	1201	GGTGATGAAGGTTCAACAATATTAGACGATAGCACAAATTAATTAAGTTTGA	1260
Db	475	GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly	494
Qy	1261	GATAATCAAAATTTACAGATAGTAACAGAAATTTATGATTTACAGTGAATATGAAGATGC	1320
Db	495	AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal	514
Qy	1321	ACAAATGATGATTTAGCCCAATTAGGAATATAATGATGTGAATATAATTTTGGTAAT	1380
Db	515	ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn	534
Qy	1381	ATAGATTCACCATATATTAAAGTTATTAGTAAATATGACCCCTAATTAAGGATGATTAC	1440
Db	535	IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr	554
Qy	1441	ACGACTATACAGCAAACTGTGCAATGCGACGACACTATAAATGAGTATACTGTGAGTTT	1500
Db	555	ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe	574
Qy	1501	AGAACAGCATCCTATGATAATCAATTGCTTCTCTACAAGTTTCAGTCAAGGACCAAGGT	1560
Db	575	ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly	594
Qy	1561	GACTTCCTCCTGAAAAAATCTTATAAAATCGGAGATTACGTATGGGAAGATGTAGATAAA	1620
Db	595	AspLeuProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys	614
Qy	1621	GATGGTATTCAAAATCAAAATGATAATGAAAAACCCCTTAGTATGTTTGGTAACCTTG	1680
Db	615	AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu	634
Qy	1681	ACGTATCCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAACATGCGAAATATCAATTT	1740
Db	635	ThrTyrProAspGlyThrSerLysSerValArgThrAspGluAspGlyLysTyrGlnPhe	654
Qy	1741	GATGGA 1746	
Db	655	AspGly 656	









```
Qy 1081 GCTAACCTTCAAGCTATGTTTACAAATATAGATACGAAATATCATACAGTTGACGAACG 1140
Db 394 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 413
Qy 1141 ATTTATATTAACCTCTCTCGTTATTTCAGCCCAAGGAAACAAATGTAAATATTTTCAGGGAAT 1200
Db 414 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 433
Qy 1201 GGTGATCAAGGTTCAACAAATATAGACGATAGCACAATTAATAAGTTTATAGGTTGGA 1260
Db 434 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 453
Qy 1261 GATAATCAAAATTTACAGATAGTAACAGAAATTTATGATTACAGTGAATGAAGATGTC 1320
Db 454 AspAsnGlnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 473
Qy 1321 ACAATGATGATTATGCCCAATTAGGAAATTAATATGATGTGAATATTAATTTTGGTAAAT 1380
Db 474 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn 493
Qy 1381 ATAGATTACCATATATTAAGTTATTAGTAAATATGACCCCTAATAAGATGATTAC 1440
Db 494 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 513
Qy 1441 ACGACTATACAGCAAACTGTGACAAATGCAGACGACTATAAATGAGTATCTGTTGAGTTT 1500
Db 514 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 533
Qy 1501 AGAACAGCATCTATGATAATACAAATTCCTTCTCAAGTTTCAGGTCAGGCAAGGT 1560
Db 534 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 553
Qy 1561 GACTTGCTCTGAAACAACTTATAAATCGGAGATTACGTATGGGGAAGATGATAGATAA 1620
Db 554 AspLeuProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys 573
Qy 1621 GATGGTATCAAAATACAAATGATAATGAAACCGCTTAGTAAATGATTGGTAACCTTG 1680
Db 574 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 593
Qy 1681 ACGTATCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT 1740
Db 594 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyrGlnPhe 613
Qy 1741 GATGGA 1746
Db 614 AspGly 615
```

## RESULT 7

```
US-10-615-383-10
; Sequence 10, Application US/10615383
; Publication No. US2004003832A1
; GENERAL INFORMATION:
; APPLICANT: FOSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCUS
; FILE REFERENCE: P06335U03/BAS
; CURRENT APPLICATION NUMBER: US/10/615,383
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: 09/386,962
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 930
; TYPE: PRN
; ORGANISM: Staphylococcus epidermidis
US-10-615-383-10
Alignment Scores:
```

```
Pred. No.: 8 11e-180 Length: 930
Score: 2810.50 Matches: 545
Percent Similarity: 96.2% Conservative: 15
Best Local Similarity: 93.6% Mismatches: 21
Query Match: 92.9% Indels: 1
DB: 4 Gaps: 1

US-10-806-288-12 (1-1746) x US-10-615-383-10 (1-930)
Qy 1 TCTAGTATGAGAAAAGAAATGATGATCAATAATAATCAGTCAATAATAAACACGACGAT 60
Db 73 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 92
Qy 61 AATAACCAATTAATTAATAAAGAAAGAAACGAATAAATCACTGATGCGATAGAAAACGCTCA 120
Db 93 AspAsnGln---IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer 111
Qy 121 GAAGATAGAACACAGTCAACAAACAAATGTAGATGAAACGAACGAACCAACATTTTACAAAAG 180
Db 112 LysAspIleThrGlnSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 131
Qy 181 ACCCTCAAGATAATATCTCATCTTACAGAAAGAGAGTAAAGAAATCCTCATCAGTCGAA 240
Db 132 ThrProGlnAspAsnThrGlnLeuLysGluGluValValLysGluProSerSerValGlu 151
Qy 241 TCCTCAATTCATCAATTCATCTGCTCCCAACACCATCTCACACACAAATAAATAGAGAA 300
Db 152 SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu 171
Qy 301 GAATCTGTTCAAAACAAAGTGTATAATGTAGAAAGATTCACACGATCAGATTTTGTAACTCT 360
Db 172 AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer 191
Qy 361 AAATAAAGAGAGTAACTGAATCTGTGTAAGAAGAGAAATACTATAGAACAACTTAAT 420
Db 192 LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn 211
Qy 421 AAGTAAAGAGAGATTCACACACACACAGTCCGCTCTGGCTATACAAATATAGATGAAAA 480
Db 212 LysValArgGluAspSerIleThrSerGlnProSerSerTyrLysAsnIleAspGluLys 231
Qy 481 ATTTCAAAATCAAGATCAGTTATTAAATTTACCAATAAATGAATATGAAAAATAGGCTAGA 540
Db 232 IleSerAsnGlnAspGluLeuLeuLeuLeuProIleAsnGluTyrGluAsnLysValArg 251
Qy 541 CCATTATCTAACACATCTGCTCCCAACCATCGATTAAACGTTAAACCGTAAATCAATTAGCG 600
Db 252 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 271
Qy 601 GCGGAACAAAGTTCCGAATGTTAACCAATTTAATAAGTTTACTGATCAAAAGTATTACTGAA 660
Db 272 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 291
Qy 661 GGATATGATGATAGTGAAGGTGTTTAAAGACACATGATGCTGAAATCTTAATCTATGAT 720
Db 292 GlyTyrAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 311
Qy 721 GTAACCTTTGAAGTAGATGATGAAGTGAATCTGGTGATACGATGACAGTGGATATGAT 780
Db 312 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 331
Qy 781 AAGAATACAGTTCATCAGATTTTAAACCGATGCTTTACATACCAATAAATAAAGATAAT 840
Db 332 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 351
Qy 841 TCTGGAGAAATCATCGCTACAGGTACTTATGATAACAAAAATAAACAATTAACCTTACT 900
Db 352 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr 371
Qy 901 TTACAGATTATGTAGATAAGTATGAAATATTAAGACACACCTTAATTAATTAAGCTATAC 960
Db 372 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 391
```



```

QY 961 ATTGTAATAATCAAGGTTCCAAATAATAATACCAAGTAGTAGTAGATAATAAAGCGCC 1020
Db 392 IleaSpLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrlsThrAla 411
QY 1021 CTTTCATCAGTAATAAATAAACAATTACGTTGAATATCAAGACCTAAAGCAAAATCGGACT 1080
Db 412 LeuSerSerValAsnLysThrIleThrValGluTyrlsProAsnGluAsnArgThr 431
QY 1081 GCTAACCTTCAAGTATGTTTCAAAATATAGATACGAAAAATCATACAGTTTGAGCAACG 1140
Db 432 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 451
QY 1141 ATTTATATATACCTCTTCGTTATTCACCAAGGAACAATATGTAATATTTTCAGGGAAT 1200
Db 452 IleyrIleAsnProLeuArgTyrlsAlaLysGluThrAsnValAsnIleSerGlyAsn 471
QY 1201 GGTGATGAAGGTTCAACAATTATAGACGATAGCACAAATAATAAGTTTATAAGTTGGA 1260
Db 472 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrlsValGly 491
QY 1261 GATAATCAAAATTTACCAAGATAGTAACAGAAATTTATGATTACAGTGAATATCAAGATGTC 1320
Db 492 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrlsAspTyrlsSerGluTyrlsGluAspVal 511
QY 1321 ACAATGATGATTATGCCCAATTAGGAATAATAATATGATGTAATATTAATTTTGGTAAT 1380
Db 512 ThrAsnAspAspTyrlsAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn 531
QY 1381 ATAGATTACCATATATTTAATTAAGTTATTAAGTAATATGTAATACCTTAATAGGATGATTAC 1440
Db 532 IleaSpSerProTyrlsIleIleLysValIleSerLysTyrlsAspProAsnLysAspAspTyrls 551
QY 1441 ACGACTATACAGCAAACTGTGACATGCGACGACTATAAATAGTATACCTGAGTGGTGGTTT 1500
Db 552 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrlsGlyGluPhe 571
QY 1501 AGAAGCATCCTATGATAATACAAATTCCTTCTTCTACAGTTCAGGTCACAGGCAAGGT 1560
Db 572 ArgThrAlaSerTyrlsAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 591
QY 1561 GACTTGCTCTGAAACAACTTATAAATCGGAGTACGTTACGTTATGCGAGATGATAGATAAA 1620
Db 592 AspLeuProProGluLysThrTyrlsIleGlyAspTyrlsValTrpGluAspValAspLys 611
QY 1621 GATGGTATTCAAAATACAAATGATAATGAAACCGCTTAGTAATGTTTCTGTAACCTTG 1680
Db 612 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 631
QY 1681 ACGTATCCTGATGAACCTTCAAAATCAAGTACAGACAGATGAAGATGGGAAATATCAATTT 1740
Db 632 ThrTyrlsProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyrlsGlnPhe 651
QY 1741 GATCGA 1746
Db 652 AspGly 653

```

## RESULT 8

US-10-690-184-10

```

; Sequence 10, Application US/10690184
; Publication No. US20040141997A1
; GENERAL INFORMATION:
; APPLICANT: POSTER, Timothy
; TITLE OF INVENTION: METHODS FOR TREATING OR PREVENTING INFECTIONS FROM COAGULASE-
; FILE OF INVENTION: NEGATIVE STAPHYLOCOCCI
; FILE REFERENCE: P06335US05/BAS
; CURRENT APPLICATION NUMBER: US/10/690,184
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 09/386,962
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25

```

```

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.11
; SEQ ID NO 10
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-690-184-10

```

```

Alignment Scores:
Pred. No.: 8,11e-180 Length: 930
Score: 2810.50 Marches: 545
Percent Similarity: 96.2% Conservatives: 15
Best Local Similarity: 93.6% Mismatches: 21
Query Match: 92.9% Indels: 1
DB: Gaps: 1

```

US-10-806-288-12 (1-1746) x US-10-690-184-10 (1-930)

```

QY 1 TCTAGTGATGAAGAAAAGAATGATGTGATCAATAATAATCAAGTCAATAAACAACCGACGAT 60
Db 73 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 92
QY 61 AATAACCAATAATAATAAAGAAAGAAACGATAACTACGATGCGATAGAAAAACGCTCA 120
Db 93 AspAsnGln---IleLysLysGluThrAsnSerAsnAspAlaIleGluAsnArgSer 111
QY 121 GAACATAGAACAGAGTCAACAAACAATGTAGATCAAAACGAAGCAACATTTTACAAAG 180
Db 112 LysAspIleThrGlnSerThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 131
QY 181 ACCCTCAAGATAATCTCTTACAGAAAGAGGTAAGAAATCTCTCATCGATCGAA 240
Db 132 ThrProGlnAspAsnThrGlnLeuLysGluValValLysGluProSerSerValGlu 151
QY 241 TCCTCAAAATTCATCAATTGATCTACCCCAACACCATCTCACACAATATAATAGAGAA 300
Db 152 SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu 171
QY 301 GAATCTGTCTCAACAAAGTGAATGTTAGAACGATTCACACGATCATCAGATTTTGTAACTCT 360
Db 172 AlaSerIleGlnThrSerAspAsnGluLysSerArgValSerAspPheAlaAsnSer 191
QY 361 AAAATAAAGAGAGTAAACACTGTAATCTGTTAAAGAGAGATACTATATAGACCAACTAAT 420
Db 192 LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn 211
QY 421 AAAGTAAAGAGATTCACACAAAGTCAGCCGCTCGCTGCTATACAAATATATAGATGAAAAA 480
Db 212 LysValArgGluAspSerIleThrSerGlnProSerSerTyrlsAsnIleAspGluLys 231
QY 481 ATTTCAAAATCAAGATGAGTTTATTAATTTACCAATAAATGAATATGAAATAAGGCTAGA 540
Db 232 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrlsGluAsnLysValArg 251
QY 541 CCATATCTCAACATCTGCCCAACCATCGATTAAACGTTGTAACCGTAAATCAATTAGCG 600
Db 252 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 271
QY 601 GCGGAACAAGTTTCGAATGTTTACCATTTAATTAAGTTACTGATCAAGATTTACTGAA 660
Db 272 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 291
QY 661 GGATATCATGATAGTGAAGGTGTTATTAAAGCACATCATGCTGAAAATCTTAATCTATGAT 720
Db 292 GlyTyrlsAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrlsAsp 311
QY 721 GTAACTTTTGAAGTAGATGATAAGGTGAAATCTGCTGATACGATGACAGTGGATATAGAT 780
Db 312 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 331
QY 781 AGAATAACAGTTTCATCAGATTTAACCGATAGCTTTTACATATACAAAAATAAAGATAAT 840
Db 332 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 351

```

```
QY 841 TCTGGAGAAATCATCGCTACAGGTACTATGATTAACAAAAATAAACAATCACCTACT 900
Db |||||
QY 352 SerGlyGluLeuIleAlaThrGlyThrTyAspAsnThrAsnLysGlnIleThrTyThr 371
Db |||||
QY 901 TTTCACGATTATGATAGTAAAGTAAATTAATTAAGCACACACCTTAATTAACGTCATAC 960
Db |||||
QY 372 PheThrAspTyValAspLysTyGluAsnIleLysAlaHisLeuLysLeuThrSerTy 391
Db |||||
QY 961 ATTGATTAATCAAGGTTCCAAATTAATAATCAACGTTAGATGATAGATTAATAACGGCC 1020
Db |||||
QY 392 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyLysThrAla 411
Db |||||
QY 1021 CTTTCATCAGTAATAAACAATTAACGTTGAATATCAAGACCTTAACGAATTCGACT 1080
Db |||||
QY 412 LeuSerSerValAsnLysThrIleThrValGluTyGlnLysProAsnGluAsnArgThr 431
Db |||||
QY 1081 GCTAACCTTCAAGTATGTTTACAAATATAGATACGAAATAATCATACAGTTTGACAAACG 1140
Db |||||
QY 432 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 451
Db |||||
QY 1141 ATTTATATTAACTCTTCGTTATTCAGCCAAAGAAACAAATGTAATATTTCAGGGAAT 1200
Db |||||
QY 452 IleTyIleAsnProLeuArgTySerAlaLysGluThrAsnValAsnIleSerGlyAsn 471
Db |||||
QY 1201 GGTGATCAAGGTTCAACAATATAGACGATAGACACATAATTAAGTTTATAGTTGGA 1260
Db |||||
QY 472 GlyAspGluGlySerThrIleIleAspAspSerThrIleLysValTyLysValGly 491
Db |||||
QY 1261 GATAATCAAAATTTACAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGC 1320
Db |||||
QY 492 AspAsnGlnAsnLeuProAspSerAsnArgIleTyAspTySerGluTyGluAspVal 511
Db |||||
QY 1321 ACAATGATGATTATGCCCAATAGGAAATAATAATGATGTGAATATTAATTTTGGTAAT 1380
Db |||||
QY 512 ThrAsnAspAspTyAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 531
Db |||||
QY 1381 ATAGATTCCACATATATTAAGTTTATAGTAAATATGACCCCTAATAGGATGATTAC 1440
Db |||||
QY 532 IleAspSerProTyIleIleLysValIleSerLysTyAspProAsnLysAspAspTy 551
Db |||||
QY 1441 ACAGACTATACAGCAAACTGTGACAACTGACAGCACTATAATGATGATGATGAGTTT 1500
Db |||||
QY 552 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyThrGlyGluPhe 571
Db |||||
QY 1501 AGAACAGCATCTATGATATATACAAATGCTTCTCTCAAGGTTCAAGTCAAGGCAAGGT 1560
Db |||||
QY 572 ArgThrAlaSerTyAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 591
Db |||||
QY 1561 GACTTGCTCTCGAAAAAATTAATAATCGAGATTACGTTACGTTGCGGAGATGTAGATAA 1620
Db |||||
QY 592 AspLeuProGluLysThrTyLysIleGlyAspTyValTrpGluAspValAspLys 611
Db |||||
QY 1621 GATGGTATTCAAAATCAAAATGATAATGAAAACCGCTTAGTAAATGATTGTTGTAACCTTG 1680
Db |||||
QY 612 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 631
Db |||||
QY 1681 ACGTATCTCATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT 1740
Db |||||
QY 632 ThrTyProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyGlnPhe 651
Db |||||
QY 1741 GATGGA 1746
Db |||||
QY 652 AspGly 653
```

## RESULT 9

```
US-10-689-082-10
; Sequence 10, Application US/10689082
; Publication No. US20040142348A1
; GENERAL INFORMATION:
; APPLICANT: FOSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCUS
; FILE REFERENCE: P06335US04/BAS
```

```
; CURRENT APPLICATION NUMBER: US/10/689,082
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 09/386,962
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-689-082-10

Alignment Scores:
Pred. No.: 8,11e-180 Length: 930
Score: 2810.50 Matches: 545
Percent Similarity: 96.2% Conservative: 15
Best Local Similarity: 93.6% Mismatches: 21
Query Match: 92.9% Indels: 1
DB: 4 Gaps: 1

US-10-806-288-12 (1-1746) x US-10-689-082-10 (1-930)

QY 1 TCTAGTGTGAGAGAAAAGAAATGATGTCAATCAATTAATCAGTCAATAAATACCGCAGAT 60
Db |||||
QY 73 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 92
Db |||||
QY 61 AATAACCAATTAATTAATAAAGAAAGAAACGAATAAATACGATGCGATAGAAAAACGCTCA 120
Db |||||
QY 93 AspAsnGln---IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer 111
Db |||||
QY 121 GAAGATAGACACAGTCAACAAACAAATGTAGATGAAACCGAAGCAACATTATTTACAAAG 180
Db |||||
QY 112 LysAspIleThrGlnSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 131
Db |||||
QY 181 ACCCTCAAGATTAATCTCATCTTACAGAAAGAGAGTAAAGAAATCCTCATCAGTGGAA 240
Db |||||
QY 132 ThrProGlnAspAsnThrGlnLeuLysGluValValLysGluProSerSerValGlu 151
Db |||||
QY 241 TCCTCAAAATTCATCAATGTGATCTGCCCAACCAACCATCTCACACAACATAAATAGAGAA 300
Db |||||
QY 152 SerSerAsnSerSerMetAspThrAlaGlnProSerHisThrThrIleAsnSerGlu 171
Db |||||
QY 301 GAATCTGTTCAACAAAGTGAATATGATAGAGATTCACGATATCAGATTTTGTAACTCT 360
Db |||||
QY 172 AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer 191
Db |||||
QY 361 AAAATAAAGAGAGTAACTGAATCTGGTAAAGAGAGAGATATCTATAGACCACTAAT 420
Db |||||
QY 192 LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn 211
Db |||||
QY 421 AAAGTAAAGAGAGATTCACAAACAAAGTCAAGCCGCTCTGGCTATACAAATATAGATGAAA 480
Db |||||
QY 212 LysValArgGluAspSerIleThrSerGlnProSerSerTyLysAsnIleAspGluLys 231
Db |||||
QY 481 ATTTCAAAATCAAGATGAGTTTAAATTTTACCAATAAATGAATATGAAAATAAGGCTAGA 540
Db |||||
QY 232 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyGluAsnLysValArg 251
Db |||||
QY 541 CGATTATCTCAACATCTGCCCAACCATCGATTAAACGTTAACCGTAACTCAATTAATAGCG 600
Db |||||
QY 252 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 271
Db |||||
QY 601 GCGGAACAAGTTTCGAATGTTAACCATTTTAAAGTTACTGATCAAGTATTACTGAA 660
Db |||||
QY 272 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 291
Db |||||
QY 661 GGATATGATGATGAGAGGTGTTATTAAAGCAGCATGATGCTGAAATCTTAATCTATGAT 720
Db |||||
QY 292 GlyTyAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyAsp 311
Db |||||
```

```
QY 721 GTAACCTTTTGAAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAGTGGATATAGAT 780
Db ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 331
QY 781 AAGAATACAGTTCATCAGATTACCATGACCTTTTCAATACCAACCAAAATAAAGATATAT 840
Db LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 351
QY 841 TCTGAGAAATCATCGCTACAGGTACTTATCATACAAAATAAACAATCACCTATACT 900
Db SerGlyGluIleAlaThrGlyThrTyxAspAsnThrAsnLysGlnIleThrTyxThr 371
QY 901 TTTACAGATTATGATAGATGATGAAATATTTAAAGCACACCTTTAAATTAACGTATAC 960
Db PheThrAspTyxValAspLysTyxGluAsnIleLysAlaHisLeuLysLeuThrSerTyx 391
QY 961 ATTGATAAATCAAAAGTTCCAAATTAATTAATCAACAGTTAGATGTAGATATAAAGCGCC 1020
Db IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyxLysThrAla 411
QY 1021 CTTTCATCAGTAAATAAAACAATTACGGTTCGAATATCAAGACCTTAACGAAAATCGGACT 1080
Db LeuSerSerValAsnLysThrIleThrValGluTyxGlnLysProAsnGluAsnArgThr 431
QY 1081 GCTAACCTTCAAAGTATGTTTCAAAATATAGATACGAAAAATCATACAGTTTGAGCAACG 1140
Db AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 451
QY 1141 ATTTATATTACCTCTTCGTTATTCACCCAGGAAGAAACAATGTAAATTTTCAGGGAAT 1200
Db IleTyxIleAsnProLeuArgTyxSerAlaLysGluThrAsnValAsnIleSerGlyAsn 471
QY 1201 GGTGATGAAGTTTCAACAATTATAGCATAGCAACAATAATTAAAGTTTATAAGTTTGA 1260
Db GlyAspGluGlySerThrIleIleAspAspSerThrIleLysValTyxLysValGly 491
QY 1261 GATAATCAAAATTTACCAGATAGTAAACAGAAATTTTATGATTACAGTGAATATGAAGATGC 1320
Db AspAsnGlnAsnLeuProAspSerAsnArgIleTyxAspTyxSerGluTyxGluAspVal 511
QY 1321 ACAATGATGATTATGCCAATTAGGAAATAATTAATGATGTGAATATTAATTTGGTAAAT 1380
Db ThrAsnAspAspTyxAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 531
QY 1381 ATAGATTACCATATATTTATAAGTTTATTAGTAATATGACCCCTTAATAGATGATTAC 1440
Db IleAspSerProTyxIleIleLysValIleSerLysTyxAspProAsnLysAspAspTyx 551
QY 1441 ACGACTATACAGCAAACTGTGACAACTGACAGCACTATAATGATGATGATGATGATGATG 1500
Db ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyxThrGlyGluPhe 571
QY 1501 AGAACAGATCCTATGATATATACAAATTTCTTCAAGTTTCAGTTCAGTTCAGTTCAGTAAA 1560
Db ArgThrAlaSerTyxAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 591
QY 1561 GACTTGCTCTGAAAAAATTAATAATCGGAGATTACGTATGCGGAGATGTAGATAAAA 1620
Db AspLeuProGluLysThrTyxLysIleGlyAspTyxValTrpGluAspValAspLys 611
QY 1621 GATGGTATTTCAAAATGATAATGAAAAACCGCTTAGTAATGTATTGTTGTAACCTTTG 1680
Db AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 631
QY 1681 ACGTATCCTGATGAACTTCAAAATCAGTCAGAACAGATGAAGATGCGAAATATCAATTT 1740
Db ThrTyxProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyxGlnPhe 651
QY 1741 GATGGA 1746
Db 652 AspGly 653
```

## RESULT 10

```
US-10-724-972A-5309
; Sequence 5309, Application US/10724972A
; Publication No. US20040147734A1
```

## GENERAL INFORMATION:

```
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
```

```
; SEQ ID NO 5309
```

```
; LENGTH: 930
```

```
; TYPE: PRT
```

```
; ORGANISM: S.epidermidis
```

```
US-10-724-972A-5309
```

## Alignment Scores:

```
Pred. No.: 8,11e-180 Length: 930
Score: 2810.50 Matches: 545
Percent Similarity: 96.2% Conservative: 15
Best Local Similarity: 93.6% Mismatches: 21
Query Match: 92.9% Indels: 1
DB: 4 Gaps: 1
```

```
US-10-806-288-12 (1-1746) x US-10-724-972A-5309 (1-930)
```

```
QY 1 TCTAGTCATGACGAAAAAGAAATGATGTCATCAATAATAATCAGTCATCAATAATAACACCGACGAT 60
Db 73 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 92
QY 61 AATAACCAATAATAATAAAAGAAAGAAACGAAATAACTACGATGGCATAGAAAAACGCTCA 120
Db 93 AspAsnGln--11eLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer 111
QY 121 GAAGATAGACAGAGTCACAAACAATGTAGATGAAACGAAACGAAACGAAATTTTACAAAAG 180
Db 112 LysAspIleThrGlnSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 131
QY 181 ACCCTCAAGATATACTCATCTTTACAGAAAGAGAGGTAAAGAAATCCTCATCAGTCGAA 240
Db 132 ThrProGlnAspAsnThrGlnLeuLysGluGluValValLysGluProSerSerValGlu 151
QY 241 TCCTCAAATTCATCAATTTGATCTACCCCAACCAACCATCTCACACAACAATAAATAGAGAA 300
Db 152 SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu 171
QY 301 GATCTGTTCAAACAGTGTATATGTAGAGATTCACAGTATCAGATTTTGTCTACTCT 360
Db 172 AlaSerIleGlnThrSerAspAsnGluAsnSerArgValSerAspPheAlaAsnSer 191
QY 361 AAAATAAAGAGAGTAACTGATGATCTGTTAAAGAGAGAAATCTATAGAGCAACCTAAT 420
Db 192 LysIleIleGluSerAsnThrGluSerAsnLysGluAsnThrIleGluGlnProAsn 211
QY 421 AAAAGTAAAGAGATTCACAAACAAGTCAGCCGCTCTGGCTATACAAATATAGATGAAAAA 480
Db 212 LysValArgGluAspSerIleThrSerGlnProSerSerTyxLysAsnIleAspGluLys 231
QY 481 ATTTCAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAATAAAGGCTAGA 540
Db 232 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyxGluAsnLysValArg 251
```

```
QY 541 CCATTATCTCAACATCTGCCACCATCGATTAAACGTGTAAACCGTAAATCAATTAGCG 600
Db 252 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 271
QY 601 GCGGAACAAGGTTTGGAAATGTTAAACCAATTAATTAAGTTACTGATCAAAAGTATTACTGAA 660
Db 272 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 291
QY 661 GGATATGATGATAGTAGTGAAGGTGTTATTAAAGCACATGCTGTAAGAACTTAATCTATGAT 720
Db 292 GlyTyrAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 311
QY 721 GTAACTTTTCAAGTAGATGATAAGCTGAAATCTGGTCATACGATGACAGTGGATATAGAT 780
Db 312 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 331
QY 781 AAGAATACAGTTCCATCAGATTTTAACCGATAGCTTTACAATACCAAAATAAAACAATCACTACT 840
Db 332 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 351
QY 841 TCTGGAGAAATCATCGCTCAGAGTACTTATGATAACAAAATAAAACAATCACTACTACT 900
Db 352 SerGlyGluIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr 371
QY 901 TTTACAGATTATGTAGATAAGTAAATATTAAGCACACACTTAAATTAACGTCATAC 960
Db 372 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 391
QY 961 ATTGATAAATCAAAGGTTCCAAATTAATAACCAAGTTAGATGATGATAATAAAACGGCC 1020
Db 392 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 411
QY 1021 CTTTCATCAGTAATAAAACAATTTACCGTTGAATATCAAGACCTTAACGAAATTCGGACT 1080
Db 412 LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr 431
QY 1081 GCTAACTTCAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTTGACGAACG 1140
Db 432 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 451
QY 1141 ATTTATATTAACCTCTCTGTTATTTCAGCCAAAGAAACAAATGTAAATATTTTCAGGGAAT 1200
Db 452 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 471
QY 1201 GGTGATGAAGTTTCAACAATATAGACGATAGCAATATTAAGTTTATAGTTTGA 1260
Db 472 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 491
QY 1261 GATAATCAAATTTTACCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGTC 1320
Db 492 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 511
QY 1321 ACAAAATGATGATTATGCCCAATTAGGAAATAATAATGATGTGAATATTAATTTTGGTAAT 1380
Db 512 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 531
QY 1381 ATAGATTCACCATATATTAAGTTATTAAGTTATATGATATGACCCCTAATAAGATGATTAC 1440
Db 532 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 551
QY 1441 ACCGACTACAGCAAACTGTGACAAATCGACAGCACTAATAATAGTAGTACTGTTGAGTTT 1500
Db 552 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 571
QY 1501 AGACAGCATCCTATGATAATACAAATTCCTTCTCAAGTTCCAGGTCAGGACACAGGT 1560
Db 572 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 591
QY 1561 GACTTGCTCTGAAAAAATTATAAATCGGAGATACGATTCGGGAAGATGTAGATAAA 1620
Db 592 AspLeuProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys 611
QY 1621 GATGGTATTCAAAATACAAATGATAATGAAAAACCGCTTAGTAATGATTGGTAACTTTG 1680
```

```
Db 612 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 631
QY 1681 ACATATCCTGATCGAACTTCAAATAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT 1740
Db 632 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyrGlnPhe 651
QY 1741 GATGGA 1746
Db 652 AspGly 653

RESULT 11
US-10-378-674-9
; Sequence 9, Application US/10378674
; Publication No. US20040006209A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATIV
; FILE OF INVENTION: STAPHYLOCOCCAL PROTEINS
; FILE REFERENCE: P07556US01/BAS
; CURRENT APPLICATION NUMBER: US/10/378,674
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: 60/361,324
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-9

Alignment Scores:
Pred. No.: 1,99e-170 Length: 549
Score: 2670.00 Matches: 519
Percent Similarity: 99.2% Conservative: 3
Best Local Similarity: 98.7% Mismatches: 4
Query Match: 88.2% Indels: 0
Db: 4 Gaps: 0

US-10-806-288-12 (1-1746) x US-10-378-674-9 (1-549)
QY 1 TCTAGTGATCAAGAAAAGAAATGATGTGATCAATAATAATCAGTCAATAATAACACCGACGAT 60
Db 24 SerSerAspGluGluGluAsnAspValIleAsnAsnAsnGlnSerIleAsnSerAspAsp 43
QY 61 AATAACCAATAATTAATAAAGAAAGAAACGAATAACTACGATGCGATAGAAAAACGCTCA 120
Db 44 AsnAsnGlnIleAsnLysLysGluGluThrAsnAsnAsnAspGlyIleGluLysSerSer 63
QY 121 GAAGATAGAACACAGTCACACAAACAAATGTAGATGAAACCAAGCAACACATTTTACAAAG 180
Db 64 GluAspArgThrGluSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 83
QY 181 ACCCTCAAGATAATCTCATCTTACAGAAAGAGAGTAAAGAATCCTCATCAGTCGAA 240
Db 84 SerProGlnAspAsnThrHisLeuThrGluGluValLysGluProSerSerValGlu 103
QY 241 TCTCAAAATTCATCAATTTGATCTGCCCCAACCAACCATCTCACACAAACAATAATAGAGAA 300
Db 104 SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrThrIleAsnArgGlu 123
QY 301 GAATCTGTTCAACAAGTGTATGTAGAGATTTACACGTCATCAGATTTTGTCTAACTCT 360
Db 124 GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer 143
QY 361 AAAATAAAGAGAGTAACTGAATCTGTGTAAGAGAGAGAAATCTATAGAGCAACCTAAT 420
Db 144 LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn 163
QY 421 AAAGTAAAGAGATTCACAAACAAAGTCAGCCGCTCTGGCTGTATACAAATATAGATGAAAAA 480
Db 164 LysValLysGluAspSerThrThrSerGlnProSerGlyTyrThrAsnIleAspGluLys 183
```

Qy	481	ATTTC	CAATCAAGT	AGTGTATTAAATTTACCAATAAATGAATATGAAATAAGCGCTAGA	540
Db	184	II	Ser	AsnGlnAAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysAlaArg	203
Qy	541	CCATTATCTACA	CAATCGCCCAACCATCGATTAAACCGTGAACCGTAAATCAATTAAGCG	600	
Db	204	ProLeuSerThrThr	SerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla	223	
Qy	601	CGCGAAC	AGGTTCCGAATGTTAAACATTTAAATTAAGTTACTGATCAAAAGTATTACTGAA	660	
Db	224	AlaGluGlnGlySer	AsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu	243	
Qy	661	GGATATGATGAT	ACTGAAGGTGTTATTAAACGACATGATCGTGAAGAACTTTAATCTATCAT	720	
Db	244	GlyTyrAspAspSer	GluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp	263	
Qy	721	GTAACTTTT	GAAAGTAGATGATAAGGTGAAATCTCGTGTATACGATCGATCGATGATATAGAT	780	
Db	264	ValThrPheGluValAsp	AspLysValLysSerGlyAspThrMetThrValAspIleAsp	283	
Qy	781	AAGAATACAGTTCCAT	CGATTTAAACCGATAGCTTTTCAATACCAAAAAATAAAAGATAAT	840	
Db	284	LysAsnThrValProSer	AspLeuThrAspSerPheThrIleProLysIleLysAspAsn	303	
Qy	841	TCTCGAGAAATCAT	CGCTACAGGTACTTATGATACCAAAAAATAACAAATCACCATCTACT	900	
Db	304	SerGlyGluIleIleAla	ThrGlyThrTyrAspAsnLysAsnLysGlnIleThrTyrThr	323	
Qy	901	TTTACAGATTATG	TAGATAAGTATTGAAATATTAAAGCACACCTTTAAATTAACGTCATAC	960	
Db	324	PheThrAspTyrValAsp	LysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr	343	
Qy	961	ATTGATAAATCA	AGGTTCCAAATAATAATACCAAGTTAGATGATAGATAATAAACCGGCC	1020	
Db	344	IleAspLysSerLysValPro	AsnAsnThrLysLeuAspValGluTyrLysThrAla	363	
Qy	1021	CTTTTCATCAGTAA	ATAAAACAAATTTACGGTTCAATATCAAGACCTCAACGAAATCGGACT	1080	
Db	364	LeuSerSerValAsnLys	ThrIleThrValGluTyrGlnArgProAsnGluAsnArgThr	383	
Qy	1081	GCTAACCTTCAA	AGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAAAACG	1140	
Db	384	AlaAsnLeuGlnSerMet	PheThrAsnIleAspThrLysAsnHisThrValGluGlnThr	403	
Qy	1141	ATTTATATTAA	CCCTCTTCGTATTTCAGCAAGGAAACAAATGTAATATTTTCAGGGAAT	1200	
Db	404	IleTyrIleAsnProLeu	ArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn	423	
Qy	1201	GGTCATGAAGGTTCA	CAATTTATAGACGATAGCACAATAATTAAGTTTATAAGGTGGGA	1260	
Db	424	GlyAspGluGlySer	ThrIleIleAspAspSerThrIleIleLysValTyrLysValGly	443	
Qy	1261	GATTAATCAAAATTT	ACCAGATAGTAACAGAAATTTATGATTACAGCTGAATATGAAGATGTC	1320	
Db	444	AspAsnGlnAsnLeuPro	AspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal	463	
Qy	1321	ACAAATGATGAT	TATGCCCAATTAGGAATAATAATGATGTAATATTAATTTTGGTAAT	1380	
Db	464	ThrAsnAspAspTyrAla	GlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn	483	
Qy	1381	ATAGATTCA	CCCATATATTATTAAAGTTATTAGTAAATATGACCCCTAATAAGGATGATTAC	1440	
Db	484	IleAspSerProTyrIle	IleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr	503	
Qy	1441	ACGACTATAC	AGCAAACTGTGCAATGCAGACGACTATAATAGTAGTATACTGGTGAGTTT	1500	
Db	504	ThrThrIleGlnGlnThr	ValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe	523	
Qy	1501	AGAACAGCATCCT	ATGATATACAAATTCGCTTCTCTACAGTTCCAGTCCAGGCAAGGT	1560	
Db	524	ArgThrAlaSerTyrAsp	AsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly	543	

Qy 1561 GACTTGCCCTCTGAAAAA 1578  
|||  
Db 544 AspLeuProGluLys 549

RESULT 12

US-10-378-674-2  
; Sequence 2, Application US/10378674  
; Publication No. US2004006209A1  
; GENERAL INFORMATION:  
; APPLICANT: PATTI, Joseph M.  
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATIVE  
; FILE REFERENCE: P07556US01/BAS  
; CURRENT APPLICATION NUMBER: US/10/378, 674  
; CURRENT FILING DATE: 2003-03-05  
; PRIOR APPLICATION NUMBER: 60/361,324  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-10-378-674-2

	Pred. No.:	Length:
Alignment Scores:	9,24e-160	560
Score:	2510.50	Matches: 490
Percent Similarity:	95.8%	Conservative: 14
Best Local Similarity:	93.2%	Mismatches: 21
Query Match:	83.0%	Indels: 1
DB:	4	Gaps: 1

US-10-806-288-12 (1-1746) x US-10-378-674-2 (1-560)

Qy 1 TCTAGTGTGAAGAAGATCATGTGATCAATAATAATCAGTCAATAAAACCGACGAT 60  
|||  
Db 36 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 55  
|||  
Qy 61 AATAACCAAATAATTAATAAAGAAGAACGATTAATACCTGATGGCATAGAAAAACGCTCA 120  
|||  
Db 56 AspaenGln--llyllysGluGluThrAsnSerAsnAspAlalleGluAsnArgSer 74  
|||  
Qy 121 GAAGATAGAACAGAGCTCAACAACAAATGTAGATGAAGAACGAGCAACATTTTACAAAAG 180  
|||  
Db 75 LysAspIleThrGlnSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 94  
|||  
Qy 181 ACCCTCAAGATAATACTCATCTTCACAGAAGAGAGGTAAAGNATCCTCATAGTCGAA 240  
|||  
Db 95 ThrProGlnAspAsnThrGlnLeuLysGluGluValLysGluProSerSerValGlu 114  
|||  
Qy 241 TCCTCAAAATTCATCAATGTATGATCTGCCCAACACCATCTCACACAACAATAAATAGAGAA 300  
|||  
Db 115 SerSerAsnSerSerMetCaspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu 134  
|||  
Qy 301 GAATCTGTTCACAAAGTAGTAATGTAGAGATTCACGATCAGATTTTTGCCTAACTCT 360  
|||  
Db 135 AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer 154  
|||  
Qy 361 AAAATAAAGAGAGTAACACTGAATCTGGTAAAGAAGAGATTAATATAGAGCAACCTAAT 420  
|||  
Db 155 LysIlelleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn 174  
|||  
Qy 421 AAAGTAAAGAAGATTCAACAACAAGTACGCGCTCGGCTATACAAATATATAGATGMAAAA 480  
|||  
Db 175 LysValArgLysAspSerIleThrSerGlnProSerSerTyrlsAsnIleAspGluLys 194  
|||  
Qy 481 ATTTCAAAATCAAGATGAGTATTAAATTTTACCAATAAATGAATATGAAAAATAAGCGTAGA 540  
|||  
Db 195 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrlsAsnLysValArg 214  
|||  
Qy 541 CCATTATCTACAAATCTGCCCCAACCATCGATTAAACGTTAAACCGTAAATCAATTAGCG 600  
|||

```
Db      215  ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 234
Qy      601  GCGGAACAAGTTCGAATGTTAACCATTTAATTAAGTTACTGATCAAGATTACTGAA 660
Db      235  AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 254
Qy      661  GGATATGATGATGATGAGGTGTTATTAAAGCACATGCTGCTGAAACTTAACTATGAT 720
Db      255  GlyTyrAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 274
Qy      721  GTAACTTTTCAAGTAGATGATAAGCTGAAATCTGGTGATACGATGACAGTGGATATAGAT 780
Db      275  ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 294
Qy      781  AAGAATACAGTTCCATCAGATTAAACCGATAGCTTTTACAATACCAAAAAATAAAGATAAT 840
Db      295  LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 314
Qy      841  TCTGGAGAAATCATCGCTACAGGTACTTATGATAACAAAAATAAACAATCACCTATACT 900
Db      315  SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr 334
Qy      901  TTTACAGATTATGATAGTAAAGTATGAAATATTAAAGCACACACCTTAAATTTAACTCATAC 960
Db      335  PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 354
Qy      961  ATTGATAAATCAAAGGTTCCAAATAATAATACCAAGTTAGATGATGATAATAAAGCGCC 1020
Db      355  IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 374
Qy      1021  CTTTCATCAGTAAATAAACAATTTACCGTTGAAATATCAAGACCTTAACGAAATCGGACT 1080
Db      375  LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr 394
Qy      1081  GCTAAACCTTCAAAGTATGTTTACAAATATAGATACGAAATAATCATACAGTTTGACCAACG 1140
Db      395  AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 414
Qy      1141  ATTTATATTAAACCTCTTCGTTATTTCAGCCAAGAAACAAATGTAATATTTCAGGGAAT 1200
Db      415  IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 434
Qy      1201  GGTGATCAAGGTTCAACAATTATAGACGATAGCACATTAATTAAGTTTAAAGTTTGA 1260
Db      435  GlyAspGluGlySerThrIleIleAspAspSerThrIleLysValTyrLysValGly 454
Qy      1261  GATAATCAAATTTACAGATAGTAAACAGAATTTATGATTACAGTGAATATGAAGATGTC 1320
Db      455  AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 474
Qy      1321  ACAATGATGATTATGCCCAATTAGGAATAATAATGATGTGAATATTATTTTGGTAAT 1380
Db      475  ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn 494
Qy      1381  ATAGATTCACCATATATTATTAAGTTATTAGTAAATATGACCTTAATRAGGATGATTAC 1440
Db      495  IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 514
Qy      1441  ACAGACTATACAGCAAACTGTGACAATCGACAGCACTATAATAGATGATCTGGTGAGTTT 1500
Db      515  ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 534
Qy      1501  AGAACAGCATCTCATGATAATAACAATTTGCTTCTCAAGTTCAAGTTCAGGCAAGGAT 1560
Db      535  ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 554
Qy      1561  GACTTGCTCTGAAAA 1578
Db      555  AspLeuProProGluLys 560
RESULT 13
US-11-016-564-3
; Sequence 3, Application US/11016564
```

```
; Publication No. US20050287146A1
; GENERAL INFORMATION:
; APPLICANT: INHIBITEX, INC.
; TITLE OF INVENTION: METHOD OF INHIBITING CANDIDA-RELATED INFECTIONS
; FILE REFERENCE: P08140US03/BAS
; CURRENT APPLICATION NUMBER: US/11/016,564
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: US 60/566,082
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: US 60/561,540
; PRIOR FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: US 60/530,654
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Candida albicans
US-11-016-564-3

Alignment Scores:
Pred. No.:      1,07e-105      Length:      331
Score:          1702.00        Matches:    325
Percent Similarity: 99.4%      Conservative: 4
Best Local Similarity: 98.2%    Mismatches: 2
Query Match:     56.2%         Indels:     0
DB:              6            Gaps:      0

US-10-806-288-12 (1-1746) x US-11-016-564-3 (1-331)

Qy      601  GCGGAACAAGTTCGAATGTTAACCATTTAATTAAGTTACTGATCAAGATTACTGAA 660
Db      1   AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 20
Qy      661  GGATATGATGATGATGAGGTGTTATTAAAGCACATGCTGCTGAAACTTAACTATGAT 720
Db      21  GlyTyrAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 40
Qy      721  GTAACTTTTCAAGTAGATGATAAGTGAATCTGGTGATACGATGACAGTGGATATAGAT 780
Db      41  ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 60
Qy      781  AAGAATACAGTTCCATCAGATTAAACCGATAGCTTTACATACCAAAAAATAAAGATAAT 840
Db      61  LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 80
Qy      841  TCTGGAGAAATCATCGCTACAGGTACTTATGATAACAAAAATAAACAATCACCTATACT 900
Db      81  SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr 100
Qy      901  TTTACAGATTATGATAGTAAAGTATGAAATATTAAAGCACACACCTTAAATTTAAAGTATAC 960
Db      101  PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 120
Qy      961  ATTGATAAATCAAAGTTCCAATAATAATAATACCAAGTTAGATGATGATAATAAAGCGCC 1020
Db      121  IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 140
Qy      1021  CTTTCATCAGTAAATAAACAATTTACGGTTGAAATATCAAGACCTTAACGAAATTCGGACT 1080
Db      141  LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr 160
Qy      1081  GCTAAACCTTCAAAGTATGTTTACAAATATAGATACGAAATAATCATACAGTTTGACCAACG 1140
Db      161  AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 180
Qy      1141  ATTTATATTAAACCTCTTCGTTATTTCAGCCAAGAAACAAATGTAATATTTCAGGGAAT 1200
Db      181  IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 200
Qy      1201  GGTGATGAAGTTCAACAATTTATAGACGATAGCACAAATTAATTAAGTTTAAAGTTTGA 1260
```







GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 12, 2006, 08:45:46 ; Search time 9.6 Seconds  
(without alignments)  
3672.712 Million cell updates/sec

Title: US-10-806-288-12  
Perfect score: 3026  
Sequence: 1 tctagtgtatgaagaaga.....ggaaatatcaattgtatgga 1746

Scoring table:  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 479828

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB.spool/US10806288/runat 11082006 163422 21500/app\_query.fasta\_1  
-DB=Published Applications AA New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DLOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-MINLEN=2000000000 -HOST=abs02p  
-USER=US10806288.OCGN 1.1 64 @runat 11082006 163422 21500 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA New.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US09\_NEW\_PUB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US08\_NEW\_PUB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2810.5	92.9	930	7	US-11-396-565-10
2	576	19.0	1349	6	US-10-471-571A-3352
3	499	16.5	1742	7	US-11-396-565-4
4	455	15.0	995	6	US-10-471-571A-3354
5	454	15.0	927	6	US-10-471-571A-2922
6	397.5	13.1	877	6	US-10-471-571A-3884
7	377	12.5	496	7	US-11-256-173-29
8	376	12.4	948	6	US-10-471-571A-3552
9	300.5	9.9	1018	6	US-10-471-571A-3554

10	262.5	8.7	1160	7	US-11-192-046-250	Sequence 250, App
11	259	8.6	1161	7	US-11-192-046-121	Sequence 121, App
12	253.5	8.4	3029	6	US-10-537-642-10	Sequence 10, Appl
13	212	7.0	2024	6	US-10-537-642-21	Sequence 21, Appl
14	211.5	7.0	1086	7	US-11-330-403-3535	Sequence 3535, Ap
15	205	6.8	774	6	US-10-471-571A-4824	Sequence 4824, Ap
16	204	6.7	1781	6	US-10-537-642-24	Sequence 24, Appl
17	201	6.6	1464	6	US-10-537-642-27	Sequence 27, Appl
18	201	6.6	2478	6	US-10-471-571A-2278	Sequence 2278, Ap
19	197	6.5	2314	7	US-11-013-711-11	Sequence 11, Appl
20	192	6.3	1234	6	US-10-537-642-14	Sequence 14, Appl
21	190.5	6.3	1992	7	US-11-013-711-3	Sequence 3, Appl
22	190.5	6.3	1992	7	US-11-013-711-13	Sequence 13, Appl
23	190.5	6.3	2047	7	US-11-013-711-4	Sequence 4, Appl
24	190.5	6.3	2047	7	US-11-013-711-7	Sequence 7, Appl
25	188.5	6.2	1421	6	US-10-630-629-18	Sequence 18, Appl
26	187.5	6.2	450	7	US-11-165-586-64	Sequence 64, Appl
27	187.5	6.2	991	7	US-11-165-586-62	Sequence 62, Appl
28	187	6.2	1274	6	US-10-471-571A-898	Sequence 898, App
29	185.5	6.1	2271	6	US-10-449-902-34842	Sequence 34842, A
30	178	5.9	800	6	US-10-471-571A-4496	Sequence 4496, Ap
31	177.5	5.9	9535	6	US-10-537-642-22	Sequence 22, Appl
32	175	5.8	1471	6	US-11-013-711-9	Sequence 9, Appl
33	175	5.8	2053	6	US-10-471-571A-860	Sequence 860, App
34	168.5	5.6	823	7	US-11-192-046-14	Sequence 14, Appl
35	168.5	5.6	851	7	US-11-192-046-13	Sequence 13, Appl
36	168.5	5.6	862	7	US-11-192-046-12	Sequence 12, Appl
37	168.5	5.6	890	7	US-11-192-046-11	Sequence 11, Appl
38	167.5	5.5	1086	6	US-10-630-629-2	Sequence 2, Appl
39	166	5.5	619	6	US-10-471-571A-3914	Sequence 3914, Ap
40	164.5	5.4	2659	7	US-11-256-173-28	Sequence 28, Appl
41	164.5	5.4	1501	6	US-10-630-629-4	Sequence 4, Appl
42	163	5.4	4544	6	US-10-537-642-20	Sequence 20, Appl
43	163	5.4	4544	6	US-10-537-642-20	Sequence 20, Appl
44	162.5	5.4	637	6	US-10-471-571A-3918	Sequence 3918, Ap
45	161	5.3	718	6	US-10-953-349-5389	Sequence 5389, Ap

ALIGNMENTS

RESULT 1  
US-11-396-565-10  
; Sequence 10, Application US/11396565  
; Publication No. US20060171964A1  
GENERAL INFORMATION:  
; APPLICANT: POSTER, Timothy  
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOC  
; FILE REFERENCE: P06335052/BAS  
; CURRENT APPLICATION NUMBER: US/11/396,565  
; CURRENT FILING DATE: 2006-04-04  
; PRIOR APPLICATION NUMBER: US/09/386,962  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: 60/098,443  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: 60/117,119  
; PRIOR FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 930  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-11-396-565-10

Alignment Scores:  
Pred. No.: 6.67e-149 Length: 930  
Score: 2810.50 Matches: 545  
Percent Similarity: 96.2% Conservative: 15  
Best Local Similarity: 93.6% Mismatches: 21  
Query Match: 92.9% Indels: 1  
DB: 7 Gaps: 1

US-10-806-288-12 (1-1746) x US-11-396-565-10 (1-930)

```
QY 1 TCTAGTCATGAGAAAGAAATGATGTGATCAATAATAATCAGTCATAAATACACCGAGCAT 60
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
73 SerSerAenGluGluLysAenAepValIleAenAenSerGlnSerIleAenThrAepAep 92
QY 61 AATAACCAATAATTAATAAAGAAAGAAACCAATACCTACGATGCGCATAGAAAAACGCTCA 120
Db ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
93 AspAenGln--lleLysLysGluGluThrAenSerAenAepAlalleGluAenAepSer 111
QY 121 GAAGATAGAACAGAGTCACAAACAATAATGTAGATGAAACGAAGCAACATTTTACAAAG 180
Db ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
112 LysAepIleThrGlnSerThrAenValAepGluAenGluAlaThrPheLeuGlnLys 131
QY 181 ACCCTCAAGATAATATCTCATCTTACAGAGAAGAGGTAAGAAGATCCTCATCAGTCGAA 240
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
132 ThrProGlnAepAenThrGlnLeuLysGluGluValLysGluProSerSerValGlu 151
QY 241 TCCTCAAAATTCATCAATTTGATCTGCCCCAACCAACATCTCACACAAACAATAAATAGAGAA 300
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
152 SerSerAenSerSerMetAepThrAlaGlnGlnProSerHisThrIleAenSerGlu 171
QY 301 GAATCTGTTCAAAAGTGAATAATGTAGAAGATTCAACAGTATCACAGATTTTGCCTACTCT 360
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
172 AlaSerIleGlnThrSerAepAenGluAenSerArgValSerAepPheAlaAenSer 191
QY 361 AATAAAGAGAGTAACTGAACTCTGGTAAAGAGAGAACTACTATAGAGCAACCTAAT 420
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
192 LysIleIleGlnSerAenThrGluSerAenLysGluAenThrIleGluGlnProAen 211
QY 421 AAGTAAAGAGAGATTCAACCAAGTCAGCGCTCGCTATACAAATATAGATGAAAAA 480
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
212 LysValArgGluAepSerIleThrSerGlnProSerSerTyrLysAenIleAepGluLys 231
QY 481 ATTTCAAAATCAAGATGAGTTAATAATTTACCAATAAATGAATATGAAAAATAAGCTPAGA 540
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
232 IleSerAenGlnAepGluLeuLeuAenLeuProIleAenGluTyrGluAenLysValArg 251
QY 541 CCATTATCTACACATCTGCCACCATCGATTAAACGTCGTACCGTAAATCAATTAGCG 600
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
252 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAenGlnLeuAla 271
QY 601 GCGAACAAGGTTCCGAATGTTAAACCAATTAATTAAGTTACTGATCAAAAGTATTACTGAA 660
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
272 AlaGluGlnGlySerAenValAenHisLeuIleLysValThrAepGlnSerIleThrGlu 291
QY 661 GGTATGATGATGATGAGGTGTTATTAAAGCATCATGATGCTGAAACCTTAATCTATGAT 720
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
292 GlyTyrAepAepSerAepGlyIleIleLysAlaHisAepAlaGluAenLeuIleTyrAep 311
QY 721 GTAACTTTCAAGTCAGTATAGGTGAATCTGGTGATACGATGACAGTGGATATAGAT 780
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
312 ValThrPheGluValAepAepLysValLysSerGlyAepThrMetThrValAenIleAep 331
QY 781 AAGAATACAGTTCATCAGATTTAAACCGATAGCTTTTACAATACCAAAATAAAAGATAAT 840
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
332 LysAenThrValProSerAepLeuThrAepSerPheAlalleProLysIleLysAepAen 351
QY 841 TCTGGAGAAATCATCGCTACAGGTACTTATGATAACAAAAATAAACAATCACCCTATPACT 900
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
352 SerGlyGluIleIleAlaThrGlyThrTyrAepAenThrAenLysGlnIleThrTyrThr 371
QY 901 TTTACAGATTTATGATAGATGATGAAATAATTAACACACACACCTTAATTAACGTCATAC 960
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
372 PheThrAepTyrValAepLysTyrGluAenIleLysAlaHisLeuLysLeuThrSerTyr 391
QY 961 ATTGATAAAATCAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATAATAAACCGCC 1020
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
392 IleAepLysSerLysValProAenAenAenThrLysLeuAepValGluTyrLysThrAla 411
QY 1021 CTTTCATCAGTAAATAAACAATTCAGGTTGAATATCAAGACCTAACGAAATTCGAGCT 1080
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
412 LeuSerSerValAenLysThrIleThrValGluTyrGlnLysProAenGluAenArgThr 431
```

```
QY 1081 GCTAACTCTCAAGATGATGTTTACAAATATATAGATACGAAATAATCATACAGTTGACCAACG 1140
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
432 AlaAenLeuGlnSerMetPheThrAenIleAepThrLysAenHisThrValGluGlnThr 451
QY 1141 ATTTATATTAAACCTCTCTGTTATTAGCCCAAGGAAACAAATGTAAATATTTTCAGGGAAT 1200
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
452 IleTyrIleAenProLeuArgTyrSerAlaLysGluThrAenValAenIleSerGlyAen 471
QY 1201 GGTGATGAAGTTTCAACAATATATAGACGATAGCACATAATTAAGTTTAAAGTTTGA 1260
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
472 GlyAepGluGlySerThrIleIleAepAepSerThrIleIleLysValTyrLysValGly 491
QY 1261 GATAATCAAAATTTACAGATAGTAAACAGATTTTATGATTACAGTGAATATGAAGATGTC 1320
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
492 AspAenGlnAenLeuProAepSerAenArgIleTyrAepTyrSerGluTyrGluAepVal 511
QY 1321 ACAAAATGATGATTATGCCAAATTAGGAAATAATAATGATGTGAATATTAATTTTGGTAAT 1380
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
512 ThrAenAepAepTyrAlaGlnLeuGlyAenAenAenAepValAenIleAenPheGlyAen 531
QY 1381 ATAGATTCACCATATATTTAAGTTTATTAGTAAATATATGACCCCTAATAAGATGATTAC 1440
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
532 IleAepSerProTyrIleIleLysValIleSerLysTyrAepProAenLysAepAepTyr 551
QY 1441 ACAGCTATACAGCAAACTGTGCAATGCAAGCAGCACTATAATGAGTATCTGTTGAGTTT 1500
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
552 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAenGluTyrThrGlyGluPhe 571
QY 1501 AGAACAGCATCTCATGATAATCAATTTGCTTCTCTACAAGTTTCAGTCAAGGACAAGGT 1560
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
572 ArgThrAlaSerTyrAepAenThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 591
QY 1561 GACTTCCTCTCGAAAAAACTTATAAAATCGGAGATACGTATGCGGAGATGATAGATAA 1620
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
592 AspLeuProGluLysThrTyrLysIleGlyAepTyrValTrpGluAepValAepLys 611
QY 1621 GATGGTATTCAAATACAAATGATAATGAAACCGCTTAGTAAATGTTGTTAACTTTG 1680
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
612 AspGlyIleGlnAenThrAenAepAenGluLysProLeuSerAenValLeuValThrLeu 631
QY 1681 ACGTATCTCTGATGGAATTCMAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT 1740
Db |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
632 ThrTyrProAepGlyThrSerLysSerValArgThrAepGluGluGlyLysTyrGlnPhe 651
QY 1741 GATGGA 1746
Db |||||
652 AspGly 653

RESULT 2
US-10-471-571A-3352
; Sequence 3352, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3352
; LENGTH: 1349
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1349)
; OTHER INFORMATION: Ser-Asp rich
US-10-471-571A-3352
Alignment Scores:
```

Pred. No.: 4,778-25 Length: 1349  
Score: 576.00 Matches: 186  
Percent Similarity: 48.2% Conservative: 112  
Best Local Similarity: 30.1% Mismatches: 228  
Query Match: 19.0% Indels: 92  
DB: 6 Gaps: 29

US-10-806-288-12 (1-1746) x US-10-471-571A-3352 (1-1349)

QY 1 TCTAGTATGAGAAAGAAATGATGTG-----ATCAATAATAATCAGTCAATAAAC 51  
DB 55 SerThrAsnLysGluLeuAsnGluAlaThrThrSerAlaSerAspAsnGlnSerSerAsp 74  
QY 52 ACCGACGATATAACCAATTAATAAAGAAAGAAACAAATACCTAGCGCATGAA 111  
DB 75 LysValAspMetGlnGlnLeuAsnGlnGluAspAsnThrLysAsnAspAsnGlnLysGlu 94  
QY 112 AAACGCTCAGAGATAGACAGACAGTCACACAAATGTAGTAA-----AACGAGCAACA 168  
DB 95 MetValSerSerGlnGlyAsnGluThrThrSerAsnGlyAsnLysLeuLeuGluLysGlu 114  
QY 169 TTTTACAAAAGACCCCTCAAGATAATACTCATCTTACAGAGAGAGAGTAAAGATCC 228  
DB 115 SerValGlnSerThrThrGlyAsnLysValGluValSerThrAlaLysSerAspGluGln 134  
QY 229 TCATCAGTCGAATCCTCAAAATTCATCAATGATGATGCTGCCAACACCATCTCACACAACA 288  
DB 135 AlaSerProLysSerThrAsnGluAspLeuAsnThrLysGln-----Thr 149  
QY 289 ATAAATAGAGAAATCTGTTCAACACAGTGAATGTAGAGATTCACAGTATCAGAT 348  
DB 150 IleSerAsnGlnGluAlaLeuGln---ProAspLeuGlnGluAsnLysSerValValAsn 168  
QY 349 TTTGCTAACTCTAAATAAAGAGAGTAACTGATCTGTAAAGAGAGAGTAACTATA 408  
DB 169 -----ValGlnProThrAsnGlnGluAsnLysLysValAsp----- 180  
QY 409 GAGCAACCTAATAAGTAAAGAGATTCACAAAGTCAAGCCTCGCTGCTATACAAAT 468  
DB 181 -----AlaLysThrGluSerThr-----LeuAsn 189  
QY 469 ATA---GATGAAAAATTTCAATCAAGATGATGATTA-----AATTTACCAATAAT 519  
DB 190 ValLysSerAspAlaLysSerAsnAspGluThrLeuValAspAsnAsnSerAsnSer 209  
QY 520 GAATATGAAATAAGGCTAGACCATATCTACACATCTGCCCAACCA----- 567  
DB 210 AsnAsnGluAsnAsnAlaAspIleLeuProLysSerThrAlaProLysArgLeuAsn 229  
QY 568 TCGATTAAACGCTGAACCGTAAATCAATTAACGCGGGAACAAAGGTTGAAATGTTAAACCAT 627  
DB 230 ThrArgMetArgIleAlaAlaValGlnProSerSerThrGluAlaLysAsnValAsnAsp 249  
QY 628 TTAATTAAGATTACTGATCAAGATTTACTCAAGATATGATGATGAGAGGTGTTATT 687  
DB 250 LeuIleThrSerAsnThrThrLeuThrValValAspAlaAspLysAsnLysIleVal 269  
QY 688 AAAGCACATGATGCTGAAACCTTAATCTATCATGTAACCTTTTGAAGTAGATGATAAGGTG 747  
DB 270 ProAlaGlnAspTyrLeuSerLeuLysSerGlnIleThr-----ValAspAspLysVal 287  
QY 748 AAATCTGCTGATCGATGACAGTGGATATAGATAGATACAGTT----- 792  
DB 288 LysSerGlyAspTyrPheThrIleLysTyr---SerAspThrValGlnValTyrGlyLeu 306  
QY 793 ---CCATCAGATTAAACCGATAGCTTTACATACCAAAATAAAGAT---AATCTCGGA 846  
DB 307 AsnProGluAspIleLysAsn-----IleGlyAspIleLysAspProAsnAsnGly 323  
QY 847 GAAATCATCGCTACAGGTACTTATGATAACAAATAAACAACAAATACCATATCTTTTACA 906  
DB 324 GluThrIleAlaThrAlaLysHieAspThrAlaAsnAsnLeuIleThrTyrPheThr 343

QY 907 GATTATGTAGATAAGTATGAAATAATTAATAACACACACCTTAATACTCACTCATATTGAT 966  
DB 344 AspTyrValAspArgPheAsnSerValGlnMetGlyIleAsnTyrSerIleTyrMetAsp 363  
QY 967 AAATCAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATATAATAAACGCGCTTCA 1026  
DB 364 AlaAspThrIlePro-----ValSerLysAsnAspValGluPheAsnValThrIleGly 381  
QY 1027 TCAGTAAATAAACAATTTACGTTGAATATCAAGACCTTAAC-----GAAATCGGACT 1080  
DB 382 AsnThrThrThrLysThrThrAlaAsnIleGlnTyrProAspTyrValValAsnGluLys 401  
QY 1081 GCTAACCTTCAAGATATGTTTCAAAATAGATAGACGAAATAATCATACA----- 1128  
DB 402 AsnSerIleGlySerAlaPheThr-----GluThrValSerHieValGlyAsnLysGlu 419  
QY 1129 -----GTTGACCAACGATTTATATTAACCTCTCTCGTTATTCAGCCAAGNA 1176  
DB 420 AsnProGlyTyrTyrLysGlnThrIleTyrValAsnProSerGluAsnSerLeuThrAsn 439  
QY 1177 ACAATGTAAATATT-----TCAGGAATGGTGATGAAGGTTCAACAATATA 1224  
DB 440 AlaLysLeuLysValGlnAlaTyrHisSerSerTyrProAsnAsnIleGlyGlnIleAsn 459  
QY 1225 GACGATAGCACATAATTAAGTTTATAAGTTGGAGATATCAAAATTTACCAGATAGT 1284  
DB 460 LysAspValThrAspIleLysIleTyrGlnValProLysGlyTyrThrLeu----- 476  
QY 1285 AACGAAATTTATGATTACAGT-----GAATATGAAGATGTCACAAATGATGATTATGCC 1338  
DB 477 AsnLysGlyTyrAspValAsnThrLysGluLeuThrAspValThrAsn---GlnTyrLeu 495  
QY 1339 CAA-----TTAGAAATAATAATGATGCTGAATATTAAATTTGGTAAATATAGATCA 1389  
DB 496 GlnLysIleThrTyrGlyAspAsnAsnSerAlaValIleAspPheGlyAsnAlaAspSer 515  
QY 1390 CCATATATATTAAAGTTATTAGTAAATATGACCTTAATAAGGATGATTACACGACTATA 1449  
DB 516 AlaTyrValValMetValAsnThrLysPheGlnTyrThrAsnSerGluSerProThrLeu 535  
QY 1450 CAGCAAACTGCAATGACAGACCATTAATAGTATGATGATGAGTTAGAACAGCA 1509  
DB 536 ValGlnMetAlaThrLeuSerSerThrGlyAsn-----LysSerVal 549  
QY 1510 TCCTATGATATAATTTCTCTCTCAAGATTCAGGTCAAGCAAGGTGACTTGCT 1569  
DB 550 SerThrGlyAsnAlaLeuGlyPheThrAsnAsnGlnSerGlyGlyAlaGly----- 566  
QY 1570 CCTGAAAAAATCTTATAAATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGTTAT 1629  
DB 567 ---GlnGluValTyrLysIleGlyAsnTyrValTrpGluAspThrAsnLysAsnGlyVal 585  
QY 1630 CAAATAACAATGATAATGAAAAACCGCTTAGTATGTTGTTAACTTTGACGTATCCT 1689  
DB 586 GlnGluLeu-----GlyGluLysGlyValGlyAsnValThrValThrVal---PheAsp 602  
QY 1690 GATCGAACTTCAAAATCAGTCAGA-----ACAGATGAAGATGGGAAATAT 1734  
DB 603 AsnAsnThrAsnThrLysValGlyGluAlaValThrLysGluAspGlySerTyr 620

RESULT 3

US-11-396-565-4  
; Sequence 4, Application US/11396565  
; Publication No. US20060171964A1  
; GENERAL INFORMATION:  
; APPLICANT: POSTER, Timothy  
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCI  
; FILE REFERENCE: P06335US2/BAS  
; CURRENT APPLICATION NUMBER: US/11/396,565  
; CURRENT FILING DATE: 2006-04-04  
; PRIOR APPLICATION NUMBER: US/09/386,962  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: 60/098,443

```
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1742
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-11-396-565-4

Alignment Scores:
Pred. No.:      8.67e-21      Length:      1742
Score:          499.00      Matches:      168
Percent Similarity: 43.9%      Conservative: 104
Best Local Similarity: 27.1%      Mismatches:  275
Query Match:      16.5%      Indels:      72
DB:              7          Gaps:       25

US-10-806-288-12 (1-1746) x US-11-396-565-4 (1-1742)
QY 1 TCTAGTATGAAGAAAGATGTGATCAATAATAATCAGTCAATAAATACACCGAGAT 60
Db 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 157 ThrSerThrThrGlnGlnAspSerThrGluLysAsnAsnProSerLeuLysAspAsnLeu 176
Db 157 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 AATAACCAATATATTAAGAAAGAAACGAAATACGTACGATGCGATAGAAAACGCTCA 120
Db 61 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 AsnSerSerSerThrThrSerLysGluSerLysThrAspGluHisSerThrLysGlnAla 196
Db 177 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 GAAGATAGACAGAGTCAACAAATGTAGATGAAACGAAGCA---ACATTTTACAA 177
Db 121 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 197 GlnMetSerThr---AsnLysSerAsnLeuaspThrAsnAspSerProThrGlnSerGlu 215
Db 197 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 178 AAGACC---CCTCAAGATATATCTATCTTACAGAAAGAGGTAAAGAAATCCTCATCA 234
Db 178 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 216 LysThrSerSerGlnAlaAsnAsnAspSerThrAspAsnGlnSerAlaProSerLysGln 235
Db 216 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 GTCGAATCCTCAATTCAC-----TCGAATGTACTGCGC 267
Db 235 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 LeuAspSerLysProSerGluGlnLysValLysThrLysPheAsnAspGluProThr 255
Db 236 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 268 CAACAAACCATCTCACAAACAAATAAT---AGAGAAGAACTCTGTCAAAACAGTGATAAT 324
Db 268 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 256 GlnAspValGluHisThrThrLysLysLysThrProSerValSerThrAspSerSer 275
Db 256 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 325 GTAGAAGATTACACGATGATGATTTTGTCTTAACCTTAAATATAAAGAGAGTAACACTGAA 384
Db 325 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 276 ValAsnAspLys-----GlnAspTyrThrArgSerAlaVal-----AlaSer 289
Db 276 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 385 TCTGTTAAGAGNAGATATCTATAGACCAACCTTAATAAGAAAGAGATTCACACACA 444
Db 385 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 290 LeuGlyValAspSerAsnGluThrGluAlaIleThrAsnAlaValArgAspAsnLeuAsp 309
Db 290 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 445 AGTCAGCGCTGCGCTATACAAATATATAGATGAAATAAT----- 483
Db 445 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 310 LeuLysAlaIleSerArgGluGlnIleAsnGluAlaIleIleAlaLeuLysLys 329
Db 310 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 484 -----TCAATCAAGATGAGTTATTAAATTTACCA-----ATAAATGAATATGAAAT 531
Db 484 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 330 AspPheSerAsnProAspTyrGlyValAspThrProLeuAlaLeuAsnArgSerGlnSer 349
Db 330 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 532 AAGCTAGACCATATCTACACATCTGCCCCAACCATCGATTAAACGTGTAAACCGTAAT 591
Db 532 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 350 LysAsnSerPro-----HisLysSerAlaSerPro-----ArgMetAsnLeuMet 364
Db 350 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 592 CAATTAGCGCGGAA-----CAAGGTTCCGAATGTTAACCATTTAATTAAGTTACTGAT 645
Db 592 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 365 SerLeuAlaIleGluProAsnSerGlyLysAsnValAsnAspLysValLysIleThrAsn 384
Db 365 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 646 CAA-----AGTATTACTGAAGATATGATGATGAGGTTGTTATTAAAGCACATGAT 699
Db 646 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 385 ProThrLeuSerLeuAsnLysSerAsnAsnHisAlaAsnAsnValIleTyrProThrSer 404
Db 385 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```
QY 700 GCTGAAACCTTAATCTATGATGATACTTTTGAAGTAGATGATAAGGTGAAATCTGGTAT 759
Db 700 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 405 AsnGluGlnPheAsnLeuLysAlaAsnTyrGluLeuAspSerIleLysGluGlyAsp 424
Db 405 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 760 ACGATGACAGTGGATATAGATAAGAATACAGTTTCCATCAGATTAAACCCGATAGCTTTACA 819
Db 760 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 425 ThrPheThrIleLysTyrGlyGlnTyrIleArgProGlyGlyLeuGluLeuProAlaIle 444
Db 425 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 820 ATACCAAAATAAAGATAATCTCTGGAGAAATCATCGCTACAGCTACTTATGATAACAAA 879
Db 820 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 445 LysThrGlnLeuArgSerLysAspGlySerIleValAlaAsnGlyValTyrAspLysThr 464
Db 445 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 880 AATAAAACAAATCACCTATCTTTTACAGATTATGTAGATAAGTAAATGAAATATATAAGCA 939
Db 880 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 465 ThrAsnThrThrThrThrPheThrAsnTyrValAspGlnTyrGlnAsnIleThrGly 484
Db 465 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 940 CACCTTAAATTTAACGTACATCATTTGATAAATCAAGGTTCCAAATATATATACCAAGTTA 999
Db 940 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 485 SerPheAspLeuIleAlaThrProLysArgGluThrAlaIleLysAspAsnGlnAsnTyr 504
Db 485 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1000 GATGTAGATATATAAAGCGCCTTTTCATCAGTAAATAAACAATACGGTTGAATATCAA 1059
Db 1000 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 505 ProMetGluValThrIleAlaAsnGluValValLysLysAspPheIleValAspTyrGly 524
Db 505 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1060 AGACCTAACGAAATCGACTCTTAACCTTCAAAGTATGTTTACAAATATAGATACGAA 1119
Db 1060 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 525 AsnLysLysAspAsnThrThrThr-----AlaAlaValAlaAsnValAspAsnVal 541
Db 525 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1120 AATCATCATAGTTGAGCAAAACGATTTATTTAATTAACCTCTTCGTTATTTCAGCAAGAAACA 1179
Db 1120 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 542 AsnAsnLysHisAsnGluValValTyrLeuAsnGlnAsnAsnGlnAsnProLysTyrAla 561
Db 542 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1180 AATGTAATATTTTCAGGGAATGCGTATGAGGTTTCAACATTTATAGACGATACACATA 1239
Db 1180 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 562 LysTyr-----PheSerThrValLysAsnGlyGluPheIle 573
Db 562 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1240 -----ATTAAAGTTTATAGGTTGGAGATAATCAAAATTTACCAGATAGT---AAC 1287
Db 1240 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 574 ProGlyGluValLysValTyrGluValThrAspThrAsnAlaMetValAspSerPheAsn 593
Db 574 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1288 AGAATTTATGATTACAGTAATATGAAGATGTCACAAATGATGATTATGCCCAATTA--- 1344
Db 1288 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 594 ProAspLeuAsnSerSerAsnValLysAspValThrSerGlnPheAlaProLysValSer 613
Db 594 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1345 GGAATAATAATGATGATGATTAATTTTGGTGAATATA-----GATTCACCATAT 1395
Db 1345 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 614 AlaAspGlyThrArgValAspIleAsnPheAlaArgSerMetAlaAsnGlyLysLysTyr 633
Db 614 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1396 ATTATTTAAAGTTATTAGTAAATATGACCTTAATAGGATGATTACACGACTATACAGCAA 1455
Db 1396 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 634 IleValThrGlnAlaValArgProThrGlyThrGlyAsnValTyrThr-----GluTyr 651
Db 634 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1456 ACTGTGACAAATGCAGACGACTATAATGATGATATCGTGGTGGATTTAGAACAGCATCCTAT 1515
Db 1456 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 652 TrpLeuThrArgAspGlyThrThrAsn-----ThrAsnAspPheTyrArgGlyThrLys 669
Db 652 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1516 GATAATACAAATTCGCTTTCTCAAGTTCAGGTCAAGGCAAGGTGACCTGCTCTCTGAA 1575
Db 1516 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 670 SerThrThrValThrTyrLeuAsnGlySerSerThrAlaGlnGlyAspAsnPro----- 687
Db 670 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1576 AAACTTATAAATCGAGATTCAGTATCGGAAGATGTAGATAAAGATGATTTTCAAAAT 1635
Db 1576 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 688 ---ThrTyrSerLeuGlyAspTyrValTrpLeuAspLysAsnLysAsnGlyValGln--- 705
Db 688 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1636 ACAAAATGATAAATGAAAACCGCTTAGTAAATGTTAGTAACTTTGACGTATCTCGATGGA 1695
Db 1636 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 706 ---AspAspAspGluLysGlyLeuAlaGlyValTyrValThrLeu-----LysAspSer 722
Db 706 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1696 ACTTCAAAATCA-----GTCAGAACAGATGAAGATCGGAAATATCAATTTGAT 1743
Db 1696 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 723 AsnAsnArgGluLeuGlnArgValThrThrAspGlnSerGlyHisTyrGlnPheAsp 741
Db 723 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 4





```

Db      515 AsnIlelelrpArgSerMetSerTrpAspAsnGluValAlaPheAsnAsnGlySerGly 534
      ::::||||::: |||:::||||| ::::|||||::: |||:::
Qy      1549 CAAGCAAGGT---GACTTGCTCT-----CCTCAAAAAAATTATAAAATCGGAGATTAC 1599
      ||| ||| ||| ||| |||::: |||:::
Db      535 SerGlyAspGlyIleAspLysProValValProGluGlnProAspGluProGlyGluIle 554
      ||| ||| ||| ||| |||::: |||:::
Qy      1600 -----GTATCGGAAGATGTAGATAAGAT---GGTATTCAAAATACAAATGATAAT 1647
      :::: ||| ||| ||| ||| |||::: |||:::
Db      555 GluProIleProGluAspSerAspSerAspProGlySerAspSerGlySerAspSer 573

RESULT 6
US-10-471-571A-3884
; Sequence 3884, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WC
; CURRENT APPLICATION NUMBER: US/10/471.571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: Seqwin99, version 1.03
; SEQ ID NO 3884
; LENGTH: 877
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(877)
; OTHER INFORMATION: Clumping factor B
US-10-471-571A-3884

```

[illegible]

QY	415	CCTAATAAGTAAAGAAGATTCAACACCAAGTCAGCGCTGGCTATACAAATATAGAT	474
DB	160	AsnSerGluLeuLysAsnSerGlnThr	168
QY	475	GA AAAAATTTCAAATCAAGATGAGTTATTAATTTACCAATAAATGAATATGAAATAAG	534
DB	169	LeuAspLeuPro	173
QY	535	GCTAGACCATTATCTACAACATCTGCCAA	582
DB	174	SerSerProGlnThrIleSerAsnAlaGlnGlyThrSerLysProSerValArgThrArg	193
QY	583	ACCCTAAATCAATTAGCGCGGCAACAA	615
DB	194	AlaValArgSerLeuAlaValAlaGluProValValAsnAlaAlaAspAlaLysGlyThr	213
QY	616	AATGTTAAACCTTTAATTAAGTTACTGATCAAAAGTATTACTGAAGGATATGATGATAGT	675
DB	214	AsnValAsn	227
QY	676	GAAGGTGTTATTAAGCACATGATGCTCGAATACTTAATCTATGATGATACTTTTGAAGTA	735
DB	228	LysThrThrPheAspProAsnGlnSerGlyAsnThrPheMetAlaAlaAsnPheThrVal	247
QY	736	GATGATAAGGTGAATCTGGTGATACGATGACAGTG	771
DB	248	ThrAspLysValLysSerGlyAspTyrPheThrAlaLysLeuProAspSerLeuThrGly	267
QY	772	GATATAGAT	813
DB	268	AsnGlyAspValAspTyrSerAsnSerAsnAsnThrMetPro	281
QY	814	TTTACAATACCAAAATAAAGATAATCTCGGAAATCATCGTCACAGGTACTTATGAT	873
DB	282	IleAlaAspIleLysSerThrAsnGlyAspValValAlaLysAlaThrTyrAsp	299
QY	874	AACAAAATAACAAATCACCTACTACTTTTACAGATTATGTAGATAAGTATGAAAAATT	933
DB	300	IleLeuThrLysThrTyrThrPheValPheThrAspTyrValAsnAsnLysGluAsnIle	319
QY	934	AAACACACCTTAATTAACGTCATCATTTGATAAATCAAGGTTCCAAATATAATATACC	993
DB	320	AsnGlyGlnPheSerLeuProLeuPheThrAspArgAlaLysAlaProLysSerGlyThr	339
QY	994	AAGTTAGATGTAGATAATAAACGGCCCTTTCATCAGTAAATAAAACAATACCGTTGAA	1053
DB	340	TyrAspAlaAsnIleAsnIleAlaAspGluMetPheAsnAsnLysIleThrTyrAsn	358
QY	1054	TATCAAAAGACCT	1101
DB	359	TyrSerSerProIleAlaGlyIleAspLysProAsnGlyAlaAsnIleSerSerGlnIle	378
QY	1102	ACAATATATAGATCAAAAAT	1155
DB	379	IleGlyValAspThrAlaSerGlyGlnAsnThrTyrLysGlnThrValPheValAsnPro	398
QY	1156	CTTCGTTTATTCAGCCAGGAACAATATTAATTTTACGGGAATGCTGATGAAGGTTCA	1215
DB	399	LysGlnArgValLeuGlyAsnThrTrpValTyrIleLysGlyTyrGlnAspLys	416
QY	1216	ACAATTATAGACGATAGC	1251
DB	417	IleGluGluSerSerGlyLysValSerAlaThrAspThrLysLeuArgIlePhe	434
QY	1252	AAGTTGGAGATATCAAAATTTACCAGATAGT	1284
DB	435	GluValAsnAspThrSerLysLeuSerAspSerTyrTyrAlaAspProAsnAspSerAsn	454
QY	1285	ACAGAAATTTATGATTTACAGTGAATATGAGAT	1317
DB	455	LeuLysGluValThrAspGlnPheLysAsnArgIleTyr	469
QY	1318	GTCAAAATGATGATTATGCCCAATTAGGAAATAAATGATGTGATAATTAATTTTGGT	1377

```
Db 470 -----HisProAsnValAlaSerIleLysPheGly 479
Qy 1378 AATATAGATTACCATATATTATTAAAGTTATTAGTAATATGACCCCTAATAAGGATGAT 1437
Db 480 AspileThrLysThrValValLeuValGluGlyHisTyAspAsnThrGlyLysAsn 499
Qy 1438 TACAGGACT-----ATACAGCAACTGTGCAATGCAGAGGACTATATAATGAGTACT 1491
Db 500 LeuLysThrGlnValIleGlnGluAsnValAspProValThr-----Asn 514
Qy 1492 GGTGAGTTAGACAGCATCTATGATAATACAAATTCGTTCTCTCAAGTTCCAGGTCAA 1551
Db 515 ArgAspTySerIlePheGlyTrpAsnAsnGluAsnValValArgTyThrGlyGlySer 534
Qy 1552 GGACAAGGTGAC 1563
Db 535 AlaAspGlyAsp 538

RESULT 7
US-11-256-173-29
; Sequence 29, Application US/11256173
; Publication No. US20060140979A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; TITLE OF INVENTION: Antigenic Peptides
; FILE REFERENCE: toxin
; CURRENT APPLICATION NUMBER: US/11/256,173
; PRIOR FILING DATE: 2005-10-24
; PRIOR FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-256-173-29

Alignment Scores:
Pred. No.: 5,6e-14 Length: 496
Score: 377.00 Matches: 127
Percent Similarity: 43.4% Conservative: 88
Best Local Similarity: 25.7% Mismatches: 210
Query Match: 12.5% Indels: 70
DB: 7 Gaps: 19

US-10-806-288-12 (1-1746) x US-11-256-173-29 (1-496)
Qy 1 TCTAGTGATGAGAAAGAATGATGTGATCAATTAATCAATGATCAATAAACACCGAGAT 60
Db 51 SerAsnGluSerLysSerAsnAspSerSerValSerAlaAlaProLysThrAspAsp 70
Qy 61 AATAACCAATAATTAATAAAGAAAGAAACGAATAACTACGATGCGATAGAAAAACGCTCA 120
Db 71 ThrAsnVal-----Ser 74
Qy 121 GAAGATAGACAGAGTCAACAAATGTAGATGAAACGAAACGAAACATTTTACAAAG 180
Db 75 AspThrLysThrSerSerAsnThrAsn-----AsnGlyGluThrSerValAlaGln 91
Qy 181 ACCCTCAAGTAACTATCTATCTTACAGAGAAGAGGTAAAGATCTCTCATCGTGCAG 240
Db 92 AsnPro-----AlaGlnGlnGluThrThrGlnSerSerSerThrAsn 105
Qy 241 TCCTCAAAATTCATCAATTGATCTGCCCAACCAACTCTCACAAACAATAAATAGAGAA 300
Db 106 AlaThrThrGluGluThrProValThrGlyGluAlaThrThrThrThrAsnGlnAla 125
Qy 301 GAATCTGTTCAACAGTGATTAATGTAGAAAGATTCACACGATATCAGATTTGCTAACTCT 360
Db 126 AsnThrProAlaThrThrGlnSer---SerAsnThrAsnAlaGluGluLeuValAsn--- 143
```

```
Qy 361 AAAATAAAGAGAGTACACTGAATCTGGTAAAGAGAGAACTACTATAGACCACTAAT 420
Db 144 -----GlnThrSerAsnGluThrThrPheAsnAspThrAsnThrVal----- 157
Qy 421 AAAATAAAGAGAGTCAACAAACAGAGTCAGCCGCTCTGGCTATACAAATATATAGATGAAAA 480
Db 158 -----SerSerValAsnSerProGlnAsnSerThrAsnAlaGluAsnVal 172
Qy 481 ATTTCAAATCAAGATGAGTTATTAAAT---TTACCAATAAATGAATATGAAAAAAGGCT 537
Db 173 SerThrThrGlnAspThrSerThrGluAlaThrProSerAsn-----AsnGluSer 189
Qy 538 AGACCATTTACTCAACATCTGCCCAACCATCGATTAAACGTGTAACCGTAAT----- 591
Db 190 AlaProGlnSerThrAspAlaSerAsnLysAspValValAsnGlnAlaValAsnThrSer 209
Qy 592 -----CAATTAGCGCGGCAACAAAGGTTTCGAATGTTAAACCATTTA 630
Db 210 AlaProArgMetArgAlaPheSerLeuAlaAlaValAlaAlaAspAlaProAlaAlaGly 229
Qy 631 ATTAAAGTTACTGATCAA-----AGTATTACTGAAGGATATGATGATGATGAGAGGTGT 684
Db 230 ThrAspIleThrAsnGlnLeuThrAsnValThrValGlyIle---AspSerGlyThrThr 248
Qy 685 ATTAAGCACATGATGCTGAAAACCTTAATCTATGATGTAACCTTTTGAAGTAGATGATAAG 744
Db 249 ValTyProHisGlnAlaGlyTyValLysLeuAsnTyThrGlyPheSerValProAsnSer 268
Qy 745 GTGAAATCTGGTGATACGATGACAGTGGATAGATAAGAAATACAGTTCATCAGATTTA 804
Db 269 AlaValLysGlyAspThrPheLysIleThrValProLysGluLeuAsnLeuAsnGlyVal 288
Qy 805 ACCGATAGCTTTACAATACCAAAAATAAAGATAAATCTCGGAGAAATCATCGCTACAGGT 864
Db 289 ThrSerThrAlaLysValProProIleMetAlaGlyAsp---GlnValLeuAlaAsnGly 307
Qy 865 ACTTATGATTAACAAAATAAACAATCACCTTACTTTTACAGATATATGATAGATAAGTAT 924
Db 308 ValIleAspSer---AspGlyAsnValIleTyThrPheThrAspTyValAsnThrLys 326
Qy 925 GAAATATTAAAGCACACCTTTAAATTAACGTCATACATTTGATTAATCAAAAGTTTCCAAT 984
Db 327 AspAspValLysAlaThrLeuThrMetProAlaTyIleAsp-----ProGlu 342
Qy 985 AATAATACCAAGTTA---GATGTAGATATATAAACGCCCTTTCATCA-----GTAAT 1035
Db 343 AsnValLysLysThrGlyAsnValThrLeuAlaThrGlyIleGlySerThrThrAlaAsn 362
Qy 1036 AAAACAATTACGGTTCGAATATCAAGACCTTAACGAAATCGGACTGCTAACCTTCAAAGT 1095
Db 363 LysThrValLeuValAspTyThrGluLysTyThrGlyLysPheTyThrAsnLeuSerIleLysGly 382
Qy 1096 ATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAAAACGATTTTATTAACCCCT 1155
Db 383 ThrIleAspGlnIleAspLysThrAsnAsnThrTyArgGlnThrIleTyValAsnPro 402
Qy 1156 CTT-----CGTTATTCAGCCCAAGGAAACAAATGTAATATTTCAGGAATGTTGATGAA 1209
Db 403 SerGlyAspAsnValIleAlaProValLeuThrGlyAsnLeuLysProAsnThrAspSer 422
Qy 1210 GGTTCACCAATTTATAGACGATAGACCAATTAATTAAGTTTATTAAGGTTGGAGATAATCAA 1269
Db 423 AsnAlaLeuIleAspGlnGlnAsnThrSerIleLysValTyLysValAspAsnAlaAla 442
Qy 1270 AATTTACGATAGTAACGAATTTATGATTACAGTGAATATGAAGATGTACAAAATGAT 1329
Db 443 AspLeuSerGluSerTyThrPheVal---AsnProGluAsnPheGluAspValThrAsnSer 461
Qy 1330 GATTATGCCCAATTAGGAATAATAATGATGTCGAATATTATTTTGT----- 1377
Db 462 ValAsnIleThrPheProAsnProAsnGlnTyLysValGluPheAsnThrProAspAsp 481
Qy 1378 AATATAGATTCACCATATATTATTAAGTTATTAGTAAATATATGAC 1422
```



[illegible]

```

Db      506 ProProValGluIysHisGluLeuThrGlyThrIleGluGluSerAsnAspSer---Lys 524
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1654 CCGCTTAGTAAATGATTGGTAACCTTTCAGC-----TATCCTGATGGAAC 1698
      |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      525 ProIleAspPheGluTyHisThrAlaValGluGlyAlaGluGlyHisAlaGluGlyThr 544
      |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1699 TCAAAATCAGTCAGAACAGATGAGAT 1725
      |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      545 -----IleGluThrGluGluAsp 550
      |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...

RESULT 9
US-10-471-571A-3554
; Sequence 3554, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
; CURRENT APPLICATION NUMBER: US/10/471.571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3554
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1018)
; OTHER INFORMATION: fibronectin-binding protein
US-10-471-571A-3554

```

```

Alignment Scores:
Pred. No.:      9.16e-10      Length:      1018
Score:          300.50      Matches:      123
Percent Similarity: 41.5%      Conservative: 118
Best Local Similarity: 21.2%      Mismatches: 243
Query Match:      9.9%      Indels:      97
DB:              6      Gaps:      25

```

US-10-806-288-12 (1-1746) x US-10-471-571A-3554 (1-1018)

```

Qy      103 GGCATAGAAAACCGCTCAGAGATAGAACAGAGTCAACAACAATGTAGATGAACGAA 162
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      30 GlyGlnAspLysGluAlaAlaAlaSerGluGlnLysThrThrValGluGluAsn--- 48
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      163 GCAACATTTTACAAAAGACCCCTCAAGATAAT-----ACTCATCTTACAGAA 210
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      49 -----GlyAsnSerAlaThrAspAsnLysThrSerGluThrGlnThrThra 64
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      211 GAAGAGGTAAAGAAGATCCTCATAGTCGAATCCTCAAAATTCATCAATGTAGTATGATGCCCAA 270
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      65 ThrAsnValAsnHisIleGluGluThrGlnSerTyraAsnAlaThrVal-----ThrGlu 82
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      271 CAACCATCTCACAAACA-----ATAAATAGAGAGAA-----TCTGTTCAACAAGT 318
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      83 GlnProSerAsnAlaThrGlnValThrGluGluAlaProLysAlaValGlnAlaPro 102
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      319 GATNAATGTAGNAGATTCACAGGTATCAGATTTTGCTAACTCTAAATATAAAGAGAGGTAAAC 378
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      103 GlnThrAlaGlnProAlaAsnIleGluThrValLysGluGluValValLysGlu----- 120
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      379 ACTGAATCTGTAAAGAGAGAACTATATAGAGCAACCTAATAAAGTAAAGAAAGAGATTCA 438
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      121 -----GluAlaLysProGlnValLysGluThrThr 130
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      439 ACAACAAGTCAGCGCTCTGGC-----TATCACAATATAGATGAACAAATTTCAAT 489
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      131 GlnSerGlnAspAsnSerGlyAspGlnArgGlnValAspLeuThrProLysLysAlaThr 150
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...

```

```

Qy      490 CRAAGATGAGTTTAAATTTACCAATAAATGAATATGAAATAAGCGTAGACCATTTACT 549
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      151 GlnAsnGlnValAlaAlaGluThrGlnVal-----GluValAlaGlnProArgThr 166
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      550 ACAACATCTGCCCAACACCATCGATTAAACGTTGAACC-----GTA 588
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      167 AlaSerGluSerLysProArgValThrArgSerAlaAspValAlaGluAlaLysGluAla 186
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      589 AATCAATTAGCGCGGGAACAAGGTTTCGAATGTTAACCATTTAATTAAGTTACTGATCAA 648
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      187 SerAsnAlaLysValGluThrGlyThrAspValThrSerLysValThrValGluIleGly 206
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      649 AGTATTACTGAAGGATATGATGATGAGGTTTATTAAAGCACACATGATGCTGAAAC 708
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      207 SerIle---GluGlyHisAsnAsnThrAsnLysVal---GluProHisAlaGlyGlnArg 224
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      709 TTAATCTATGATGATACTTTTGAAGTAGATGATAAGGTGAAATCTGCTGATGATGACA 768
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      225 AlaValLeuLysTyrlLysLeuLysPheGluAsnGlyLeuHisGlnGlyAspTyrlPheAsp 244
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      769 GTGGATATAGATAAGAATACAGTTCATCCATCAGATTAAACCATGCTTTACAAATACCAAA 828
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      245 PheThrLeuSerAsnAsnValAsnThrHisGlyValSerThrAlaArgLysValProGlu 264
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      829 ATAAAGATAATTTCT-----GGAGAAATCATCGCTACAGGTACTTATGAT 873
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      265 IleLysAsnGlySerValValMetAlaThrGlyGluValLeuGluGlyGly----- 281
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      874 AACAAAAATAAACAAATCACCTTATCTTTTACAGATTATGTAGATGAATGAATAATT 933
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      282 -----LysIleArgTyrlThrPheThrAsnAspIleGluAspLysValAspVal 297
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      934 AAGCACACCTTAATTAACGTATACATGATTAATCAAGGTTCCCAATATATATACC 993
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      298 ThrAlaGluLeuGluIleAsnLeuPheIleAspProLysThrValGlnThrAsnGlyAsn 317
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      994 AAGTTAGATGTAGATAATAAAACGGCCCTTTTCATCAGTAAAT-----AAA 1038
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      318 -----GlnThrIleThrSerThrLeuAsnGluGluGlnThrSerLys 331
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1039 ACAATTACGGTTGAATATCAAGACCTAACGAAAAATCGGACTCTCTAACCTTCAAAGTATG 1098
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      332 GluLeuAspValLysTyrlLysAspGlyIleGlyAsnTyrlTyrlAlaAsnLeuAsnGlySer 351
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1099 TTTACAAATATAGATACGAAATATACATACAGTTGACGCAACGATTATATTAACCTCTT 1158
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      352 IleGluThrPheAsnLysAlaAsnAsnArgPheSerHisValAlaPheIleLysPro--- 370
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1159 CGTTATTTCAGCCCAAGAAACAAATGTAAATATTTCAGGGAATGCTGATGAAGTTCAACA 1218
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      371 ---AsnAsnGlyLysThrThrSerValThrValThrGlyThrLeuMetLysGlySerAsn 389
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1219 ATTATAGACATAGACAATAATAAGTTTATAAG---GTTGGAGATATCAAAATTTA 1275
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      390 GlnAsnGlyAsnGlnProLysValArgIlePheGluTyrlLeuGlyAsnAsnGluAspIle 409
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1276 CCAGATAGTAACAGATTAT-----GATTACAGTCAATATGAAGTGTCA 1323
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      410 AlaLysSer-----ValTyrlAlaAsnThrThrAspThrSerLysPheLysGluValThr 427
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1324 AATGATGATTATGCCCAATTAGGA-----AATAATAATGATGTAATATTAATTTTGGT 1377
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      428 SerAsnMetSerGlyAsnLeuAsnLeuGlnAsnAsnGlySerTyrlSerLeuAsnIleGlu 447
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1378 AATATAGATTCACATATATATTAAAGTTATTAGTAATATGACCCCTAATAAGAT--- 1434
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      448 AsnLeuAspLysThrTyrlValValHisTyrlAspGlyGluTyrlLeuAsnGlyThrAspGlu 467
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1435 ---GATTACAGCTATACAGCAAACTGTGACAATGCAGACACTATATAATAGTACT 1491
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Db      468 ValAspPheArgThr---GlnMetValGlyHisProGluGlnLeuTyrlLysTyrlTyrl 486
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...
Qy      1492 GGTGAGTTTAGAACAGCATCCTATGATATAACAATTGCTTTCTCTACAAGTTCAGGTCAA 1551
      |||  ...  |||...  |||...  |||...  |||...  |||...  |||...  |||...  |||...

```

```

Db      487 AspArgGlyTyrThrLeuThrTrpAspAsnGlyLeuValLeuTyrSerAsnLysAlaAsn 506
Qy      1552 GGACAAAGTGACTGCTCTCCT-----GAAAAAACTTATAAAATCGGAGAT 1596
Db      507 GlyAsnGluLysAsnGlyProIleLeuGlnAsnAsnLysPheGluTyrLys-----523
Qy      1597 TACGTATGGGAAGATGATAGATAAGATGGTATTCAAATACAAATGATAATGAAAAACCG 1656
Db      524 -----GluAspThrIleLysGluThrLeuThrGlyGlnTyrAspLysAsn-----538
Qy      1657 CTAGTATGATGTTGTAACCTTGACGTATCCTGATGGAACCTCAAAATCAGTCAGACACA 1716
Db      539 -----LeuValThrValGluGluTyrAspSerSerThrLeuAspIle 554
Qy      1717 GAT 1719
Db      555 Asp 555

RESULT 10
US-11-192-046-250
; Sequence 250, Application US/11192046
; Publication No. US20060165716A1
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Barocchi, Michelle
; APPLICANT: Rappugli, Rino
; APPLICANT: Grandi, Guido
; APPLICANT: Lauer, Peter
; APPLICANT: Mora, Marirosa
; APPLICANT: Y Ros, Immaculada
; APPLICANT: Malone, Domenico
; APPLICANT: Bensi, Guiliano
; APPLICANT: Rinaudo, Daniela
; APPLICANT: Massignani, Vega
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR GRAM POSITIVE BACTERIA SUCH AS
; TITLE OF INVENTION: STREPTOCOCCUS AGALACTIAE
; FILE REFERENCE: 002441.00168/PP22811.011
; CURRENT APPLICATION NUMBER: US/11/192.046
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US 60/592,805
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US 60/609,833
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 60/616,833
; PRIOR FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US 60/633,418
; PRIOR FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US 60/640,069
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US 60/660,321
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/673,754
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/693,001
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: US 60/695,453
; PRIOR FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/697,643
; PRIOR FILING DATE: 2005-07-11
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 250
; LENGTH: 1160
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-11-192-046-250

Alignment Scores:
Pred. No.: 1.16e-07 Length: 1160
Score: 262.50 Matches: 126
Percent Similarity: 38.3% Conservative: 101
Best Local Similarity: 21.3% Mismatches: 246

```

```

Query Match: 8.7% Indels: 119
DB: 7 Gaps: 23
US-10-806-288-12 (1-1746) x US-11-192-046-250 (1-1160)
Qy      103 GGCAATAGAAAACGCTCAGAGATAGAACAGAGTCAACAACAATGTAGATGAAACGAA 162
Db      28 GlyLeuSerGlyValSerValGlyHisAlaGluThrArgAsnGlyAlaAsnLysGlnGly 47
Qy      163 GCAACATTTTACAAAAAGACCCCTCAAGATAATACTCATCTTACAGAGAAGAGGTAAAA 222
Db      48 TyrPheGluIleLysValAspGlnAsn-----Lys 59
Qy      223 GAATCCTCATCAGTCGAATCCTCAAAATTCATCAATTTGATCTGCGCAACAACCATCTCAC 282
Db      60 ProLeuSerGlyAlaThrPheSerLeuThrProLysAspGlyLysGlyValProValGln 79
Qy      283 ACAACAATAATAGAGAGAATCTGTTCAACAACAAGTATGATAATGTAAGATTCACACGTA 342
Db      80 ThrPheThrSerSerGluGluGlyIleLeuAspAlaGlnAsnLeuGlnProGlyThrTyr 99
Qy      343 TCAGATTTTGCTAACTCTAAATAATAAGAGAGTAACTGAATCTGGTAAAGAGAGAAAT 402
Db      100 Thr-----LeuLysGluGluThrAlaProAspGlyTyrAspLysThr 113
Qy      403 ACTATAGAGCAACCTAATAAAGTAAAGAGAGATTCACAACAAGTCAAGCGCTCGCTAT 462
Db      114 Ser-----ArgThrTrpThrValThrValTyrGluAsnGlyTyr 126
Qy      463 ACAATATAGATGAAAAAATTTTCAAAATCAAGATGAGTTATTAAATTTTACCAATAAATGAA 522
Db      127 ThrLysLeuValGluAsnProTyrAsn-----GlyGlu 137
Qy      523 TATGAAATAGGCTAGACCATTCATCTACAACATCTGCC-----CAACCATCGATTAAACGT 579
Db      138 IleIleSerLysAlaGlySerLysAspValSerSerLeuGlnLeuGluAsnProLys 157
Qy      580 GTAACCGCTAAATCAATAGCGGCAACAAGTTGCGAATGTTAACCATTTTAAATTAAGATT 639
Db      158 MetSerValSerLysTyrGlyGluGln-----167
Qy      640 ACTGATCAAAAGTATTACTGAAGATATGATGATAGTGAAGGTGTATTAAAGCACATGAT 699
Db      168 -----GluLysThrSerAsnSerAlaAspPheTyrArgAsnHisAla 181
Qy      700 GCTGAAACCTTAATCTATGATGTAACCTTTTGAAGTAGATGATAGGTGAATCT-----753
Db      182 Ala-----TyrPheLysMetSerPheGluLysGlnLysAspLysSerGluThr 198
Qy      754 -----GGTGATACGATGACAGTCGATATAGATAAGAATACAGTTCCATCAGATTTA 804
Db      199 IleAsnProGlyAspThrPheValLeuGlnLeuAspArgLeuAsnProLysGlyTyr 218
Qy      805 ACCGATAGCTTTACAAATACCAAAA-----ATAAAAGATAAATCTCGAGAAATCATCGCTACA 861
Db      219 SerGlnAsp-----IleProLysIleIleTyrAspSerGluAsnSerProLeuAlaIle 236
Qy      862 GGTACTTATGATAACAAAAATAACAATCACCTATACTTTTACAGATTATGTAGATAAG 921
Db      237 GlyLysTyrAspAlaLysThrHisGlnLeuThrTyrThrPheThrAsnTyrIleAlaGly 256
Qy      922 TATGAAAAATATAAAGCACACCTTTAAATTAACGTACATACATTAATCAAGGTTCACA 981
Db      257 LeuAspLysValGlnLeuSerAlaGluLeuSerLeuPheLeuGluAsnLysGluValLeu 276
Qy      982 AATAATAATACCAAGTTAGATGTAATAATAAAACGCGCCCTTTCATCATCAGTAAATAAACA 1041
Db      277 GluAsnThrAsnIleSerAspPheLysSerThrIleGlyGlnGluIleThrTyrLys 296
Qy      1042 ATTACGGTTGAATATCAAGACCTCAACGAA-----AAT 1074
Db      297 GlyThrValAsnValLeuTyrGlyAsnGluSerThrLysGluSerAsnTyrIleThrAsn 316

```

```
QY 1075 CGGACTGCTAACCTTCAAAGTATGTTTACAAATATAGATACGAAATAATACATACAGTTGAG 1134
Db :|||:
317 GlyLeuSerAsnValGlyGlySerIleGluSerTyrAsnThrGluThrGlyGluPheVal 336
QY 1135 CAACAGATTATTAACCTCTCGTATTACGCCAAGAAACAAATGTGAATATAT 1191
Db :|||:
337 TriPtyrValTyrValAsnProAsnArgThrAsnIleProTyrAlaValLeuAsnLeuTyr 356
QY 1192 -----TCAGGAATGGTGATGCAAGGTTCAACAATATAGAGAT 1230
Db :|||:
357 GlyPheAlaLysArgThrAlaGlnGlyGluAsnAspAsnSerValSerSerAlaGln 376
QY 1231 AGCACATAATTAAGTTTATAAGTTGGAGATAATCAAAATTTACCAGATAGTAACAGA 1290
Db :|||:
377 LeuThrGlyTyrAspIleTyrGluValProHisAsnTyrArgLeuProThrSerTyrGly 396
QY 1291 ATTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCAATTA----- 1344
Db :|||:
397 Val---AspIleSerArgLeu---AsnLeuArgLysAspLeuGluAlaLysLeuProGln 414
QY 1345 -----CGAATAATAATGATGCTGAATATTAATTTGCT---AATATAGAT--- 1386
Db :|||:
415 GlySerThrGlnGlyAlaAsnLysArgLeuArgIleAspPheGlyGluAsnLeuGlnGly 434
QY 1387 TCACCATATATTAAAGTTATTAGTAAATATAGACCTAATAAGGATGATTACACGACT 1446
Db :|||:
435 LysAlaPheValValLysValThrGlyLysAlaAspGlnSerGlyLysGlu----- 451
QY 1447 ATACAGCAAACTGTGCAACTGCAGACGACTATAAATGAGTATACT-----GGTGAGTTT 1500
Db :|||:
452 -----LeuIleValGlnSerHisLeuSerSerPheAsnAsnTyrGlySerTyr 467
QY 1501 AGAACA-----GCATCTATGATAATAACAATTCGTTCTCTACAGT 1542
Db :|||:
468 LysThrLeuArgProAsnSerHisValSerPheThrAsnGluIleAlaLeuSerProSer 487
QY 1543 TCAGGTCAAGGACAAGGTGAC-----TTGCTCTCGAATAAACT 1581
Db :|||:
488 LysGlySerGlySerGlyThrSerGluPheThrLysProAlaIleThrValAlaAsnLeu 507
QY 1582 TATAAATCGGAGATTACGTATGGAGAGATGATAGATAAAGATGGTATT----- 1629
Db :|||:
508 LysArgValAlaGlnLeuArgPheLysLysValSerThrAspAsnValProLeuProGlu 527
QY 1630 -----CAAAATACAAATGATAAATGAAACCGCTT-----AGTAAT 1665
Db :|||:
528 AlaAlaPheGluLeuArgSerSerAsnGlyAsnSerGlnLysLeuGluAlaSerSerAsn 547
QY 1666 GTATTGGTAACCTTTGAGGTATCCTGATGGAACCTTCA 1701
Db :|||:
548 ThrGlnGlyGluIleHisPheLysAspLeuThrSer 559

RESULT 11
US-11-192-046-121
; Sequence 121, Application US/11192046
; Publication No. US20060165716A1
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Barocchi, Michelle
; APPLICANT: Rappuoli, Rino
; APPLICANT: Grandi, Guido
; APPLICANT: Lauer, Peter
; APPLICANT: Mora, Marirosa
; APPLICANT: Y Ros, Immaculada
; APPLICANT: Malone, Domenico
; APPLICANT: Bensi, Guilianno
; APPLICANT: Rinaudo, Daniela
; APPLICANT: Maignani, Vega
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR GRAM POSITIVE BACTERIA SUCH AS
; FILE OF INVENTION: STREPTOCOCCUS AGALACTIAE
; FILE REFERENCES: 002441.00168/PP22811.011
; CURRENT APPLICATION NUMBER: US/11/192_046
; CURRENT FILING DATE: 2005-07-29
```

```
; PRIOR APPLICATION NUMBER: US 60/592,805
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US 60/609,833
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 60/616,833
; PRIOR FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US 60/633,418
; PRIOR FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US 60/640,069
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US 60/660,321
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/673,754
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/693,001
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: US 60/695,453
; PRIOR FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/697,643
; PRIOR FILING DATE: 2005-07-11
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 121
; LENGTH: 1161
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
; US-11-192-046-121

Alignment Scores:
Pred. No.: 1,81e-07 Length: 1161
Score: 259.00 Matches: 113
Percent Similarity: 39.3% Conservative: 95
Best Local Similarity: 21.4% Mismatches: 205
Query Match: 8.6% Indels: 116
DB: 7 Gaps: 21

US-10-806-288-12 (1-1746) x US-11-192-046-121 (1-1161)

QY 373 AGTACACGTGATCTCGTTAAAGAGAGATATCTATAGACCACTAATAAGTAAAGAA 432
Db :|||:
70 SerLysAspGlyLysGlyThrSerValGlnThrPheThrSerAsnAspLysGlyIleVal 89
QY 433 GATTCAACAACAAGTCAGCGCTGCTGCTATACAAATATAGATCAAAAAATTTCAAATCAA 492
Db :|||:
90 AspAlaGlnAsnLeuGlnProGlyThrTyrThrLeuLysGluThrAlaPro----- 107
QY 493 GATGAGTTTAAATTTACCAATAAATGAATATGAAATAAGCTAGACCATTTATCTACA 552
Db :|||:
108 -----AspGlyTyrAspLysThrSerArgThrTyrThrVal 119
QY 553 ACATCTGCCCAACCATCGATTAAACGTGTAAACCGTAAAT-----CAATTAGCG 600
Db :|||:
120 ThrValTyrGluAsnGlyTyrThrLysLeuValGluAsnProTyrAsnGlyGluIle 139
QY 601 GCGGAACAAGGTTTCG---AATGTTAACCATTAATTAAGTTACTGAT-----CAAAGT 651
Db :|||:
140 SerLysAlaGlySerLysAspValSerSerSerLeuGlnLeuAsnProLysMetSer 159
QY 652 ATTACTGAAGGATGATGATGATGAA-----GGTGTATTAAAGCACATGATGCT 702
Db :|||:
160 ValValSerLysTyrGlyLysThrGluValSerSerGlyAlaAlaAspPheTyrArgAsn 179
QY 703 GAAACTTAATCTATGATGTTACTTTTGAAGTAGATGATAAGGTGAATCT----- 753
Db :|||:
180 HisAlaAlaTyrPheLysMetSerPheGluLeuLysGlnLeuLysAspLysSerGluThrIle 199
QY 754 -----GGTGATACGATGATGATGATGATAAGATAACAGTCCATCCAGATTTAAACC 807
Db :|||:
200 AsnProGlyAspThrPheValLeuGlnLeuAspArgArgLeuAsnProLysGlyIleSer 219
QY 808 GATAGCTTTACAATACCAAAA---ATPAAAGATAATTTCTGGAGAAATCATCGTTACAGGT 864
Db :|||:
220 GlnAsp-----IleProLysIleIleTyrAspSerAlaAsnSerProLeuAlaIleGly 237
```

```

QY 865 ACTTATGATAACAAATAAACAATACCTTACCTTATCTTTTACAGATTATAGATAAGTAT 924
Db 238 LysTyrHisAlaGluAsnHisGlnLeuIleTyrThrPheThrAspTyrIleAlaGlyLeu 257
QY 925 GAAATATATTAAGACACACCTTAAATTAAGCTCATACATTGATAAATCAAGGTTCCAAT 984
Db 258 AspLysValGlnLeuSerAlaGluLeuSerLeuPheLeuGluAsnLysGluValLeuGlu 277
QY 985 AATAATACCAAGTTAGATAGATAATATAAAGCGCCCTTTCATCAGTAAATAAACAAT 1044
Db 278 Asn-----ThrSerIleSerAsnPhelySerThrIle 288
QY 1045 -----ACGGTTGAATATCAAGAACCCTTAACAA----- 1071
Db 289 GlyGlyGlnGluIleThrTyrLysGlyThrValAsnValLeuTyrGlyAsnGluSerThr 308
QY 1072 -----AATCGGACTGCTTAACCTTCAAGATGTTCAAGATGTTTACAATATA 1110
Db 309 LysGluSerAsnTyrIleThrAsnGlyLeuSerAsnValGlyGlySerIleGluSerTyr 328
QY 1111 GATACGAAATAATCATACAGTTGAGCAACAGATTATATTAACCTCTTCGTTATTACGCC 1170
Db 329 AsnThrGluThrGlyGluPheValTyrValTyrValAsnProAsnArgThrAsnIle 348
QY 1171 AAGGAAACAATGTAATATTTACGGGAATGTT----- 1203
Db 349 ProTyrAlaThrMetAsnLeuTyrGlyPheGlyArgAlaArgSerAsnThrSerAspLeu 368
QY 1204 ---GATGAAGTTTCAACATATATACATAGACATAGACACAATAATAAGTTTAAAGTTGGA 1260
Db 369 GluAsnAspAlaAsnThrSerSerAlaGluLeuGlyGluIleGlnValTyrGluValPro 388
QY 1261 GATAATCAAAATTTACAGATAGTAGTAACAAGATTTATGATTACAGTGAATATGAAGATGTC 1320
Db 389 GluGlyGluLysLeuProSerSerTyrGlyVal-----AspVal 401
QY 1321 ACA-----AATGATGATTATGCCCAATTAGGAATAATAATGATGTTG--- 1362
Db 402 ThrLysLeuThrLeuArgThrAspIleThrAlaGlyLeuGlyAsnGlyPheGlnMetThr 421
QY 1363 -----AATATTAATTTTGGTAAT-----ATAGATTCCACATATATTTAAAGTT 1407
Db 422 LysArgGlnArgIleAspPheGlyAsnAsnIleGlnAsnLysAlaPheIleIleLysVal 441
QY 1408 ATTAGTAATATGACCTTAATAAGGATGATTACAGACTATACAGCAAACTGTGCACATG 1467
Db 442 ThrGlyLysThrAspGlnSer-----GlyLysProLeuValVal 454
QY 1468 CAGACGACTATAAATAGTATACTGGTGAGTTTAGAACAGCATCC----- 1512
Db 455 GlnSerAsnLeuAlaSerPheArgGlyAlaSerGluTyrAlaAlaPheThrProValGly 474
QY 1513 -----TATGATAATACAAATCTCTTCTTCTACAGTTCCAGTCAAGGCAAGGT 1560
Db 475 GlyAsnValTyrPheGlnAsnGluIleAlaLeuSerProSerLysGlySerGly 494
QY 1561 -----GACTTGCCTCTCGAATAAATCTTATAAATCGGAGATTAC 1599
Db 495 LysSerGluPheThrLysProSerIleThrValAlaAsnLeuLysArgValAlaGlnLeu 514
QY 1600 GTATGGGAAGATGTAGATAAAGATGGTATTCAAAATACAAATGATATGAAAAACCGGTT 1659
Db 515 ArgPheLysLysMetSerThrAspAsnVal-----ProLeu 526
QY 1660 AGTAATGTATGGTAACCTTTCAGCTATCTCTGATGGAACCTTCAAAATCAGTCAGA----- 1713
Db 527 ProGluAlaAlaPheGluLeuArgSerSerAsnGlyAsnSerGlnLysLeuGluAlaSer 546
QY 1714 ACAGATGAAGATGGGAATATCAATTT 1740
Db 547 SerAsnThrGlnGlyGluValHisPhe 555

```

## RESULT 12

```

US-10-537-642-10
; Sequence 10, Application US/10537642
; Publication No. US20060165719A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: The United States of America as Represented by the
; APPLICANT: Secretary of the Navy
; APPLICANT: Sette, Alessandro
; APPLICANT: Doolan, Denise L.
; APPLICANT: Carucci, Daniel J.
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
; FILE REFERENCE: EPI-103X
; CURRENT APPLICATION NUMBER: US/10/537,642
; PRIORITY FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US 60/431,494
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1161
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 3029
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-537-642-10

```

## Alignment Scores:

```

Pred. No.: 3,36e-07 Length: 3029
Score: 253.50 Matches: 150
Percent Similarity: 34.8% Conservative: 95
Best Local Similarity: 21.3% Mismatches: 265
Query Match: 8.4% Indels: 195
DB: 6 Gaps: 31

```

US-10-806-288-12 (1-1746) x US-10-537-642-10 (1-3029)

```

QY 16 AAGTAATGATGTGATCAATAATAATCAAGTCAATAAACACCGACGATAATAACCAATAATT 75
Db 926 LysAsnGluAsnAspAsnIleProSerSerTyrSerGlnIleHisAsnHisGlnIleCys 945
QY 76 AAAAAAGAGAAACGAATAAATACGATGGCATAGAAAACGCTCAGAAAGATAGACAGAG 135
Db 946 LysLysValGluGluTyrThrTyrAsnSerIleAsnGln----- 958
QY 136 TCACACAAATGTAGATGAAACGAAACCAACATTTTACAAAAGACC----- 183
Db 959 ---AsnThrAsnAsnPheAsnAsnAsnValMetMetLeuMetAsnThrSerAsnAsnIle 977
QY 184 CCTCAAGATATAACT-----CATCTTACA 207
Db 978 ProLeuAspAsnAsnThrTyrAsnSerAsnLysAsnLysIleIleTyrLysHisIleIle 997
QY 208 GAAGAAGAGGTAAAGAAATCCTCATCA-----GTCCGAATCCTCAAAATTCATCAATT 258
Db 998 AsnAspHisIleAsnGlnLysAspAsnAsnValGluTyrGluAsnLeuAsnAsnSerCys 1017
QY 259 GATACTCCCAA----- 270
Db 1018 AspAsnThrGlnAsnLysGluThrPheCysAsnGlnAspLeuIleAsnSerSerAsnIle 1037
QY 271 -----CAACCATCTCACACACAATAAATAGAGAGAA 303
Db 1038 AsnAsnAsnIleSerSerTyrThrPheGlnAsnAsnAspPheTyrThrLysLysLys 1057
QY 304 TCTGTTCAA-----ACAAGTGAATAGTAGAA 330
Db 1058 SerMetGlnTyrAsnHisAspAsnIleTyrLysIleAsnThrThrSerGluAsnValGly 1077
QY 331 GATTACACATATCAGATTTTGTCTTAACCTTAATAAAGAGAGATGAATCTGGT 390
Db 1078 SerProHis-----ThrAsnAsnLysThrSerIleTyrAsnHisLysLysGly 1093

```

```
QY 391 AAAGAAGAGAATACTATAGACGACCTAATAAAGTAAAGAAAGATTCAACAACAAAGTCAG 450
Db 1094 GlyTyrGluGlnHisThrGluGlnAsnAsnGluGlnAsnGluGlnAsnSerGluGln 1113
QY 451 CCCTCTGGCTATACAAATATAGATGAAATAATTTCA-----AATCAAGATGAGTTA 501
Db 1114 -----AsnIleGluGlnAsnIleGluGlnAsnIleGluGlnAsnValala 1128
QY 502 TTAATTTTACCAATAATGAATATGAAATAAGCTAGACCATTTATCTACACATCTGCC 561
Db 1129 GlnAsnValalaGlnAsnValalaGlnAsnValGluGlnAsnValala 1148
QY 562 CAACCATCGATTAAACGTGTAACCGTAAAT---CAATTAGCGGCGGAACAAAGTTGCAAT 618
Db 1149 GlnAsnValGluGlnAsnValGluGlnAsnValGluGlnLysAlaGluGlnAsnSerAsn 1168
QY 619 GTTAACCATTTTAATTAAGTT-----ACTGATCAAAAGTATTACTGAAGGATAT 666
Db 1169 ---AsnGluSerIleLysThrAsnThrValGluThrPheLysArgAsnLysAsnGlnIle 1187
QY 667 GATGATAGTGAAGGTGTTATT-----AAAGCATGATGCTGMAAACTTAATCTATGAT 720
Db 1188 ThrAsnSerAsnAsnValIleSerLysGlnGlnHisAspThrAsnAsnIleLeuAsnAsn 1207
QY 721 GTAACCTTTTGAAGTATGATAAGTG-----747
Db 1208 IleAsnIleAsnIleLysGluAsnIleAsnArgHisLysIleAsnGluPheGlnTrpGlu 1227
QY 748 AAATCTCGTGATACGATGACAGTGGATATAGTAAGAATACAGTTTCCATCAGATTTTAACC 807
Db 1228 LysSerAsn-----LysIleAspIleGluLysAsnAsnCys-----LeuThr 1241
QY 808 GATAGCTTTTCAATACCAAAAATAAAGATAATTTCTCGGAGAAATCATCGCTACAGGTACT 867
Db 1242 ThrLysTyr-----AspLysAspAsnAspAsnGluAsnAspAsnGluAsnAspAsnThr 1259
QY 868 TATGATAACAAAATAAACAATCAACCTATACTTTTACAGATTATGTAGATAAGTATGAA 927
Db 1260 Tyr---AsnLysAsnAsnAspIleVal-----IleCysAsnAsnHis 1272
QY 928 AATATTAAAGCACACCTTAAATTAACGTCTATACATATGATAAATCAAAAGTTTCCAAATAT 987
Db 1273 AsnAsnSerSerHisValGlnLysAsnTyrTyrAsnMetAsnGluSerMetIleAsnGlu 1292
QY 988 AATACCAAGTATGATGATAGATAATAAACCGCCCTTTCATCA-----GTA 1032
Db 1293 AsnAsnIleIleIleThrGluGluAsnLeuMetAsnSerThrGluGluTyrPheThr 1312
QY 1033 AATAAAACAATTACGGTTGTAATATCAAGAGCCTAACGAAATCGACTGTAACTTCAA 1092
Db 1313 AsnGluLeuIleLysLysAspSerLeuGluLysAsnLysSerAspThrLysPheLeuIle 1332
QY 1093 AGTATGTTTCAAAATATAGATACGAAATAATCATACAGTTGAGCAA---ACGATTATATT 1149
Db 1333 LysLeuAsnAsnGluIleLysLysGluGluLysLysAspAsnIleAsnIlePheIle 1352
QY 1150 AACCTCTCTGTTATTCAGCCCAAGCAACAAT-----1182
Db 1353 AsnAsnAsnIleTyrGluLeuLysGluIleAsnGlyAsnLysAsnArgSerAspTyrPhe 1372
QY 1183 -----GTAATAATTTTCAGGGAAT-----1200
Db 1373 HisAsnThrLysAspAspLysGluAsnIleThrAsnValSerSerAsnAsnHisLeuSer 1392
QY 1201 -----GGTGAATGAAGTTTCAAAATTTATAGACGATAGCACAAATATT 1242
Db 1393 ValProLeuAsnLysTyrAsnAspGlu-----AspLysGlnLeuIle 1406
QY 1243 AAAGTTTATAGGTGGAGATAATCAAAATTTTACCAGATAGTAAACAGAAATTTATGATAC 1302
Db 1407 LysGlnMetAsnHisAlaSerAsnMetAsnPhe-----IleTyrAspTyr 1421
QY 1303 AGTGAATATGAAGTGTACAAATGATGATTTATGCCCAATTTAGGAAATATATATGATGTG 1362
```

```
Db 1422 AsnTyrHisAsnAsnTyrSerSerThrAsnSerGlnGlnLeuIleLysAsnAsnThrGlu 1441
QY 1363 AATATT---AATTTTGGTAATATAGATTACCATATATATTAAAGTTATTAGTAAATAT 1419
Db 1442 AsnLeuHisSerPheLysAsnGluThrHisSerThrTyrValLysTyrIleLysSerGlu 1461
QY 1420 GACCTTAAT---AAGGATGATTAC-----1440
Db 1462 IleAsnAsnMetAsnAsnSerIleGlyValProThrLysLysAsnAspTyrMetTyrThr 1481
QY 1441 -----ACGACTATACAGCAAACTGTGCACAAATGCAG 1470
Db 1482 AsnTyrLeuAsnMetGluHisIleLysMetAsnAsnMetGluLysGluIleLysLys 1501
QY 1471 ACGACTATTAATGAGTATATCTGTGAGTTTAGAACAGCATCTTATGATATATACAAATGCT 1530
Db 1502 GlyAsnAspAsnGluIleLysGlyGlnArgIleGlnValGluHisAspArgAspValHis 1521
QY 1531 TTCTCTACAGTTTCAGGTCAAGGACCAAGGTGACTTGCCTCTGAAAAAACTTATAAATC 1590
Db 1522 TyrAsnThrThrGlnGluAsnAsnIleIleAsnAsnGlnAsnProGlnThr-----1538
QY 1591 GGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAATACAAATGATAATGAA 1650
Db 1539 -----AsnHisAspGlyAspMetAsnIleAsnIleAsn---1549
QY 1651 AAACCGCTTAGTAAATGTTGGTAACT---TTGACGTATCTCTGATGGAACTTCAAAATCA 1707
Db 1550 -----SerAsnLysPheMetThrProThrThrLeuLysGluLysTyrGlnAsnAsn 1566
QY 1708 GTCAGAACAGATGAA 1722
Db 1567 IleAsnThrAsnGlu 1571

RESULT 13
US-10-537-642-21
; Sequence 21, Application US/10537642
; Publication No. US20060165719A1
; GENERAL INFORMATION:
; APPLICANT: EpiImmune, Inc.
; APPLICANT: The United States of America as Represented by the
; APPLICANT: Secretary of the Navy
; APPLICANT: Sette, Alessandro
; APPLICANT: Doonan, Denise L.
; APPLICANT: Carucci, Daniel J.
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE
; FILE REFERENCE: EPI-103X
; CURRENT APPLICATION NUMBER: US/10/537,642
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US 60/431,494
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1161
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 2024
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; US-10-537-642-21

Alignment Scores:
Pred. No.: 6.95e-05 Length: 2024
Score: 212.00 Matches: 132
Percent Similarity: 39.7% Conservative: 121
Best Local Similarity: 20.7% Mismatches: 249
Query Match: 7.0% Indels: 136
DB: 6 Gaps: 33

US-10-806-288-12 (1-1746) x US-10-537-642-21 (1-2024)
QY 43 TCAATAAACACCGCAGCATATAACCAATAATTAATAAAGAAAGAAACGAAT-----93
```

```
Db 31 SerLeuAsnTyrSerLysAsnAsnTyrGlyLeuAsnAspGlnGluLeuAArgAlaMetLeu 50
|||:||||| ||||| :||| :|||
94 -----AACTACGATGGCATAAGAAAACGCTCAGAAAGATAGAACAGAGTCAACAACA 144
|||:||||| :||| :||| :|||
Db 51 PheGlyLeuAsnTyrAspProSerLysArgAsnLysAsnAsnLysVal-----AsnArg 68
|||:||||| :||| :||| :|||
145 AATGTAGTAAAGCAAGCAACATTTTTCACAAAGACCCCTCAAGATAAATACTCATCTT 204
|||:||||| :||| :||| :|||
Db 69 AspValIleLysAsnGluSerSerLeuLeuLeuArgAsnLeuIleAsnGluGluThrLeu 88
|||:||||| :||| :||| :|||
205 ACAGAAAGAGGTAAGAAATCCTCATCAGTCGAAATCCTCAAAATTCATCA----- 255
|||:||||| :||| :||| :|||
Db 89 SerGluLysAsnAspLysValValAsnAspIleLysAsnMetAsnAsnSerThrGluLys 108
|||:||||| :||| :||| :|||
256 ---ATTGATACTGCCCAACACCTCTCACACAACAATAAATAGAGAAGATCTGTTCAA 312
|||:||||| :||| :||| :|||
Db 109 LysIleAsnSerIleSerLysGlyAsnAsnAsnIleHisAsnIleAsnGluAsnGlnAsn 128
|||:||||| :||| :||| :|||
313 ACAAGTGAATAGTAGAAGATTCACAGTATCAGATTTTGTCTAACTTAA-----ATA 366
|||:||||| :||| :||| :|||
Db 129 AlaAsnValGluLeuLysThrAspAsnIleLeuAspAsnThrSerGluGlnAspAspIle 148
|||:||||| :||| :||| :|||
367 AAAGAGACTAACACTGAATCTGTTAA-----GAAGAAATACTATA 408
|||:||||| :||| :||| :|||
Db 149 AsnGluLysAsnAsnAspAsnGlyAspMetValHisLysAsnIleTyrAsnAsnIleLeu 168
|||:||||| :||| :||| :|||
409 GAGCAACCTAATAAGTAAAGAAAGATTCACAACAACAGTCAGCCGCTCGGTCTATACAAAT 468
|||:||||| :||| :||| :|||
Db 169 SerAspProTyrAspIleAsnSerThrAsnAlaTyrIleAsnLysSerAspIleThrAsn 188
|||:||||| :||| :||| :|||
469 ATAGATGAAAATTTCAAAATCAAGATGAGTTTAAATTTTCAAAATTAATGAA---TAT 525
|||:||||| :||| :||| :|||
Db 189 LeuAsn-----TyrSerSerAsnAspValIleAsnAsnAspLysValAsnLysSerTyr 206
|||:||||| :||| :||| :|||
526 GAAATAGGCTAGACCATTTATCTACAACATCTGCCCAACCATCGATTAACGTTGTAACC 585
|||:||||| :||| :||| :|||
Db 207 GluGluLys-----AsnIleValAsnAsnThrGlu 216
|||:||||| :||| :||| :|||
586 GTAATCAATTA---GCGCGGAACAGGTTTGAATGTTTGAACCATTTAATTAAGTTACT 642
|||:||||| :||| :||| :|||
Db 217 LeuAsnLysLeuIleGluSerAspAspHisSerAsnLysAsnAspIleAsnLysLysThr 236
|||:||||| :||| :||| :|||
643 GATCAA-----AGTATTACTGAAGGATATGATAGTAGAGGTTGTTATT 687
|||:||||| :||| :||| :|||
Db 237 GluLysAsnLysThrPheAsnSerSerSerThrSerAspGluLysLysGlnThrAspIle 256
|||:||||| :||| :||| :|||
688 AAAGCACATGATGCTGAAACTTTAATCTATGATGTAACCTTT-----GAAGTAGAT 738
|||:||||| :||| :||| :|||
Db 257 LysGlyGlnAsnLysAsnAspLeuAsnAsnGluHisIlePheAsnAsnAsnAspIleAsn 276
|||:||||| :||| :||| :|||
739 GATAAGGTGAATCTGGTGATACGATGACA---GTGGATATAGATAGAAATACAGTTCCA 795
|||:||||| :||| :||| :|||
Db 277 AsnAsnValGlnTyrLysAsnLysValAsnIleIleSerValAspLysAsnAsnThrAsp 296
|||:||||| :||| :||| :|||
796 TCAGATTAAACCGATAGCTTTTACAATACCAAAAAATAAAGATAATTTCTGGA----- 846
|||:||||| :||| :||| :|||
Db 297 ArgAspAsnAsnAsnLeuTyr-----GluThrAsnAsnGlyAspLeuLys 311
|||:||||| :||| :||| :|||
847 -----GAAATCATCGCTACAGGTACTTATGATACAAAATAAACAATACACCTAT 897
|||:||||| :||| :||| :|||
Db 312 TyrAsnAsnAspLeuIleLysGluGlyGluAsnLysArgAsnAsnLysLeuAsnAsnTyr 331
|||:||||| :||| :||| :|||
898 ACTTTTACAGATTATGATAGTAACTATGAAATATTAAGCACACCTTTAAATTAACCTCA 957
|||:||||| :||| :||| :|||
Db 332 LysPheAsn-----MetAsnLysValAsnAspAsnLysAsnPheAsnLysTyrThrGlu 349
|||:||||| :||| :||| :|||
958 TACATTGATAAATCAAAAGTTTCCA-----AATAATAAT----- 990
|||:||||| :||| :||| :|||
Db 350 IleTyrAsnLysGluSerGluProGluLysGlnAsnAsnSerAsnAsnAsnLeuGlyIle 369
|||:||||| :||| :||| :|||
991 -----ACCAAGTTAGATGATAGATATAA-----ACGGCCCTTTCTATCAGTAAT 1035
|||:||||| :||| :||| :|||
```

```
Db 370 ProThrLeuIleLysLysGluValHisIleLysAsnHisAsnThrPheSerSerAsnGly 389
1036 AAAACAAT-----ACGGTTGAATATCAAGACCTAACGAA 1071
|||:||||| :||| :||| :|||
Db 390 LysIleLeuGluAsnLysAspIleAspLysMetSerAspThrSerLysLysAsnAspArg 409
|||:||||| :||| :||| :|||
1072 AATCGGACTGTAACCTTCAAAAGTATGTTTACAAATATATAGATACGAAATATCAT---ACA 1128
|||:||||| :||| :||| :|||
Db 410 AsnPheArgSerAsnAspIleLysAsnPheLysAsnAsnAspThrLysAsnAsnAlaThr 429
|||:||||| :||| :||| :|||
1129 GTTGAAGCAACGATTTATATTAACCTCTTGGTTATTCAGCCAGGAACAATGTAAAT 1188
|||:||||| :||| :||| :|||
Db 430 LeuSerGluAsp-----AsnLysAsnArgTyr-----AsnIleThr 441
|||:||||| :||| :||| :|||
1189 ATTTTCAGGGAATGTTGATGAAGGTTTCAACAATTATAGACGATAGCACAAATTAAGTT 1248
|||:||||| :||| :||| :|||
Db 442 ThrAsnLysAsnAsnGluLys-----LysGlu 450
|||:||||| :||| :||| :|||
1249 TATAAGGTTGAGATAATCAAAATTTTACCAGATAGTAACAGAAATTTATGATTTACAGTAA 1308
|||:||||| :||| :||| :|||
Db 451 Tyr-----AsnMetLysLysSerAsnGluAsnGluTyrAlaPheAsnThrGlu 466
|||:||||| :||| :||| :|||
1309 TATGAAGATGTCACAAATGAT-----GATTATGCCCAATTAGA 1347
|||:||||| :||| :||| :|||
Db 467 LysThrAsnValAsnAsnAspAlaLeuLysGluGluArgAsnAsnTyrLysTyrLeuAsn 486
|||:||||| :||| :||| :|||
1348 AATAATAATGATGTAATATTAATTTTGGTAAATATAGATTCACCATATATTTAAAGTT 1407
|||:||||| :||| :||| :|||
Db 487 AsnGlnThrAspValAsnIleAsn-----AsnLeuGlnGlu-----ArgAsp 500
|||:||||| :||| :||| :|||
1408 ATTAGTAATATGACCCCTAATAAGGATGATTACACGATATACAGCAAACTGTGACAATG 1467
|||:||||| :||| :||| :|||
Db 501 IleAsnLeuTyrAsnLysAsnGluSerAsp---LysLysLeuGluGlnSerPheArgGlu 519
|||:||||| :||| :||| :|||
1468 CAGACGACTAATAGTATATCTGCTGAGTTTGAACAGCATCTCTATGATAAATCAAT 1527
|||:||||| :||| :||| :|||
Db 520 GluAspIleLysAsnAlaTyrLeuProGlu-----AsnLysAsnPheGlnLysThrLeu 537
|||:||||| :||| :||| :|||
1528 GCTTCTCTCAAGCTTCAGGTCAAGGACAGGTCACCTGCTCCTCGAAATATATAA 1587
|||:||||| :||| :||| :|||
Db 538 -----ThrAsnAsnGluLysAsnGluAsnLysIleProHisIle----- 551
|||:||||| :||| :||| :|||
1588 ATCGAGATTACGTTATGGGAAGATGTAGATAAAGATGGTATTCAAAAT----- 1635
|||:||||| :||| :||| :|||
Db 552 -----AspProSerAsnAsnGluLeuAspLysLysGlyAsnTyrAsnLysTyrGluIle 569
|||:||||| :||| :||| :|||
1636 -----ACAATGATATGAAAAACCGCTTAGTAAATGTTGGTAACTTTGACGAT 1686
|||:||||| :||| :||| :|||
Db 570 GlyLysIleLysLysAsnAsnGluGluAsnLysGlnAsnValThrValGlu----- 586
|||:||||| :||| :||| :|||
1687 CCTGATGGAATTCAAAATCAGTCAGACACAGATCAAGATGGGAATATCAATTT 1740
|||:||||| :||| :||| :|||
Db 587 GluAsnIleAsnProGluLysIleArgLysAspHisGluGlnAsnIleGlnTyr 604
|||:||||| :||| :||| :|||
RESULT 14
US-11-330-403-3535
; Sequence 3535, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 3535
; LENGTH: 1086
; TYPE: prt
; ORGANISM: Candida albicans SC5314
US-11-330-403-3535
Alignment Scores: 7.82e-05 Length: 1086
Pred. No.:
```

```
Score: 211.50 Matches: 125
Percent Similarity: 34.5% Conservative: 80
Best Local Similarity: 21.0% Mismatches: 253
Query Match: 7.0% Indels: 137
DB: 7 Gaps: 20

US-10-806-288-12 (1-1746) x US-11-330-403-3535 (1-1086)

Qy 10 GAAGAAAAGATGATGATCAATAAATCAAGTCAATAAACACCGAGCAATAAACCAA 69
Dy 344 AspGluSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 363
Qy 70 ATATTAAAAAAGAAAGAACCAATACCTACGATGGCATAGAAAACGCTCAGAGATAGA 129
Dy 364 SerValSerAlaSerGluThrSerSerSerSerSerSerSerSerSerSerSerSer 383
Qy 130 ACAGAGTCAACAAATAGATGAAACCAAGCAACATTTTACAAAAGACCCCTCAA 189
Dy 384 GluValSerSerThrGluProSerSer-----SerThrProGlu 397
Qy 190 GATAATCTACTCTTACAGAAAGAGAGTAAAGAAATCCTCATCAGTCGAATCCTCAAT 249
Dy 398 ProSerSerSerSerGluThrSerSerSerThrGlnGluSerSerSerThrGluGlyProSer 417
Qy 250 TCATCAATTGATCTGCCCAACAA-----CCATCTCAC 282
Dy 418 SerSerThrSerSerSerSerThrGluAlaSerSerSerSerSerSerSerSerSerSer 437
Qy 283 ACAACAAATAAGAGAGAAATCTGTTCAACAAAGTGAATATGTAAGAGATTCACAGTA 342
Dy 438 SerThr-----GluAlaSerSerSerSerSerSerSerSerSerSerSerSerSerSer 454
Qy 343 TCAGATTTCCTAACTCTAAATAAAGAGAGTAAAC----- 378
Dy 455 SerThrGluGlyProSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 474
Qy 379 -----ACTGAATCTGTAAGAGAGAACTATAGCAACCTCAATAAAGTAAAGAA 432
Dy 475 GluProSerSerSerSerThrGlySerSerSerSerSerSerSerSerSerSerSerSer 494
Qy 433 GATTCAACAAAGTACGCGCTGCGGTATACAAATATAGATGAAATAATTT----- 483
Dy 495 SerSerSerThrGluGlyProSerSerSerSerSerSerSerSerSerSerSerSerAla 514
Qy 484 TCAATCAAGATGATGATTAAATTTACCAATAAATGAATGAATAAGGCTAGACCA 543
Dy 515 SerSerThrSerGluGlnSerSerSerSerSerSerSerSerSerSerSerSerSerSer 534
Qy 544 TTATCTCAACATCTGCCCAACCACTGATTAAACGTTAAACCGTAAATCAATTAGCGCG 603
Dy 535 IleAspSerThrGluSerAspThrSer----- 543
Qy 604 GAACAAGGTTTGAATGTTAAACCATTTAATTAAGTTTACTGATCAAAAGTATTACTGAAGGA 663
Dy 544 -----SerAlaThrAspSerSer----- 549
Qy 664 TATGATGATAGTGAAGGTGTTATTAAGAGCATGATCTGAAACCTTAATCTATGATGA 723
Dy 550 -----ThrAlaThrAspSerSerSerSerSerSerSerSerSerSerSerSer 561
Qy 724 ACTTTTGAAGTAGATGATAAGTGAATCTGGTATACGATGACAGTGGATATAGATAAG 783
Dy 562 AsnSerGluSerThrAspSerSerThrAlaThrAspThrSerSerSer-----AspSer 579
Qy 784 AATAACAGTTCCATCA-----GATTAAACCGATAGCTTTTACAAATACCAAA 828
Dy 580 AsnThrAlaSerSerThrGluThrAsnThrAspValThrAspSerSerThr----- 596
Qy 829 ATAAAGATATTTCTGAGAAATCATCGCTACAGGTACTTATGATACAAAATAAACAA 888
Dy 597 ---AspSerAsnThrGlyAla-----ThrGluSerSerThr 607
Qy 889 ATCACCTATATCTTTTACGATTTATGTAGATAAGTATGAAATAATTAAGCACACCTTAAA 948
```

---

```
608 AlaThrAspThrAsnThrAspAlaThrAsp----- 617
949 TTAACGCTATACATTTGATAAATCAAGGTTTCAAAATTAATAATACCAAGTTAGATGTAGAA 1008
618 ---SerSerThrValSerGluThrGlyAlaThrAspSerSerSerThrAlaThrAspThrAsn 636
1009 TATAAAACGCGCTTTTCATCAGTAATAAACAATTAACGTTGATTAATCAAGACCTAAC 1068
637 ThrGlyAlaThrGluSerSerThrAspSerAsnThrGlyAla-----Thr 651
1069 GAAAATCGGAGTCTCT-----AACCTTCAAAAGTATGTTTACAAATATATAGATACGAAA 1119
652 GluSerSerThrAlaThrAspThrAsnThrSerAlaThrAsnThrAspThrAsnThrGly 671
1120 AATCATACAGTTGAGCAACAGATTTATATTAACCTCTTCGTTATTTCAGCAAGAAACA 1179
672 SerAsnThrAlaThrAsnThrAspAspAsnThrAlaThrAspThrSerSerThrGluThr 691
1180 AATGTAATATTTTCAGGAATGCTGATGAGGTTCAACA---ATTATAGACGATAGCACA 1236
692 AsnThrAlaThrAsnThrAspGlyThrGluThrAsnThrGlyAlaThrGluThrAsnThr 711
1237 ATAAATTAAGTTTATTAAGGTTGAGATTAATCAAAATTTTACCAGATAGTAAACAGAAATTTAT 1296
712 AspThrSerAlaSerAsnThrAspAspAsnThrGly-----SerAsnThrAlaThr 728
1297 GATTACAGTGAATATGAAGATGTCACAAATGATGATATGCCCAATTAGGAAATAATAAT 1356
729 AsnThrGlyGlyThrAsp-----ThrAsnThrAspThrAsnThrGlyGlyThrAspThr 746
1357 GATGTGAATATTAATTTTGGTAATATAGATTCCACCATATATATTATAAGTTATTAGTAAA 1416
747 AsnThrGlyThrAsnThrGlyThrAspThr----- 757
1417 TATGACCTTAATAAGGATGATTACACGACTATACAGCAAACTGTGACAAATGCAGACGACT 1476
758 -----Ly8ThrGlyThrAsnThrAlaThr 765
1477 ATAAATGATGATATCTGGTGAAGTTTGAACAGCATCTCTATGATTAATACAAATGCTTCTCT 1536
766 GlyAsnAsn---ThrGlyAlaThrGluThrAsnThrAlaThrAsnThrAsnGly 784
1537 ACAAGTTTCAGGTCAAGCAAGGCTGACTTCCTCTCGAAATACTTATAAATCGGAGAT 1596
785 ThrAsnThrAsnThrGlyAlaThrAspThrAlaThrAsnThrAlaThrGlyThrAsn--- 803
1597 TACGTATGGAAGATGATAGATAAAGATGGTATTTCAAAATACAAATGATAATGAAAACCG 1656
804 -----ThrAsnThrGlyAlaThrAspThrAsnThrAsnThrAsnThr 817
1657 CTTAGTAATGATTTGTTAACTTTGACGTATCTCTGATGGAACTTCA 1701
818 GlyAlaThrValThrAsnThrAlaThrAsnThrAspAsnValSer 832

RESULT 15
US-10-471-571A-4824
; Sequence 4824, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: Seqwin99, version 1.03
; SEQ ID NO 4824
; LENGTH: 774
; TYPE: PRP
; ORGANISM: Staphylococcus aureus
```



```

; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(774)
; OTHER INFORMATION: serine protease Htra
US-10-471-571A-4824

```

**Alignment Scores:**

Pred. No.:	0.000184	Length:	774
Score:	205.00	Matches:	119
Percent Similarity:	37.8%	Conservative:	121
Best Local Similarity:	18.7%	Mismatches:	209
Query Match:	6.8%	Indels:	186
DB:	6	Gaps:	26

US-10-806-288-12 (1-1746) X US-10-471-571A-4824 (1-774)

QY	7	GATGAAGAAAGAAATGATGTGATCAATTAATCAGTCACAATAAACACCGCAGATAATAAC	66
DB	29	AsnGluAspGluAsnLeuAsnGlnHisGlnAspLysGlnAsnIleAspAsnThr	48
QY	67	CAAAATAATTAAGAAAGAAACGAAATAACTACGATGCGATAGAAAACGC	117
DB	49	ThrSerLysLysAlaAspLysGlnIleHisLysAspSerIleAspLysHisGluArgPhe	68
QY	118	-----TCAGAAGATAGAACACAGCATCAACAATAATGTAGATGAAAAACGAACGA	165
DB	69	LysAsnSerLeuSerSerHisLeuGluGlnArgAsnArgAspValAsnGluAsnLysAla	88
QY	166	ACATTTTACAAAAGACCCCTCAAGATAATACT-----CATCTT	204
DB	89	Glu--GluSerLysSerAsnGlnAspSerLysSerAlaTyAsnArgAspHisTyLeu	107
QY	205	ACAGAAGAGAGGTAAAGAACTTCATCAGTCGAATCCTCAAAATTCATCAATTCGATACT	264
DB	108	ThrAspAspValSerLysLysGlnAsnSerLeuAspSerValAspGlnAspThrGluLys	127
QY	265	GCC-----CAACAACCATCTCACACACAATAATAGAGAGAAGATCTGTTCAACA	315
DB	128	SerLysTyTyGluGlnAsnSerGluAlaThrLeu-----SerThrLysSer	143
QY	316	AGTGATAATGTAGAAGATTCACACGTATCAGATTTTCTGAATCTCTAAAAATAAAGAGAGCT	375
DB	144	ThrAspLysValGluSerThrGluMetArgLysLeuSerSerAspLysAsnLysValGly	163
QY	376	AAACCTGAA-----	384
DB	164	HisGluGluGlnHisValLeuSerLysProSerGluHisAspLysGluThrArgIleAsp	183
QY	385	-----TCGTGTAAGAGAGAGATACTATAGCGAACCTAATAAGTAAAGAGAAGAT	435
DB	184	SerGluSerSerArgThrAspSerAspSerMetGlnThrGluLysIleLysLysAsp	203
QY	436	TCAACAACAAGTCAGCCGCTCTGCG-----TATACAAAT	468
DB	204	SerSerAspGlyAsnLysSerSerAsnLeuLysSerGluValIleSerAspLysSerAsn	223
QY	469	ATAGATGAAAAATTTCAATCAAGATCAGATTATAATTTCAACATAAATGAATATGAA	528
DB	224	ThrValProLysLeuSerGluSerAspGluVal-----	235
QY	529	AATAAGGCTAGACCATTTACTACAACATCTGCCAACCATCGATTAACGTGAACCGTA	588
DB	236	AsnAsnGlnLysProLeuThrLeuProGluGluGln-----	247
QY	589	ATCAATTAAGCGCGGAACAAGGTTTCGAATGTTTAACCATTTAATAAGTTACTGATCAA	648
DB	248	---LysLeuLysArgGlnGlnSerGlnAsn-----GluGln	258
QY	649	AGPATTTACTGAAGGATATCATGATAGTCAAGGTGTTTATAAGCCACATGATGCTGGAAC	708
DB	259	ThrLysTyThrTyThrTyGlyAspSerGluGlnAsnAspLysSerAsnHisGluAsnAsp	278
QY	709	TTAATCTATGATGAACCTTTTGAAGTACATGAAG-----	744

Search completed: August 12, 2006, 08:57:03

Job time : 93 secs

-----

Result No.	Score	Query Match	Length	DB	ID	Description
1	3013	99.6	1092	2	T30214	fibrinogen-binding
2	1144.5	37.8	1166	2	T28680	fibrinogen-binding
3	1137.5	37.6	1141	2	E89824	hypothetical prote
4	576	19.0	1315	2	T28679	fibrinogen-binding
5	559	18.5	1385	2	E89824	hypothetical prote
6	489	16.2	953	3	S41539	hypothetical prote
7	452	14.9	933	2	S41539	fibrinogen-binding
8	452	14.9	989	2	E89852	fibrinogen-binding
9	397.5	13.1	877	2	F90070	Clumping factor B
10	376	12.4	940	2	S15702	fibrinectin-bindin
11	344.5	11.4	961	2	G90053	hypothetical prote
12	326	10.8	1038	2	H90053	hypothetical prote
13	300.5	9.9	1018	2	A32192	fibrinectin-bindin
14	239	7.9	1039	2	T30856	protein F2 - Strep

QY 181 ACCCTCAAGATAATACTCATCTTACAGAAGAAGAGTAAAGAAATCCTCATCGTCGAA 240  
Db |||||  
135 ThrProGlnAspAsnThrHisLeuThrGluGluValLysGluSerSerValGlu 154  
QY 241 TCCTCAAAATTCATCAATGATACTGCCCAACAACCATCTCACACAATAAATAGAGAA 300  
Db |||||  
155 SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrThrIleAsnArgGlu 174  
QY 301 GAATCTGTTCAACAAGTGATTAATGTAGAAGATTCACACGGTATCAGATTTGCTAACTCT 360  
Db |||||  
175 GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer 194  
QY 361 AAAATAAAGAGAGTAAACACTGTAACCTGTAAGAAGAGAGATCTATATAGAGCAACTAAT 420  
Db |||||  
195 LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn 214  
QY 421 AAAGTAAAGAAGATTCAACAACAGTCAGCCGCTCTGGCTATACAAAATATAGATGAAAAA 480  
Db |||||  
215 LysValLysGluAspSerThrThrSerGlnProSerGlyTyrThrAsnIleAspGluLys 234  
QY 481 ATTTCAAAATCAAGATGAGTTAATTAATTTACCAATAATGAATATGAAAAATAAGGCTAGA 540  
Db |||||  
235 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysAlaArg 254  
QY 541 CCATTATCTACAACATCTGCCCAACCATCGATTAAACGTGTAAACCGTAAATCAATTAGCG 600  
Db |||||  
255 ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla 274  
QY 601 CGGGAACAAGGTTTCAAGATTTAAACCAATTTAAAGTTACTGTATCAAAAGTATTACTGAA 660  
Db |||||  
275 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 294  
QY 661 GAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Db |||||  
295 GlyTyrAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 314  
QY 721 GTAACTTTTGAAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
Db |||||  
315 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAspIleAsp 334  
QY 781 AAGAATACAGATTCCATCAGATTAAACCGATAGCTTTTACAATAACCAAAATAAAGATAAT 840  
Db |||||  
335 LysAsnThrValProSerAspLeuThrAspSerPheThrIleProLysIleLysAspAsn 354  
QY 841 TCTGAGAAATCATCGCTACAGGTACTTATGATAACAAAATAAACAATCACTATACT 900  
Db |||||  
355 SerGlyGluIleAlaThrGlyThrTyrAspAsnLysAsnLysGlnIleThrTyrThr 374  
QY 901 TTTACAGATTATGTAGATAAGTATGAAATATTTAAAGCACACCTTTAAATTTAACGTCATAC 960  
Db |||||  
375 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 394  
QY 961 ATTTGATAAATCAAAGGTTCCAAATAATAATACCAAGTTAGATGTAGAATATAAAACGCC 1020  
Db |||||  
395 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 414  
QY 1021 CTTTCATCGTAAATAAACAATTAACGGTTGATATCAAGACCTTAACGAAATCGGACT 1080  
Db |||||  
415 LeuSerSerValAsnLysThrIleThrValGluTyrGlnArgProAsnGluAsnArgThr 434  
QY 1081 GCTAACCTTCAAAGTATGTTTACAATAATAGATACGAAAAATCATACAGTTTCAGCAACG 1140  
Db |||||  
435 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 454  
QY 1141 ATTTATATTAAACCTCTTCGTTTATTCAGCCAAGGAAACAATATGTAATTTTCAGGGAAT 1200  
Db |||||  
455 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 474  
QY 1201 GGTGATGAAGGTTCAACAATATAGACGATAGCACAAATAATTAAGTTTATAGGTTGGA 1260  
Db |||||  
475 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 494  
QY 1261 GATAATCAAAATTTTACCAGATAGTAACAGAAATTTTATGATTACAGTGAATATGAAATGTC 1320

Db |||||  
495 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 514  
QY 1321 ACAATGATGATTATGCCAATTAGGAAATAATTAATGATGTGAATATTAATTTTGGTAAT 1380  
Db |||||  
515 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 534  
QY 1381 ATAGATTCCACATATATTAATTAAGTTATTAGTAAATATGACCCCTTAATAAGGATGATTAC 1440  
Db |||||  
535 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 554  
QY 1441 ACGACTATACAGCAAACTGTGACCAATCGACACGACTATAAAATGATATACCTGGTGAGTTT 1500  
Db |||||  
555 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 574  
QY 1501 AGAACAGATCCTATGATATAACAATTCGTTCTCTACAACTTCAGTTCAGGCACAGCAAGGT 1560  
Db |||||  
575 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 594  
QY 1561 GACTTGCTCTCGAAAAAATCTTATAAATCGAGATTACGTATCGGAAGATGTAGATAAA 1620  
Db |||||  
595 AspLeuProProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys 614  
QY 1621 GATGTTATTCAAAAATACAAATGATAATCAAAAAACCGCTTACTAGTATGTTTGGTAACTTTG 1680  
Db |||||  
615 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 634  
QY 1681 ACGTATCTGATGAACTTCAAAATCAGTCAGACAGATGAAGATGGGAAATATCAATTT 1740  
Db |||||  
635 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluAspGlyLysTyrGlnPhe 654  
QY 1741 GATCGA 1746  
Db |||||  
655 AspGly 656

RESULT 2  
T28680  
fibrinogen-binding protein homolog - Staphylococcus aureus  
C:Species: Staphylococcus aureus  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T28680  
R:Josefsson, E.; Mccrea, K.; Ni Eidhin, D.; O'Connell, D.; Cox, J.; Hook, M.; Foster, T.  
Microbiology 144, 3387-3395, 1998  
A:Title: Three new members of the serine-aspartate repeat protein multigene family of St  
A:Reference number: 220510; MUID:95098700; PMID:9884231  
A:Accession: T28680  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1166 <JOS>  
A:Cross-references: UNIPROT:O86489; UNIPARC:UPI00000B74A6; EMBL:AJ005647; NID:e1318793;  
C:Genetics:  
A:Gene: sdze

Alignment Scores:  
Pred. No.: 4,31e-51 Length: 1166  
Score: 1144.50 Matches: 263  
Percent Similarity: 60.1% Conservative: 108  
Best Local Similarity: 42.8% Mismatches: 191  
Query Match: 37.8% Indels: 55  
DB: 2 Gaps: 18

US-10-806-288-12 (1-1746) x T28680 (1-1166)

QY 1 TCTAGTGTGAAGAAAGAAGATGATGTGATCAATTAATCACTCAATTAACACACCGACGAT 60  
Db |||||  
66 AlaThrThrSerAspAsnLysGluValValSerGluThrGluAsnAsnSerThrThrGlu 85  
QY 61 AATAACCAATA-----ATTAAAAAGAAAGAAACGAATACTACGATGGCATAGAAAAA 114  
Db |||||  
86 AsnAsnSerThrAsnProIleLysLysGlu-----ThrAsnThrAspSerGlnProGlu 103  
QY 115 CGCTCAGAGATGAACAGAGTCAACAAATGTAGATGAACAAACGAAGACGACATTTT 174

Qy	1189	ATTTCAGGGAATGGT-----GATGAAGGTTTCAACAATT	1221
Db	468	IleAlaGlySerGlnValAspAspTyrGlyAsnIleLysLeuGlyAsnGlySerThrIle	487
Qy	1222	ATAGACGATAGCACAAATAATAAGTTTATAAGGTTTCGAGATAATCAAAATTTACACAGAT	1261
Db	488	IleAspGlnAsnThrGluIleLysValTyrLysValAsnSerAspGlnLeuProGln	507
Qy	1282	AGTAACAGAAATTATGATTACAGTGAATATGAGAGATGTCACAAATGAT--GATTATGCC	1338
Db	508	SerAsnArgIleTyrAspPheSerGlnTyrGluAspValThrSerGlnPheAspAsnLys	527
Qy	1339	CAATTAGGAATAATAATGATGTGAATATTAATTTGGTAAATATAGATTACCAATATATT	1398
Db	528	LysSerPheSerAsnAsnValAlaThrLeuAspPheGlyAspIleAsnSerAlaTyrIle	547
Qy	1399	ATTAAAGCTTATTAGTAAATATGACCCCTAATAAGATGATTACACGACTATACAGCAACT	1458
Db	548	IleLysValValSerLysTyrThrProThrSerAspGlyGluLeuAspIleAlaGlnGly	567
Qy	1459	GTGCACATGACAGACGACTATAAAATAGTATACTCGTGAGTTTATGAAACAGACTCCTATGAT	1518
Db	568	ThrSerMetArgThrThr---AspLysTyr---GlyTyrTyrAsnTyrAlaGlyTyrSer	585
Qy	1519	AATACAAATTCGTTTCTCTCAAGTTCAGGTCACAGGCAAGGTGACTTGG---CCTCCTGAA	1575
Db	586	AsnPheIleValThrSerAsnAspThrGlyGlyLysAspGlyThrValLysProGluGlu	605
Qy	1576	AAAACTTATAAAATCCGAGATTACGATTCGGAGATGCTAGATAAAGATGCTATTCAAAT	1635
Db	606	LysLeuTyrLysIleGlyAspTyrValTrpGluAspValAspLysAspGlyValGlnGly	625
Qy	1636	ACAAATGATAATGAAAAACCGCTTAGTAAATGTATTGGTAACTTTGACGTATCCTGATGGA	1695
Db	626	ThrAspSerLysGluLysProMetAlaAsnValLeuValThrLeuThrTyrProAspGly	645
Qy	1696	ACTTCAAAATCAGTCAGAACAGATGAAGATGGGAAAATATCAATTTGATGGA	1746
Db	646	ThrThyLysSerValArgThrAspAlaAsnGlyVhiStyGlnPheGlyGlyVal	662

RESULT 3  
E89824

R.; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekim, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.

A;Accession: E89824

A;Molecule type: DNA

**A;Cross-references: UNIP**

**C;Genetics:**

Pred. No.:

Percent Similarity: 59.0%

Query Match: 37.6%

118-10-906-388-13 (1-1746) x F888

ON 1 TCTAGTGTGATGAAAGAAAAC



Query Match: 19.0% Indels: 92  
DB: 2 Gaps: 29  
US-10-806-288-12 (1-1746) x T28679 (1-1315)

QY 1 TCTAGTGATGAAGAAAGATGATG-----ATCAATAATAATCAGTCAATAAAC 51  
DB 55 SerThrAsnLysGluLeuAsnGluAlaThrSerAlaSerAspAsnGlnSerSerAsp 74  
QY 52 ACCGACGATATAACCAATAATATAAAGAAAGAAACGAATAACTACGATGCATAGAA 111  
DB 75 LysValAspMetGlnGlnLeuAsnGlnLysAsnThrLysAsnAspAsnGlnLysGlu 94  
QY 112 AACGCTCAGAAATAGAACAGAGTCAACAAATAGTAGTAA---AACGAAGCAACA 168  
DB 95 MetValSerSerGlnGlnAsnGluThrThrSerAsnGlyAsnLysLeuLysGlu 114  
QY 169 TTTTTCACAAAGACCCTCAAGATAATCTCATCTTACAGAAAGAGGTAAAGATCC 228  
DB 115 SerValGlnSerThrGlyAsnLysValGluValSerThrAlaLysSerAspGluGln 134  
QY 229 TCATCAGTGCATCTCAATTCATCAATTCATCAATTCATCAATTCATCAATTCATCA 288  
DB 135 AlaSerProLysSerThrAsnGluAspLeuAsnThrLysGln-----Thr 149  
QY 289 ATAATAGAGAAATCTGTTCAACAAAGTGAATAATGTAGAAGATTCACACGTCATGAT 348  
DB 150 IleSerAsnGlnGluAlaLeuGln---ProAspLeuGlnGluAsnLysSerValValAsn 168  
QY 349 TTGCTTAACCTTAATAAAGAGAGTAACTGATCTGTTAAAGAGAGATATCTATA 408  
DB 169 -----ValGlnProThrAsnGlnGluAsnLysValAsp-----180  
QY 409 GAGCAACCTTAATAAAGAAAGATTCACAAACAAAGTCAGCGCTGCTGCATACAAAT 468  
DB 181 -----AlaLysThrGluSerThr-----LeuAsn 189  
QY 469 ATA---GATGAAATAATTCAAATCAAGATGATGATTA-----AATTTCACATTAAT 519  
DB 190 ValLysSerAspAlaLysSerAsnAspGluThrLeuValAspAsnAsnSerAsnSer 209  
QY 520 GAATATGAATAAAGCTAGACCATTCATCTACACATCTGCCCAACA-----567  
DB 210 AsnAsnGluAsnAlaAspLysLeuProLysSerThrAlaProLysArgLeuAsn 229  
QY 568 TCGATTAAACGCTGTAACCTTAATCAATGAGCGCGGCAACAGGTTCCGATGTAAACCAT 627  
DB 230 ThrArgMetArgLysAlaValGlnProSerSerThrGluAlaLysAsnValAsnAsp 249  
QY 628 TTAATTAAAGTTACTGATCAAGATATTACTGAAGGATATGATGATGATGATGATGAT 687  
DB 250 LeuLysThrSerAsnThrThrLeuThrValValAspAlaAspLysAsnAsnLysLysVal 269  
QY 688 AAAGCACATGATGCTCAAACTTAATCTATGATGATGATGATGATGATGATGATGATG 747  
DB 270 ProAlaGlnAspPyrLeuSerLeuLysSerGlnLysThr-----ValAspAspLysVal 287  
QY 748 AAATCTGGTGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 792  
DB 288 LysSerGlyAspPyrPheThrLysLysTyr---SerAspThrValGlnValThrGlyLeu 306  
QY 793 ---CCATCAGATTAAACCGATAGCTTTTACAATACCAAAATAAAGAT---AATTTCGA 846  
DB 307 AsnProGluAspLysLysAsn-----IleGlyAspLysLysAspProAsnAsnGly 323  
QY 847 GAAATCATGCTACAGGTACTTATGATTAACAAATAAATAAATAAATAAATAAATAAATA 906  
DB 324 GluThrIleAlaThrAlaLysHisAspThrAlaAsnAsnLeuLysThrPheThr 343  
QY 907 GATTATGTAGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 966  
DB 344 AspTyrValAspArgPheAsnSerValGlnMetGlyLysAsnTyrSerIleThrMetAsp 363

QY 967 AAATCAAGAGTTCCTCAAAATAATAATACCAAGTGTAGATGATGATGATGATGATGAT 1026  
DB 364 AlaAspThrIlePro-----ValSerLysAsnAspValGluPheAsnValThrIleGly 381  
QY 1027 TCAGTAAATAAACAATACGGTTGAATATCAAGACCTAAC-----GAAATATCGACT 1080  
DB 382 AsnThrThrThrLysThrThrAlaAsnIleGlnTyrProAspPyrValValAsnGluLys 401  
QY 1081 GCTAACCTTCAAAAGTATGTTTACAAATATATACCAATATACCAATATATACCAAT 1128  
DB 402 AsnSerIleGlySerAlaPheThr-----GluThrValSerHisValGlyAsnLysGlu 419  
QY 1129 -----GTTGAGCAACAGATTTATATTAACCTCTTCGTTGTTTATTCAGCAAGGAA 1176  
DB 420 AsnProGlyTyrTyrLysGlnThrIleTyrValAsnProSerGluAsnSerLeuThrAsn 439  
QY 1177 ACAATGTAAATATT-----TCAGGGAATGGTGATGAAGGTTCAACAATTTATA 1224  
DB 440 AlaLysLeuLysValGlnAlaTyrHisSerSerTyrProAsnAsnIleGlyGlnIleAsn 459  
QY 1225 GACGATAGCACCAATAATTAAGTTTATAGGTTGGAGATAATCAAAATTTTACCAGATAGT 1284  
DB 460 LysAspValThrAspLysLysIleTyrGlnValProLysGlyTyrThrLeu-----476  
QY 1285 AACAGATTTATGATACAGT-----GAATATGAAGATGTCAAAATGATGATGATGCC 1338  
DB 477 AsnLysGlyTyrAspValAsnThrLysGluLeuThrAspValThrAsn---GlnTyrLeu 495  
QY 1339 CAA-----TTAGGAATAATGATGATGATGATGATGATGATGATGATGATGATGAT 1389  
DB 496 GlnLysIleThrTyrGlyAspAsnAsnSerAlaValIleAspPheGlyAsnAlaAspSer 515  
QY 1390 CCATATATTAAAGATTATTAGTAAATATGACCCCTTAATAAGGATGATTCACAGCATATA 1449  
DB 516 AlaTyrValValMetValAsnThrLysPheGlnTyrThrAsnSerGluSerProThrLeu 535  
QY 1450 CAGCAAACTGTGCAATCAGACGACGATATAATAGTACTACTGTTGAGTTTGAACAGCA 1509  
DB 536 ValGlnMetAlaThrLeuSerSerThrGlyAsn-----LysSerVal 549  
QY 1510 TCCTATGATAATCAATTCCTTCTCAAGTTCAGGTCAGGTCAGGTCAGGTCAGGTCCT 1569  
DB 550 SerThrGlyAsnAlaLeuGlyPheThrAsnAsnGlnSerGlyGlyAlaGly-----566  
QY 1570 CCTGAAAAAATTTAAATTCGAGATTCAGTATGGAAGATGATGATGATGATGATGATG 1629  
DB 567 ---GlnGluValTyrLysIleGlyAsnTyrValTyrGluAspThrAsnLysAsnGlyVal 585  
QY 1630 CAAATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1689  
DB 586 GlnGluLeu-----GlyGluLysGlyValGlyAsnValThrValThrVal---PheAsp 602  
QY 1690 GATGGAATTCAAAATCAGTCAGA-----ACAGATGAGATGCGGAATATAT 1734  
DB 603 AsnAsnThrAsnThrLysValGlyGluAlaValThrLysGluAspGlySerTyr 620

RESULT 5  
D89824  
hypothetical protein sdRD [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
R:Accession: D89824  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89759; MUID:21311952; PMID:11418146  
A:Accession: D89824  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1385 <KUR>  
A:Cross-references: UNIPROT:Q99W47; UNIPARC:UPI00000CAA1F; GB:BA000018; PFD:g13700454;

A; Experimental source: strain N315

C; Genetics:

A; Gene: sdrD

# Alignment Scores:

Pred. No.: 1,76e-21 Length: 1385  
 Score: 559.00 Matches: 177  
 Percent Similarity: 47.8% Conservatives: 117  
 Best Local Similarity: 28.8% Mismatches: 235  
 Query Match: 18.5% Indels: 86  
 DB: 2 Gaps: 27

US-10-806-288-12 (1-1746) x D89824 (1-1385)

```

QY 1 TCTAGTGAAGAAAGAAAGATGATG-----ATCAATAATAATCAGTCATAAATAC 51
DB 55 SerThrAsnLysGluLeuAsnGluAlaThrThrSerAlaSerAspAsnGlnSerSerAsp 74
QY 52 ACCGACGATAATAACCAATAATTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 111
DB 75 LysValAspMetGlnGlnLeuAsnGlnGluAspAsnThrLysAsnAspAsnGlnLysGlu 94
QY 112 AAACCTCAGAGATAGACAGAGTCAACAAACAAATGTAGATGAAAC---GAAGCAACA 168
DB 95 MetValSerSerGlnGlyAsnGluThrThrSerAsnGlyAsnLysSerIleGluLysGlu 114
QY 169 TTTTACAAAGACCCCTCAGATTAATCTACTCTTACAGAAAGAAAGAGAGTAAAGATCC 228
DB 115 SerValGlnSerThrThrGlyAsnLysValGluValSerThrAlaLysSerAspGluGln 134
QY 229 TCATCAGTCGAATCTCAATTCATCAATGTGATCTGCCCAACACCATCTCACACAACA 288
DB 135 AlaSerProLysSerThrAsnGluAspLeuAsnThrLysGln-----Thr 149
QY 289 ATAAATAGAGAGAACTGTCTTCAACAAAGTGAATAATGTAGAGATTCACAGTATCAGAT 348
DB 150 IleSerAsnGlnGluGlnLeuGln---ProAspLeuLeuGluAsnLysSerValValAsn 168
QY 349 TTTGCTAACTCTAAATTAAGAGAGTAACTGATCTGTAATCTGTTAAAGAGAGAACTATA 408
DB 169 -----ValGlnProThrAsnGluGluAsnLysLysValAspAlaLysThr 183
QY 409 GAGCAACCTAAT---AAAGTAAAGAGATTCACAAACAAAGTCAGCCGCTGGCTATACA 465
DB 184 GluSerThrThrLeuAsnValLysSerAspAlaIleLysSer----- 197
QY 466 AATATAGATGAAAAAATTTCAAATCAAGATGAGTTATTAAATTTTACCAATAAATGAATAT 525
DB 198 AsnAlaGluThrLeuValAspAsnAsnSerAsnSerAsnAsn----- 211
QY 526 GAAATAGAGGTAGACCATTTATCTACACATCTGCCCAACCATGATTAACGTGTAAACC 585
DB 212 GluAsnAsnAlaAspIleLeuProLysSerThrAlaProLysSerLeuAsnThrArg 231
QY 586 GTAAATCAATTAGCGCGGCAACAGGTCG-----AATGTTAAACATTTAATT 633
DB 232 MetArgMetAlaAlaIleGlnProAsnSerThrAspSerLysAsnValAsnAspLeuIle 251
QY 634 AAAGTTACTGATCAAAAGTATTACTGAAGATATGATGATGAGTGAAGGTGTTATTAAAGCA 693
DB 252 ThrSerAsnThrThrLeuThrValValAspAlaAspAsnSerLysThrIleValProAla 271
QY 694 CATGATGCTGAAACCTTAATCTATGATGTAATCTTTTGAAGTAGATGATGAAGTGAATCT 753
DB 272 GlnAspTyrLeuSerLeuLysSerGlnIleThr-----ValAspAspLysValLysSer 289
QY 754 GGTGATCAGTACAGATGATATAGATATAGATATAGATATAGATATAGATATAGATATAG 795
DB 290 GlyAspTyrPheThrIleLysTyr---SerAspThrValGlnValThrGlyLeuAsnPro 308
QY 796 TCAGATTTAACCGATAGCTTTTCAATATACCAAAATAAAAGAT---AATTCGGGAAATC 852
DB 309 GluAspIleLysAsn-----IleGlyAspIleLysAspProAsnAsnGlyGluThr 325

```

```

QY 853 ATCGCTACAGCTACTTATGATAACAAAAATAAAACAAATCACCTATCTTTTACAGATTAT 912
DB 326 IleAlaThrAlaLysHisAspThrAlaAsnAsnLeuIleThrTyrThrPheThrAspTyr 345
QY 913 GTAGATAAGTATGAAATAATATTAAAGCACACACCTTAAATTTAAAGCTATACATTTGATAAATCA 972
DB 346 ValAspArgPheAsnSerValLysMetGlyIleAsnTyrSerIleTyrMetAspAlaAsp 365
QY 973 AAGTTTCAAATAATAATCAACAGATTAGATAGATAATAAAACGGCCCTTTTCATCAGTA 1032
DB 366 ThrIleProValAsp-----LysLysAspValProPheSerValThrIleGlyAsnGln 383
QY 1033 AATAAAACAAATTACGGTTGAATATCAAGACCT-----AACGAAATCGGACTGCTAAC 1086
DB 384 IleThrThrThrAlaAspIleThrTyrProAlaTyrLysGluAlaAspAsnAsnSer 403
QY 1087 CTTCAAAGTAGTGTTTACAAATATATAGATACGAAAAATCATACA----- 1128
DB 404 IleGlySerAlaPheThr-----GluThrValSerHisValGlyAsnValGluAspPro 421
QY 1129 -----GTTGAGCAACGATTTATATTAAACCTCTTCTGTTTATTCAGCCAGCAACAAT 1182
DB 422 GlyTyrTyrAsnGlnValValTyrValAsnProMetAspLysAspLeuLysGlyAlaLys 441
QY 1183 GTAATATTTTTCAGGGAATGGTGATGAAGGTTCAACA-----ATTATAGACGAT 1230
DB 442 LeuLysValGluAlaTyrHisProLysThrAsnIleGlyGlnIleAsnGlnAsn 461
QY 1231 AGCACAATAATTAAGTTTATAAGTTGGAGATTAATCAAAATTTTACCAGATAGTAACAGA 1290
DB 462 ValThrAsnIleLysIleTyrArgValProGluGlyTyrThrLeu-----AsnLys 478
QY 1291 ATTATGATTATAC-----AGTGAATATGAAGATGTCACAAATGAT-----GATTATGCC 1338
DB 479 GlyTyrAspValAsnThrAsnAspLeuValAspValThrAspGluPheLysAsnLysMet 498
QY 1339 CAATTAGGAATAATATGATGCAATTAATTAATTTTGGTAAATATAGATTTACCATATATT 1398
DB 499 ThrTyrGlySerAsnGlnSerValAsnLeuAspPheGlyAspIleThrSerAlaTyrVal 518
QY 1399 ATTAAAGTTATTAGTAAATATGACCTCAATAAGATGATTACAGACTATACAGCAAACT 1458
DB 519 ValMetValAsnThrLysPheGlnTyrThrAsnSerGluSerProThrLeuValGlnMet 538
QY 1459 GTGCAATGTCAGACGACTATAAATGAGTATGACTGGTGATTTAGAACAGCATCTCATGAT 1518
DB 539 AlaThrLeuSerSerThrGlyAsn-----LysSerValSerThrGly 552
QY 1519 AATCAATTTGCTTCTCTACAGTTTCAGTCAAGGCAAGCAAGGTGACTTCCTCGCTGAAAAA 1578
DB 553 AsnAlaLeuGlyPheThrAsnAsnGlnSerGlyGlyAlaGly-----GlnGlu 568
QY 1579 ACTTATAAAATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAATAACA 1638
DB 569 ValTyrLysIleGlyAsnTyrValTyrGluAspThrAsnLysAsnGlyValGlnGluLeu 588
QY 1639 AATGATTAATGAAACCGCTTAGTAAATGATTTGTTAGTACCTTTGACGTATCTCTGATGGA 1698
DB 589 -----GlyGluLysGlyValGlyAsnValThrValThrVal---PheAspAsnAsnThr 605
QY 1699 TCAAAATCAGTACAGA-----ACAGATCAAGATGGAATAT 1734
DB 606 AsnThrLysValGlyGluAlaValThrLysGluAspGlySerTyr 620

```

## RESULT 6

C89824

hypothetical protein sdrC [imported] - Staphylococcus aureus (strain N315)

C; Species: Staphylococcus aureus

C; Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C; Accession: C89824

R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;



C.: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Lancet 357, 1225-1240, 2001  
 A:Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.  
 A:Reference number: A89758; MUID:21311952; PMID:11418146  
 A:Accession: C89824  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-953 <KUR>  
 A:Cross-references: UNIPROT:Q99W48; UNIPARC:UPI00000CAB80; GB:BA000018; PID:g13700453; E  
 A:Experimental source: strain N315  
 C:Genetics:  
 A:Gene: sdrc

Alignment Scores:  
 Pred. No.: 6.34e-18 Length: 953  
 Score: 489.00 Matches: 162  
 Percent Similarity: 42.5% Conservative: 82  
 Best Local Similarity: 28.2% Mismatches: 236  
 Query Match: 16.2% Indels: 94  
 DB: 2 Gaps: 22

US-10-806-288-12 (1-1746) x C89824 (1-953)

```

QY 103 GCATAGAAAACGCTCAGAGATAGACAGAGTCAACAACTAGTAGATGAAACGAA 162
DB 45 GlyHisGluAlaLysAlaAlaGluHisThrAsnGlyGluLeuAsnGlnSerLysAsnGlu 64
QY 163 GCACATATTTTCAAAAGACCCTCAAGATATATCTCATCTTACAGAGAAGAGGTAA 222
DB 65 ThrThr-----AlaProSerGluAsnLys-----ThrThrGluLysVal--- 77
QY 223 GAATCCTCATAGTCGAATCCTCAATTCATCAATTCATGACTGCCCAACCAACATCTCAC 282
DB 78 ---AspSerArgGlnLeuLysAspAsnThrGlnThrAlaThrAlaAspGlnProLysVal 96
QY 283 ACAACAATAAATAGAGAAGAACTCTGTTCAACAAGTGATATGTAGAGAATTCACAGT 342
DB 97 Thr-----Met 98
QY 343 TCAGATTTTGCTAACTCTAAATAAAGAGAGTAACTGTAATCTGGTAAAGAGAGAT 402
DB 99 SerAspSerAlaThrValLysGluThrSerSerAsnMetGlnSer----- 113
QY 403 ACTATAGAGCAACCTAATAAAGTAAAGAAAGATTCACAAACAAGTCAGCGCTCGCTAT 462
DB 114 -----ProGlnAsnAlaThrAlaSerGlnSerThrThrGlnThrSerAsnVal 129
QY 463 ACAATATAGATGAAAA-----ATTCAAATCAAGATGAGTTATTAATTTACCA 513
DB 130 ThrThrAsnAspLysSerSerThrThrTyrSerAsnGluThrAspLysSerAsnLeu--- 148
QY 514 ATAAATGAATATGAAAT---AAGCTAGACCATTTATCTACCAACATCTGCCCAACATCG 570
DB 149 ---ThrGlnAlaLysAsnValSerThrThrProLysThrThrThrIleLysGlnArgAla 167
QY 571 ATTAACGTGTAAACCGTAAATCAATTAGCGCG---GAACAAGTTCCGAATCTTAACCAT 627
DB 168 LeuAsnArgMetAlaValAsnThrValAlaAlaProGlnGlnGlyThrAsnValAsnAsp 187
QY 628 TTAATTAAGTTACTGATCAAAAGTATT----- 654
DB 188 LysValHisPheThrAsnIleAspIleAlaLysGlyHisValAsnLysThrThr 207
QY 655 -----ACTGAAGGATATGATGATGAGTGAAGTGTATTAAAGCACATGATGCTGAAAC 708
DB 208 GlyAsnThrGluPheThrPalaThrSerSerAspValLeuLys----- 221
QY 709 TTAATCTATGATGAATCTTTGAAGTAGATGAAGGTGAATCTGGTATACGATGACA 768
DB 222 -----LeuLysAlaAsnTyrThrIleAspAspSerValLysGluGlyAspThrPheThr 239
QY 769 GTGGATATAGATAGAATACATGTTCCATCAGATTTTAAACCGATGCTTTTCAATACCAAA 828
DB 828 -----Met 829

```

# RESULT 7

S41539  
 fibrinogen-binding protein - *Staphylococcus aureus*  
 N:Alternate names: clumping factor  
 C:Species: *Staphylococcus aureus*  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
 C:Accession: S41539; S36630

```

DB 240 PheLysTyrGlyGlnTyrPheArgProGlySerValArgLeuProSerGlnThrGlnAsn 259
QY 829 ATAAAGATAAATCTCGAGAAATCATCGCTACAGGTACTATGATACAAACAAAATAACAA 888
DB 260 LeuTyrAsnAlaGlnGlyAsnIleAlaLysGlyIleTyrAspSerLysThrAsnThr 279
QY 889 ATCACTATACCTTTTACAGATATGTAGATAAGTATGAAAAATATTAAGACACACCTTAA 948
DB 280 ThrThrTyrThrPheThrAsnTyrValAspGlnTyrThrAsnValSerGlySerPheGlu 299
QY 949 TTAACGTCTATCATTCATTAATCAAGGTTCCAAATATAATAATACCAAGTTAGATGAG 1008
DB 300 GlnValAlaPheAlaLysArgGluAsnAlaThrThrAspLysThrAlaTyrLysMetGlu 319
QY 1009 TATAAAACGGCCCTTTTCATCAGTAAATAAAACAAATTTACCGTTTGAATATCAAGACCT 1068
DB 320 ValThrLeuGlyAsnAspThrTyrSerLysAspValIleValAspTyr-----Gly 336
QY 1069 GAAATCGGACTGCTAACCTTCAAAAGTATGTTTACAAATATAGATACGAAAAATCATAC 1128
DB 337 AsnGlnLysGlyGlnGlnLeuIleSerSerThrAsnTyrIleAsnAsnGluAspLeuSer 356
QY 1129 GTTGAGCAAAACGATTTATATTAAC---CCTCTTCGTTATTCAGCCAGGAACAAATGTA 1185
DB 357 ArgAsnMetThrValTyrValAsnGlnProLysLysThrTyrThrLysGluThrPheVal 376
QY 1186 ---AATATTTTCAAGGAAATGGTGAAGTTCAACAAATATATAGACGATAGCAAAATTA 1242
DB 377 ThrAsnLeuThr-----GlyTyrLysPheAsnProAspAlaLysAsnPhe 391
QY 1243 AAAGTTTATAAGTTTGGAGATAATCAAAATTTTACCAGATAGTAAACAGAAATTTATGAT 1302
DB 392 LysIleTyrGluValThrAspGlnAsnGlnPheValAspSer---PheThrProAspThr 410
QY 1303 ACTGAATATGAAGTGTCAAAATGAT---GATTATGCCCAATTAGGAAATATAATATGAT 1359
DB 411 SerLysLeuLysAspValThrGlyGlnPheAspValIleTyrSerAsnAspAsnLysThr 430
QY 1360 TGAATATTAATTTTGGTAAT-----ATAGATTCACCATATATATTATTAAGTT 1407
DB 431 AlaThrValAspLeuAsnGlyGlnSerSerAspLysGlnTyrIleIleGlnGln 450
QY 1408 ATTAGTAATATGACCCCTAATAAGGATGATTACAGACTATATACAGCAACTGTGCAATG 1467
DB 451 ValAlaTyrProAspAsnSerSerThrAspAsnGlyLysIleAspTyrThrLeuGluThr 470
QY 1468 CAGACGACTAATAATGATGATATCTCGTGAGTTTAGAACAGCATCTTATGATTAATCAAT 1527
DB 471 GlnAsnGlyLysSerSerTrpSerAsn-----SerTyrSerAsnValAsn 485
QY 1528 GCTTTCTCTACAGTTTCAGGTCAAGGACAGGTCAGTTCCTCTCGAAAAAACTTATAA 1587
DB 486 GlySerSerThrAlaAsnGlyAsp-----GlnLysLysTyrAsn 498
QY 1588 ATCGAGATTAACGTATGCGAAGATGATAGATAAGATGCTATTCAAAATACAAATGATAT 1647
DB 499 LeuGlyAspTyrValTrpGluAspThrAsnLysAspGlyLysGlnAspAla-----Asn 516
QY 1648 GAAAAACCGCTTAGTAATGTAATGTAATCTTTGCGATCTCTGATGCGAATCTTCA---AAA 1704
DB 517 GluLysGlyIleLysGlyValTyrValIleLeuLysAspSerAsnGlyLysGluLeuAsp 536
QY 1705 TCAGTCAGAACAGATGAAGATGGGAATATCAATTTTGATGGA 1746
DB 537 ArgThrThrThrAspGluAsnGlyLysTyrGlnPheThrGly 550

```



A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
A;Reference number: A89758; MUID:21311952; PMID:11418146  
A;Accession: D89952  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-989 <KUR>  
A;Cross-references: UNIPROT:Q99VJ4; UNIPARC:UP100000C7F65; GB:BA000018; PID:g13700678; E  
A;Experimental source: strain N315

Alignment Scores:	
Pred. No.:	4 7e-16
Score:	454.00
Percent Similarity:	44.5%
Best Local Similarity:	25.9%
Query Match:	14.9%
DB:	2
Length:	989
Matches:	152
Conservative:	109
Mismatches:	224
Indels:	102
Gaps:	27

US-10-806-288-12 (1-1746) x D89852 (1-989)

Qy	1	TCTAGTCATCAAGAAAGAGTGTGATCAATAAATCACTCAATAAACCGACGAT	60
Db	51	SerAsnLysSerLysSerAsnSerSerSerValSerAlaAlaProLysThrAspAsp	70
Qy	61	AATAACCAATAATTTAAAAAAGAAAGAAACGAATACTACGATGGCATAGAAAAACGCTCA	120
Db	71	ThrAsnVal-----Ser	74

QY 121 GAAGATACGACAGAGTCACCAACAATGTAGATGAAGAAGCAACATTTTTCAAAAG 180  
:: :: :: ::  
Db 75 AspThrLysThrSerSerAsnThrAsn-----AanGLygluThrSerValAlaGln 91

Qy	181	ACCCCTCAAGATAA	TACTCATCTCTT	CAGAAAGAGAGAGG	TAAAGAATCCTCATCTCGAA	240
Db	92	AsnPro-----	-----AlaGlnGln	ThrThrGlnSerSer	ThrAsn	105

**Oy**      241    TCCTCAANTCATNTGATCTGCCCAAACCATCTCACACAATAAATAGAGAA    300  
         : : : : :  
**Db**      106    ATATrThrGlUgluthrProvalThrGlVglualatThrThrThrAsnGlnAla    125  
         : : : : :  
         : : : : :

QY 301 GAATCTGTTCAAACAAGATGTAATAGAGATTACACGTTATCAGATTTTCTAACTCT 360

Db 126 AsnThrProAlaThrThrGlnSer---SerAsnThrAsnAlaGluGlnLeuValAsn--- 143

QY 361 AAAATAAAGAGAGTAACTCTGTAATCTGTTAAAGAGAGAACTACTATAGAGCAACCTAAT 420  
 Db 144 -----GlnThrSerGlnThrThrSerAsnGlnThrVal----- 157

```
Qy      421 AAAGTAAAGAAGATTCAACAACCAAGTCAGCCGCTCGGTATACAATAATAGTAGCAAAA   480
         |||:::|||||||:::
Db      158 -----getServerValueSeriProClnSenseThrtgnaIgaCnAcvAl       172
```

**OY**    481   ATTTCAAATCAAGATGAGTATTAAAT---TTACCAATAAATGAATATGAAAAATAAGGCT   537  
         ||||| |  
         ::  
**bh**     173   SerTbThrArgIleLysophSerMetbClnAlamb-ProSerDnSph-AspPheValProThrLeuLeuGluTrp 190  
         ||||| |  
         ::

[illegible]

QY	571	ATTAAACGTGTAAACCGTAAATCAATTAGCGCG	-----GAACAAGT	612
572				
573				
574				
575				
576				
577				
578				
579				
580				
581				
582				
583				
584				
585				
586				
587				
588				
589				
590				
591				
592				
593				
594				
595				
596				
597				
598				
599				
600				
601				
602				
603				
604				
605				
606				
607				
608				
609				
610				
611				

[illegible]

QY 673 AGTGAAGGTGTTATTAAAGCACATGATGCTGAAACCTTTAATCTATGATGTAACTTTTGA 732

220    *See also* 219, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029,

Qy	733	GTAGATGATAAGGTGAATCTCGTGATACGCATGACAGTGGATATAGATAGAATAACAGTT	792
Db	265	ValProAsnSerAlaValIysGlyAspThrPheLysIleThrValProLysGluLeuAsn	284
Qy	793	CCATCAGATTAAACCGTAGCTTTACAATACCAAAAATAAAGCATTAATCTCGAGAAATC	852
Db	285	LeuAsnGlyValThrSerThrAlaLysValProIleMetAlaGlyAsp---	GlnVal 303
Qy	853	ATCGCTACAGGTACTTATGATAACAAAAATAAACAAATACCCTATATCTTTACAGATTAT	912
Db	304	LeuAlaAsnGlyValIleAspSer---AspGlyAsnValIleTyrThrPheThrAspTyr	322
Qy	913	GTAGATAAGTATCAAATAATTAAAGCACACACCTTAAATTAACGTCATACATTTGATAATCA	972
Db	323	ValAspAsnLysGluAsnValThrAlaAsnIleThrMetProAlaTyrIleAsp-----	340
Qy	973	AAGGTTTCCAATATAATACCAAGTTA---GATGTAGAATATAAAACGCCCTT-----	1023
Db	341	----ProgluAsnValThrLysThrGlyAsnValThrLeuThrThrGlyIleGlyThr	358
Qy	1024	TCATCAGTAATAAAACAATTACCGTTGTAATATCAAAGACCTTAACGAAATCGGACTGCT	1083
Db	359	AsnThrAlaSerLysThrValLeuIleAspTyrGluLysTyrGlyGlnPheHisAsnLeu	378
Qy	1084	AACCTTCAAAGTATGTTTACAAATATAGATACGAAAAATCATACGCTTCGCGCAACGATT	1143
Db	379	SerIleLysGlyThrIleAspGlnIleAspLysThrAsnAsnThrTyrArgGlnThrIle	398
Qy	1144	TATATTAAACCTCTTCGTTATTTCAGCCAAAGAAACAAATGTA-----	1185
Db	399	TyrValAsnPro-----SerGlyAspAsnValValLeuProAlaLeuThr	413
Qy	1186	---AATATTTCAGGGAAATCGTGATGAAGTTCAACAATTTATAGACATGACCAATAATT	1242
Db	414	GlyAsnLeuIleProAsnThrLysSerAsnAlaLeuIleAspAlaLysAsnThrAspIle	433
Qy	1243	AAAGTTTATAAGGTTCGAGATAATCAAAATTTACCAGATAGTAACAGAAATTTATGATGAT	1302
Db	434	LysValTyrArgVal---AspAsnAlaAsnAspLeuSerGluSerTyrTyrValAsnPro	452
Qy	1303	AGTGAATATGAAGATGTCACAAATGATGATTAATGCCCAATTAGGAAATAATATGATGTG	1362
Db	453	SerAspPheGluAspValThrAsnGlnValArgIleSerPheProAsnAlaAsnGlnTyr	472
Qy	1363	AATATTAAATTT-----GCTAATATAGATTCCACATATATATTATTAAAGTTATT	1410
Db	473	LysValGluPheProThrAspAspAspGlnIleThrThrProTyrIleValValValAsn	492
Qy	1411	AGTAAATATGACCTAATAAGGATGATTACACGCACTATACAGCAAACTCTGCAATGCAAG	1470
Db	493	GlyHisIleAspProAlaSerThrGly-----AspLeuAlaLeuArg	506
Qy	1471	ACGACTATAAATGATGATFACTCGTGAGTTT-----AGAACAGCATCTCATGATATACA	1524
Db	507	SerThrPheTyrGlyTyrAspSerAsnPheIleTrpArgSerMetSerTrpAspAsnGlu	526
Qy	1525	ATTGCTTCTCTACAGTTTCAGTCAAGCAACAAGT---GACTTCGCT-----CCTGAA	1575
Db	527	ValAlaPheAsnAsnGlySerGlyAspGlyIleAspLysProValValProGlu	546
Qy	1576	AAACTTATAAATCGGAGTTATC-----GTATCGGAAGATGTAGATAAGAT---	GST 1626
Db	547	GlnProAspGluProGlyGluIleGluProIleProGluAspSerAspSerAspProGly	566
Qy	1627	ATTCAAAATACAAATGATTAAT	1647
Db	567	SerAspSerGlySerAspSer	573

## RESULT 9

F90070

Clumping factor B [imported] - *Staphylococcus aureus* (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

Qy	676	GAAGGTGTTATTAAAGCACAATGATGCTGGAGAAACCTTAATCTATGATGTAACCTTTTGAAGTA	735
Db	228	LyseThrPheAspProAsnGlnSerGlyAsnThrPheMetAlaAlaAsnPheThrVal	247
Qy	736	GATGATAAGGTGAATCTCGTGATACGATCACAGTG	771
Db	248	ThrAspLysValLysSerGlyAspTyrPheThrAlaLysLeuProAspSerLeuThrGly	267
Qy	772	-----GATATAGAT	813
Db	268	AsnGlyAspValAspTyrSerAsnSerAsnAsnThrMetPro	281
Qy	814	TTTACATACCAAAATAAAGATAATCTCGGAGAAATCATCGCTACAGCTACTTATGAT	873
Db	282	-----IleAlaAspIleLysSerThrAsnGlyAspValValAlaLysAlaThrTyrAsp	299
Qy	874	AACAAAATAAACAAATCACCTACTCTTTTACAGATTATAGATAGTATGAAAAATATT	933
Db	300	IleLeuThrLysThrTyrThrPheValPheThrAspTyrValAsnAsnLysGluAsnIle	319
Qy	934	AAAGCACACCTTAAATTAACGTCATCATTTGATAAATCAAAGTTCCAAATATAATATACC	993
Db	320	AsnGlyGlnPheSerLeuProLeuPheThrAspArgAlaLysAlaProLysSerGlyThr	339
Qy	994	AAGTTAGATGATAGATATAAAGCGCCCTTTCATCAGTAAATAAACAATATTCGGTTGAA	1053
Db	340	---TyrAspAlaAsnIleAlaAspGluMetPheAsnAsnLysIleThrTyrAsn	358
Qy	1054	TATCAAGACCT	1101
Db	359	TyrSerSerProIleAlaGlyIleAspLysProAsnGlyAlaAsnIleSerSerGlnIle	378
Qy	1102	ACAAATATAGATACGAAAT	1155
Db	379	IleGlyValAspThrAlaSerGlyGlnAsnThrTyrLysGlnThrValPheValAsnPro	398
Qy	1156	CTTCGGTTATTCAGCCAGGAAACAAATATTTACGGGAATGGTGTAAGGTTCA	1215
Db	399	LysGlnArgValLeuGlyAsnThrTrpValTyrIleLysGlyTyrGlnAspLys	416
Qy	1216	ACAATTATAGACATAGC	1251
Db	417	-----IleGluGluSerSerGlyLysValSerAlaThrAspThrLysLeuArgIlePhe	434
Qy	1252	AAAGTTGGAGATATAACAAATTTACAGATAGT	1284
Db	435	GluValAsnAspThrSerLysLeuSerAspSerTyrTyrAlaAspProAsnAspSerAsn	454
Qy	1285	-----ACAGAAATTTATGATTACGTACGTGAATATGAAGAT	1317
Db	455	LeuLysGluValThrAspGlnPheLysAsnArgIleTyr	469
Qy	1318	GTCAAAATGATGATTATGCCCAATTAGGAAATAATAATGATCGTGAATATTAATTTTGGT	1377
Db	470	-----HisProAsnValAlaSerIleLysPheGly	479
Qy	1378	AATATAGATTCACCATATATTTAAAGTPTATTAGTAAATATGACCCCTAATAAGGATGAT	1437
Db	480	AspIleThrLysThrTyrValValLeuValGluGlyHisTyrAspAsnThrGlyLysAsn	499
Qy	1438	TACACGACT	1491
Db	500	LeuLysThrGlnValIleGlnGluAsnValAspProValThr	514
Qy	1492	GGTGAGTTTGAACACGATCCTCATGATAATACAAATGCTTCTCTACAGTTCAGGTCAA	1551
Db	515	ArgAspTyrSerIlePheGlyTyrProAsnAsnGluAsnValValArgTyrGlyGlySer	534
Qy	1552	GGACAGGTGAC	1563
Db	535	AlaAspGlyAsp	538

Qy	676	GAAGGTGTTATTAAAGCACAATGATGCTGGAGAAACCTTAATCTATGATGTAACCTTTTGAAGTA	735
Db	228	LyseThrPheAspProAsnGlnSerGlyAsnThrPheMetAlaAlaAsnPheThrVal	247
Qy	736	GATGATAAGGTGAATCTCGTGATACGATCAGACAGTG	771
Db	248	ThrAspLysValLysSerGlyAspTyrPheThrAlaLysLeuProAspSerLeuThrGly	267
Qy	772	-----GATATAGAT-----AGAATAACAGTTCCTCCATCAGATTTAACCGATAGC	813
Db	268	AsnGlyAspValAspTyrSerAsnSerAsnAsnThrMetPro	281
Qy	814	TTTACAAATCAAAAATAAAGATAATTCGGAGAAATCATCCTACAGCTACTCTATGAT	873
Db	282	-----IleAlaAspIleLysSerThrAsnGlyAspValValAlaLysAlaThrTyrAsp	299
Qy	874	AACAAAATAAACAATCACCTACTCTTTTACAGATTATAGATAGTATGAAAAATATT	933
Db	300	IleLeuThrLysThrTyrThrPheValPheThrAspTyrValAsnAsnLysGluAsnIle	319
Qy	934	AAAGCACACCTTAAATTAACGTCATCATTTGATAAATCAAAGTTCCAAATAATAATACC	993
Db	320	AsnGlyGlnPheSerLeuProLeuPheThrAspArgAlaLysAlaProLysSerGlyThr	339
Qy	994	AAGTTAGATGATAGATATAAACAAGCGCCCTTTCATCAGTAAATAAACAATTCACGGTTGAA	1053
Db	340	---TyrAspAlaAsnIleAlaAspGluMetPheAsnAsnLysIleThrTyrAsn	358
Qy	1054	TATCAAAAGACCT-----AACGAAAATCGGACTGCTCAACCTTCAAAGTATGTTT	1101
Db	359	TyrSerSerProIleAlaGlyIleAspLysProAsnGlyAlaAsnIleSerSerGlnIle	378
Qy	1102	ACAAATATAGATACGAAAAT-----CATACAGTTTGAGCAACAGATTTATATTAACCT	1155
Db	379	IleGlyValAspThrAlaSerGlyGlnAsnThrTyrLysGlnThrValPheValAsnPro	398
Qy	1156	CTTCGGTTATTTCAGCCAGGAAACAAATATTTTACGGGAATGGTGAAGGTTCA	1215
Db	399	LysGlnArgValLeuGlyAsnThrTrpValTyrIleLysGlyTyrGlnAspLys	416
Qy	1216	ACAATTATAGACATAGC-----ACAATAATTAAGATTTAT	1251
Db	417	-----IleGluGluSerSerGlyLysValSerAlaThrAspThrLysLeuArgIlePhe	434
Qy	1252	AAAGTTGGAGATATAATCAAAATTTTACAGACATAGT-----	1284
Db	435	GluValAsnAspThrSerLysLeuSerAspSerTyrTyrAlaAspProAsnAspSerAsn	454
Qy	1285	-----AACAGATTTTATGATTACGTACGTGAATATGAAGAT	1317
Db	455	LeuLysGluValThrAspGlnPheLysAsnArgIleTyr-----TyrGlu	469
Qy	1318	GTCAAAATGATGATTATGCCCAATTAGGAAATAATAATGATCGTAATATTAATTTTGGT	1377
Db	470	-----HisProAsnValAlaSerIleLysPheGly	479
Qy	1378	AATATAGATTCACCATATATTTAAAGTPTATTAGTAATAATCATCCCTAATAAGGATGAT	1437
Db	480	AspIleThrLysThrTyrValValLeuValGluGlyHisTyrAspAsnThrGlyLysAsn	499
Qy	1438	TACACGACT-----ATACAGCAACCTGTGACCAATGCAGACGACTATAATGAGTACT	1491
Db	500	LeuLysThrGlnValIleGlnGluAsnValAspProValThr-----Asn	514
Qy	1492	GGTGAGTTTGAACAAGCATCCTCATGATAATACAATTCGCTTCTCTACAGTTCAGGTCAA	1551
Db	515	ArgAspTyrSerIlePheGlyTyrProAsnAsnGluAsnValValArgTyrGlyGlySer	534
Qy	1552	GGACAAGGTGAC	1563
Db	535	AlaAspGlyAsp	538

## RESULT 10

S19702  
 fibronectin-binding protein B - Staphylococcus aureus  
 C:Species: Staphylococcus aureus  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
 C:Accession: S19702  
 R:Joenisson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.  
 Eur. J. Biochem. 202, 1041-1048, 1991  
 A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus  
 A:Reference number: S19702; PMID:92111475; PMID:1837266  
 A:Accession: S19702  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-940 <OE>  
 A:Cross-references: UNIPROT:Q53682; UNIPARC:UPI000008B7719; EMBL:X62992; NID:g49040; PIDN  
 C:Keywords: fibronectin binding

Alignment Scores:  
 Pred. No.: 3,3e-12 Length: 940  
 Score: 376.00 Matches: 138  
 Percent Similarity: 42.1% Conservative: 110  
 Best Local Similarity: 23.4% Mismatches: 217  
 Query Match: 12.4% Indels: 124  
 DB: 2 Gaps: 22

US-10-806-288-12 (1-1746) x S19702 (1-940)

QY	103	GGCATAGAAAAACGCTCAGAAAGATAGAACAGAGTCAACAAATGCTAGATGAAACGAA	162
DB	30	GlyGlnGluysGluAlaAlaSerGluGlnAsnThrThrValGluGluSer---	48
QY	163	GCAACATTTTACAAAGACCCCTCAAGATAATCTCTTACAGAGAAGAGGTAAAA	222
DB	49	-----GlySerSerAlaThrGluSerLysAlaSer	58
QY	223	GAATCTCATAGTCGAATCCTCAAAATTCATCAATTCATGACTGCCAA	270
DB	59	GluThrGlnThrThrThrAsnAsnValAsnThrIleAspGluThrGlnSerTyrSerAla	78
QY	271	-----CAACCATCTCACACAACA-----ATAAATAGAGAAGAACTGTGTTCAACA	315
DB	79	ThrSerThrGluGlnProSerGlnSerThrGlnValThrGluGluAlaProLysThr	98
QY	316	-----AGTGATAAGTAGAAGATTCACACGTATACAGATTTTGCTAACTTAAATATAAA	369
DB	99	ValGlnAlaProLysValGluThrSerArgVal---AspLeuProSerGluysValAla	117
QY	370	GAGAGTAACACTGAATCTCGTAAAGAGAAGATACTATAGACCACTTAATAAGTAAAA	429
DB	118	AspLysGluThrThrGlyThrGlnValAsp-----IleAlaGlnProSerAsnValSer	135
QY	430	GAAGATTCAACAACAGTCAGCGCTCTGGCTATACAAATATAGATGAAAAAATTTCAAT	489
DB	136	Glu-----	136
QY	490	CAAGATGAGTTATTAATTTTACCATAAATGAATGAATGAAATAAGGCTAGACCATTTCT	549
DB	136	-----	136
QY	550	ACAACATCTGCCAACCATCGATTAAACGTGTAACCGTAAATCAATTAGCGGGAACAA	609
DB	137	-----IleLysProArgMetLysArgSerThrAspValThrAlaValAlaGluLys	153
QY	610	-----GGTTCGAATTTAACCATTTAATTAAGTTACT	642
DB	154	GluValValGluGluThrLysAlaThrGlyThrAspValThrAsnLysValGluValGlu	173
QY	643	GATCAAGTATTACTGAAGATATGATGATGAGGAGGTGTTATTAAAGCACATGATGCT	702
DB	174	GluGlySerGluIleValGlyHisLysGlnAspThrAsnValValAsnProHisAsnAla	193
QY	703	GAATACTTAATCTATGATGAATCTTTTGAAGTAGATGATAAGTGAATCTGGTGATACG	762

DB	194	GluArgValThrLeuLysTyrLysTrpLysPheGlyGluGlyIleLysAlaGlyAspTyr	213
QY	763	ATGACAGTGGATATAGATAAGAAATACAGTTCATCAGATTTCACCGATAGCTTTTCAACA	822
DB	214	PheAspPheThrLeuSerAspAsnValGluThrHisGlyLysSerThrLeuArgLysVal	233
QY	823	CMAAAATAAAGATAATTTCTGGAGAAATCATCGTACAGGTACTTATGATAACAANAAT	882
DB	234	ProGluIleLysSerThrAspGlyGlnValMetAlaThrGlyGluIleIleGlyGluArg	253
QY	883	AAACAAATCACCTATATCTTTACAGATTATGTAGATAAGTATCAAAATATTAAAGCACAC	942
DB	254	Lys---ValArgTyrThrPheLysGluTyrValGlnGluLysLysAspLeuThrAlaGlu	272
QY	943	CTTAAATTAACGTCATACATTAATAAATCAAGGTTCCAAATAATAATCAACAGTTAGAT	1002
DB	273	LeuSerLeuAsnLeuPheIleAspProThrThrValThrGlnLysGlyAsnGln---Asn	291
QY	1003	GTAGAATATAAAACGGCCCTTTTCATCAGTAAATAAAACAATACGGTGTGAATAT---	1056
DB	292	ValGluValLysLeuGlyGluThrThrValSerLysIlePheAsnIleGlnTyrLeuGly	311
QY	1057	---CAAAGACCTAACGAAATCGGACTGCTAACCTTCAAGATGATGTTTCAAAATATAGAT	1113
DB	312	GlyValArgAspAsnTrpGlyValThrAlaAsn-----GlyArgIleAsp	326
QY	1114	ACGAAAAATCATACA-----GTTGAGCAACGATTATATTAACCTCTTCGTTAT	1164
DB	327	ThrLeuAsnLysValAspGlyLysPheSerHisPheAlaTyrMetLysProAsnAsnGln	346
QY	1165	TCAGCCAGGAAACAAATGTAATATTTTCAGGGAATGGTGAGGTTCACCAATTTATA	1224
DB	347	SerLeu-----SerSerValThrValThrGlyGlnValThrLysGlyAsnLysProGly	364
QY	1225	GACGATAGCACAAATTAATTAAGTTTATTAAGTTGGAGATAATCAAAATTTACAGATAGT	1284
DB	365	ValAsnAsnProThrValLysValTyrLysHisIleGlySerAspAspLeuAlaGluSer	384
QY	1285	---AACAGAATTTATGATTACAGTGAATATGAAGATGTCACAATCATGATTATGCC	1338
DB	385	ValTyrAlaLysLeuAspAspValSerLysPheGluAspValThrAspAsnMetSerLeu	404
QY	1339	CAATTAGGAAATTAATGATGTAATTAATTTTGGTAATATAGATTACCA-----	1392
DB	405	AspPheAspThrAsnGlyGlyTyrSerLeuAsnPheAsnAsnLeuAspGlnSerLysAsn	424
QY	1393	TATATTATTAAGTTTATGATAATATGACCCCTTAATAAGATGATTAACGACTATACAG	1452
DB	425	TyrValIleLysTyrGluGlyTyrTyrAspSerAsnAlaSerAsn-----	439
QY	1453	CAACCTGTCACAATGCAGACGACTAATATGATGATGCTGCTGAGTTTAGAACAGCA---	1509
DB	440	LeuGluPheGlnThrHisLeuPheGlyTyrTyrAsnTyrTyrThrSerAsn	457
QY	1510	---TCCTATGATAATACAAATCTCTTCTACAAAGTTTCAGGTCAAGCAAGCT-----	1560
DB	458	LeuThrTrpLysAsnGlyValAlaPheTyrSerAsnAsnAlaGlnGlyAspGlyLysAsp	477
QY	1561	-----GACTTGCCTCTCGAAAAAATTTATATAATTCGGA	1593
DB	478	LysLeuLysGluProIleGluHisSerThrProIleGluGluPheLysSerGlu	497
QY	1594	GATTACGATGGGAAGATGATAGATAAGATGTTTCAAAATCAAAATCAATGATAAANA	1653
DB	498	ProProValGluLysHisGluLeuThrGlyThrIleGluGluSerAsnAspSer---Lys	516
QY	1654	CCGCTTAGTAATGATGTTGTAATCTTTCAGC-----TATCCTGATGAACT	1698
DB	517	ProIleAspPheGluTyrHisThrAlaValGluGlyAlaGluGlyHisAlaGluGlyThr	536
QY	1699	TCAAAATCAGTCAGAACAGATGAAGAT	1725
DB	537	-----IleGluThrGluGluAsp	542



103	GGCATAGAAAAACGCTCAGAAGATAGACAAGACTCAACAATAATCTTAGATGAAGAAACGAA	162
	:    :	
30	GlyGlnAspLysGluAlaalaaserGluGlnLysThrThrValGluGluAen---	48
	:    :	
163	GCAACATTTTTCAAAAGACCCTCAAGATNAAT-----ACTCATCTTACAGAA	210
	:::	
49	-----GlyAsnSerAlaThrAspAsnLysThrSerGluThrGlnThrThrAla	64
	:    :	
211	GAAGAGGTAAAAAGAACCTCATCAGTCGAATCTCAAATTTCATCTCAATGATGATGCCCAA	270
	:    :	
65	ThrAsnValAsnHisIleGluGluThrGlnSerTyrAsnAlaThrVal-----ThrGlu	82
	:    :	
271	CAACCATCTCACACAACA--ATAAATAGAGAAGAAATCTGTTCAACAAGAATGATAATGTA	327
	:    :	
83	GlnProSerAsnAlaThrGlnValThrThrGluGluAlaProLysAlaValGln-----	100
	:    :	
328	GAAGATTCCACGTCATCAGATTTTGCTAACTCTAAATAATAAAGAGAGTAGTAACCTG	387
	:    :	
101	-----AlaProGlnThrAlaGlnProAlaAsnValGluThr	112
	:    :	
388	GGTAAAGAAGAGAATACTATAGAGCAACCTTAATAAGTAAAGATAAGATTCAACAAC	447
	:    :	
113	ValLysGluGlu-----GluLysPro---GlnValLysGlu-----ThrThr	125
	:    :	
448	CAGCGCTCTGGCTATACAAATATAGATGAAAAAATTTCAAATCAAGATCAGTTATTAAAT	507
	:    :	
126	GlnPro-----GlnAspAsnSerGlyAsnGlnArgGlnValAspLeu	139
	:    :	
508	TTACCNATAAATGAATATGAAAATAG-----GCTPAGACA	543
	:    :	
140	ThrProLysLysValThrGlnAsnGlnGlyThrGluThrGlnValGluValAlaGlnPro	159
	:    :	
544	TATCTACAACTCTGCCCAACCATCGATTAAACGTGTAAACCGTAAATCAATAGCGCG	603
	:    :	
160	ArgThrAlaSerGluSerLysProArgValThrArg---SerAlaAspValAlaGluAla	178
	:    :	
604	GAACAGGTTTCGAATCTTAACCATTTAAATTAAGTTTACTGTCAAGTAGTATTACTGAAGA	663
	:    :	
179	LysGluAlaSerAspValSerGlu---ValLysGlyThrAsp-----ValThrSerLys	195
	:    :	
664	TATGATGATGAGGAGGCTGTTATTAAAGCA-----CATGAT	699
	:    :	
196	ValThrValGluSerGlySerIleGluAlaProGlnGlyAsnLysValGluProHisAla	215
	:    :	
700	GCTGAAAACCTTAATCTATGATGTAACCTTTTGAAGTAGATGATAAGGTGAATCTGGTGAT	759
	:    :	
216	GlyGlnArgValValLeuLysTyrLysLeuLysPheAlaAspGlyLeuLysArgGlyAsp	235
	:    :	

```

Db      563 VallaspGly 565
|||||
RESULT 13
A32192
fibronectin-binding protein - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 16-Feb-1997
C:Accession: A32192
R:Signaes, C.; Raucchi, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hosoe, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989
A:Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Staphylo
A:Reference number: A32192; MUID:89088998; PMID:2521391
A:Accession: A32192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <SIG>
A:Cross-references: UNIPARC:UPI0000054887; GB:J04151
C:Keywords: fibronectin binding

Alignment Scores:
Pred. No.:      2,166-08      Length:      1018
Score:          300.50      Matches:      123
Percent Similarity: 41.5%      Conservative: 118
Best Local Similarity: 21.2%      Mismatches:  243
Query Match:     9.9%      Indels:      97
Db:              2          Gaps:         25

US-10-806-288-12 (1-1746) x A32192 (1-1018)
QY      103 GCATAGAAAACGGCTCAGNAGATAGACAGAGTCAACACAAATGTAGATGAAACGAA 162
Db      30 GlyGlnAspLysGluAlaAlaSerGluGlnLysThrThrValGluGluAsn--- 48
QY      163 GCAACATTTTACAAAAGACCCCTCAAGATAT-----ACTCATCTTACAGAA 210
Db      49 -----GlyAsnSerAlaThrAspAsnLysThrSerGluThrGlnThrThra 64
QY      211 GAAGAGGTAAAGAAATCTCATCGATCGAATCTCAATTCATCAATTCATGACTGCCCA 270
Db      65 ThrAsnValAsnHisIleGluGluThrGlnValThrGluGluAlaProLysAlaValGlnAlaPro 102
QY      271 CAACCATCTCACACAACA---ATAATAGAGAGAA-----TCGTTCACAAACAGT 318
Db      83 GlnProSerAsnAlaThrGlnValThrGluGluAlaProLysAlaValGlnAlaPro 102
QY      319 GATATGTAGAGAGATTCACAGTATCAGATTTTGTCAATCTTAAATATAAAGAGAGAGTAAC 378
Db      103 GlnThrAlaGlnProAlaAsnIleGluThrValLysGluGluValValLysGlu----- 120
QY      379 ACTGAATCTGGTAAAGAGAGAAATCTATAGAGCAACCTATAAAGTAAAGTAAAGAGAGATTC 438
Db      121 -----GluAlaLysProGlnValLysGluThrThr 130
QY      439 ACAACAAGTCAGCCCTCTGGC-----TATACAAATATAGTGAATAATTTCAAT 489
Db      131 GlnSerGlnAspAsnSerGlyAspGlnArgGlnValAspLeuThrProLysLysAlaThr 150
QY      490 CAAGATGAGTTATTAATTTTACCAATAAATGAATATGAATAAAGTAAAGTAAAGTAAAGTAAAGT 549
Db      151 GlnAsnGlnValAlaGluThrGlnVal-----GluValAlaGlnProArgThr 166
QY      550 ACAACATCTGCCCAACCATCGATTAAACGTGTAAAC-----GTA 588
Db      167 AlaSerGluSerLysProArgValThrArgSerAlaAspValAlaGluAlaLysGluAla 186
QY      589 AATCAATTAGCGCGGACACAGGTTCGAATGTTAACCAATTTAATTAAGTTACTACTGATCAA 648
Db      187 SerAsnAlaLysValGluThrGlyThrAspValThrSerLysValThrValGluIleGly 206
QY      649 AGTATTACTGAGGATATGATGATGAGGTGAAAGTGTATTATAAGCACATGATGCTGAAAC 708
Db      207 SerIle---GluGlyHisAsnAsnThrAsnLysVal---GluProHisAlaGlyGlnArg 224

```

```

QY      709 TTAATCTATGATGTAACCTTTTGAAGTAGATGATGAAGGTGAATCTGGTGATACGATGACA 768
Db      225 AlaValLeuLysTyrLysLeuLysPheGluAsnGlyLeuHisGlnGlyAspTyrPheAsp 244
QY      769 GTGGATATAGATAAGAAATACAGATTTCCATCAGATTTAAACCGATAGCTTTACCAATACCAAAA 828
Db      245 PheThrLeuSerAsnAsnValAsnThrHisGlyValSerThrAlaAspLysValProGlu 264
QY      829 ATAAAGATATATCT-----CGAGAAATCATCGCTPACAGGATCTTATGAT 873
Db      265 IleLysAsnGlySerValValMetAlaThrGlyGluValLeuGluGlyGly----- 281
QY      874 AACAAAAATAAACAAATCACCCTATCTTTTACAGATATGTAGATAAGTAAATAATATT 933
Db      282 -----LysIleArgTyrThrPheThrAsnAspIleGluAspLysValAspVal 297
QY      934 AAGCACACACCTTAAATTAACGTATACATTAATCAAAAGTTCACAAATTAATTAATACC 993
Db      298 ThrAlaGluLeuGluIleAsnLeuPheIleAspProLysThrValGlnThrAsnGlyAsn 317
QY      994 AAGTTAGATGTAGAATATATAAACCGCCCTTTTCATCAGTAAAT-----AAA 1038
Db      318 -----GlnThrIleThrSerThrLeuAsnGluGluGlnThrSerLys 331
QY      1039 ACAATTACGGTTGAATATCAAGACCTAACGAAATCGGACTGCTTAACCTTCAAGATATG 1098
Db      332 GluLeuAspValLysTyrLysAspGlyIleGlyAsnTyrTyrAlaAsnLeuAsnGlySer 351
QY      1099 TTTCAAAATATAGATACGAAAAATCATACAGTTCAGCAACGATTTTATTAACCCCTCTT 1158
Db      352 IleGluThrPheAsnLysAlaAsnAsnArgPheSerHisValAlaPheIleLysPro--- 370
QY      1159 CGTTATTACGCCAAGCAAAATGTAATATTTTCAAGGAATGTGTAGTAGAGTTCAACA 1218
Db      371 ---AsnAsnGlyLysThrThrSerValThrValThrGlyThrLeuMetLysGlySerAsn 389
QY      1219 ATTATAGACGATACACACATTAATTAAGTTTATAAG---GTTGGAGATAATCAAAATTTA 1275
Db      390 GlnAsnGlyAsnGlnProLysValArgIlePheGluTyrLeuGlyAsnAsnGluAspIle 409
QY      1276 CCAGATAGTACACAAATTTAT-----GATTACAGTGAATATGAAGATGTACACA 1323
Db      410 AlalysSer-----ValTyrAlaAsnThrThrAspThrSerLysPheLysGluValThr 427
QY      1324 AATGATGATTATGCCCAATTAGGA-----AATTAATATGATGTGAATATTAATTTTGGT 1377
Db      428 SerAsnMetSerGlyAsnLeuAsnLeuGlnAsnAsnGlySerTyrSerLysAsnIleGlu 447
QY      1378 AATATAGATTCCACCATATATTATTAAAGTTATTAGTAATATGACCCCTAATAAGAT--- 1434
Db      448 AsnLeuAspLysThrTyrValValHisTyrAspGlyGluTyrLeuAsnGlyThrAspGlu 467
QY      1435 ---GATTACACGACTATACAGCAAACTGTGCAATATGCAGACGACTATAAATGAGTATACT 1491
Db      468 ValAspPheArgThr---GlnMetValGlyHisProGluGlnLeuTyrLysTyrTyr 486
QY      1492 GGTGAGTTTAAAGACGACATCTATGATAATACAAATGCTTTCTCTACAGTTTCAGGTCAA 1551
Db      487 AspArgGlyTyrThrLeuThrTrpAspAsnGlyLeuValLeuTyrSerAsnLysAlaAsn 506
QY      1552 GGACACAGGTGATGTCCTCT-----GAAAAAATCTATAAATCGGAGAT 1596
Db      507 GlyAsnGluLysAsnGlyProIleIleGlnAsnAsnLysPheGluTyrLys----- 523
QY      1597 TACGTATGGGAAGATGTAGATAAAGATGTTATCAAAATACAAATATGATAATGAAAAACCG 1656
Db      524 -----GluAspThrIleLysGluThrLeuThrGlyGlnTyrAspLysAsn----- 538
QY      1657 CTTAGTATGTTGTTAACTTTGACGTATCCTGATGGAACCTTCAAAATCAGTCAGAAC 1716
Db      539 -----LeuValThrThrValGluGluTyrAspSerSerThrLeuAspIle 554

```



1501	AGACA-----GCATCTTATGATAATACAAATGCTTTCTCTCAAGT	1542
QY		
1502	-----	
1503	-----	
1504	-----	
1505	-----	
1506	-----	
1507	-----	
1508	-----	
1509	-----	
1510	-----	
1511	-----	
1512	-----	
1513	-----	
1514	-----	
1515	-----	
1516	-----	
1517	-----	
1518	-----	
1519	-----	
1520	-----	
1521	-----	
1522	-----	
1523	-----	
1524	-----	
1525	-----	
1526	-----	
1527	-----	
1528	-----	
1529	-----	
1530	-----	
1531	-----	
1532	-----	
1533	-----	
1534	-----	
1535	-----	
1536	-----	
1537	-----	
1538	-----	
1539	-----	
1540	-----	
1541	-----	
1542	-----	
1543	TCAGGTCAAGGACAAGGT-----GACTTGCCTCTCAAAAAAAGCT	1581
QY		

55 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

	QY	1362	IATAAATTCGGAGATTAAGTATGCGGAGAGAATGAATAAAGATGGTAAI			-----	1622
	Db	387	LysArgValAlaGlnLeuArgPheLysLysValSerThrAspAsnValProLeuProGlu			-----	406
	QY	1630	-----CAAAATACAATGNTAATGAAAAACCCCTT-----AGTAT			-----	1665
	Db	407	AlaAlaPheGluLeuArgSerSerAsnGlyAsnSerGlnLysLeuGluAlaSerAsn			-----	426

QY 1666 GTATTGTAACTTTTCACGATCCTTGATGGAACCTTCA 1701

DD 427 INTELLECTUAL PROPERTY RIGHTS ACT OF 1980

PAGE 15

T30290 AAS surface protein - Staphylococcus saprophyticus

C;Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: T30290

Mol. Microbiol. 29, 871-881, 1998

A;Accession: T30290  
A;Status: preliminary; translated from GR/EMBL/DDBT  
A;Reference number: 420600; MOLID:96030316; EMLD:9723923

A;Molecule type: DNA  
A;Residues: 1-1463 <HEL>

C;Genetics:  
A;Gene: aag

Alignment Scores: 0.000138 Length: 1463

Percent Similarity:	36.3%	Conservative:	105
Best Local Similarity:	20.9%	Mismatches:	263

Query Match:	7.7%	Index:	1.7%
DB:	2	Gaps:	33

US-10-806-288-12 (1-1/46) X T30290 (1-1463)

## RESULT 15

AAS surface protein - *Staphylococcus saprophyticus*  
130230

C/Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C/Accession: T30290

Mol. Microbiol. 29, 871-881, 1998

A;Accession: T30290  
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-1463 <HEL>  
n;Molecule type: DNA  
A;Cross-references: UNIPROT:O86319. UNIPARC:UPI000000AER76. EMBL:AT000007. NID:ai

C/Genetics: A/Gene: aas

Alignment Scores:  
Pred. No.: 0.000138 Length: 1463

Percent Similarity: 36.3% Conservative: 105  
Best Local Similarity: 20.9% Mismatches: 263

DB:	2	Gaps:	33
-----	---	-------	----

US-10-000-200-12 (1-1/4) X 130250 (1-1403)  
On 1 TOTACGATCACAAGAAATCATCTCATCAATACTCTCAATA----- 48

[illegible]

Db 180 AsnThrAspGluAsnSerSerAspValAlaAsnGlnAsnGluProValAlaGlnAsnAsp 199  
Qy 49 -----AACCCGACGATAATAACCAATAATTAATAAAGAGAAACGAAT 93  
Db 200 LysAlaGluThrSerAsnGluAspValAlaSerSerAspValLysGlnAspGlyThrHis 219  
Qy 94 AACTACGATGGCATAGAAAACGCTCAGAGTAGACAGAGTCAACAACA----- 144  
Db 220 SerAspAspAsnAlaSerAspAspLeuThrAspGlnAsnGluSerGluThrLeuAsnAsp 239  
Qy 145 ---AATGTAGATGAACCGAACCAATTTTACAAAAGACCCCTCAAGATAATACTCAT 201  
Db 240 AsnAlaValSerSerAsnGluAspValAlaSerSerAspValLysGlnAspGlyThrHis 259  
Qy 202 -----CTTACAGAA-----GAAGAGGTAAAAAGAAATCTCTCA 231  
Db 260 SerAspAspAsnAlaSerAspAspLeuThrAspGlnAsnGluSerValAlaGlnAsnAsp 279  
Qy 232 TCAGTCGAATCCTCAAT-----TCATCAATTTGATCTGCCCAACCAACCATCTCAC 282  
Db 280 LysAlaGluThrSerAsnGluAspValAlaSerSerAspValLysGlnAspAspThrHis 299  
Qy 283 ACAACAATAAAT-----AGAGAAGATCTGTTCAAAACAAGTCAAT 324  
Db 300 SerAspAlaAsnAlaSerAspValAlaAspGlnAsnGluSerGluThrGlnAsnAspAsn 319  
Qy 325 GPAGAAGATTACAGTATTCAGATTTTCTAACTCTAAATAAAGAGAGATCAACTGAA 384  
Db 320 AlaGluSerSerAsnGluAspAspValAlaSerSerAspValAsnGlnAspAspThrHis 339  
Qy 385 TCTGCT-----AAAGAGAGATCTATATAGACCACTCAAT--- 420  
Db 340 SerAspAlaAsnAlaSerAspValLysAspGlnAsnGluSerGluThrGlnAsnAsp 359  
Qy 421 -----AAAGTAAAGAGATCAACA 441  
Db 360 LysAlaGluThrSerAsnGluAspAspValAlaSerSerAspValLysGlnAspAspThr 379  
Qy 442 ACAAGT-----CAGCCGCTCGGTATACAAATATAGATGAATAAATTTCAATCAAGAT 495  
Db 380 HisSerAspAlaAsnAlaSerAspAlaAspGlnAsnGluSerValAlaGlnAsnAsp 399  
Qy 496 GAGTATTAAATTTACCAATAATGAATATGAATAAGGCTAGACCATTATCTACAACA 555  
Db 400 LysAla-----GluThrSerAsnGluAspValAlaSerSer 411  
Qy 556 TCTGCCCAACCATCGATTAAACGCTGAACCGTAATCAATTAAGCCGCGAAACAAGGTCG 615  
Db 412 AspLysGlnAspAspThrHisSerAspAlaAsnAlaSerAspAlaAspGlnAsnGlu 431  
Qy 616 AATGTTAACCATTTAATTAAGTTACT-----GATCAAGTATTACTGAAGGATAT 666  
Db 432 SerAlaThrGlnAspAspLysAlaThrSerLysGluAspAspValAlaSerAsnAspLys 451  
Qy 667 GATGATAGT-----GAAGGTGTTATTA-----GCACATGATCTGCAAACTTAATC 714  
Db 452 GlnAspAsnAlaLysValSerAsnIleIleLysGluAlaSerThrAlaGlnAsnLysVal 471  
Qy 715 TATGATGTAACTTTT-----GAAGTAGATGATAAGGTGAATCTGGTGATACGATG--- 765  
Db 472 GlnProAlaThrPheSerAlaLysValThrProLysLeuArgValAlaThrThrSerAla 491  
Qy 766 ---ACAGTGGATATAGATAAGAAATACAGTTCATCAGATTTAAACGATAGCTTTTCAATA 822  
Db 492 AsnThrAlaValAlaThrArgSerAlaValThrLysGluAlaThrThrArgAlaAlaLeu 511  
Qy 823 CCAAAATAAAGATAATTTCTCGAGAAATCATCGCTACAGGTACTTATGATATCAACAAAT 882  
Db 512 ProLysTyr-----Ser 515  
Qy 883 AAACAAATCACCTATCTTTTACAGATTATGTAGATAAGTATGAATAATTAAGCA--- 939  
Db 516 ProLysValAsnSerSerIleAsnAsnTyrIleArgLys---AsnAsnPheLysAlaPro 534

Qy 940 -----CACCTTAATTAACGTCATACATTTGATTAATCAAAAGTTTCCAAATAATAATACC 993  
Db 535 AsnTyrGluGlnAspIleAlaAsnTyrLeuProGlnTyrAsnTyrArgTyrGlyLysPro 554  
Qy 994 AAGTTAGATGTAGATAATAAAACGCCCTTTTCATCAGTAAATAAAACAATTAACGTTGAA 1053  
Db 555 GluGlyIleValMetHisAspThrAla-----AsnAspAsnSerThrIleThrGlyGlu 572  
Qy 1054 TATCAAAAGACCTAAACGAAATCGGACCTGCTAACCTTCAAGCTATGTTTACAAATATAGAT 1113  
Db 573 IleAsnTyrMetLysAsnAsnTyrThr-----SerAlaPheValHisAlaTyr 588  
Qy 1114 ACGAAAATCATACAGTTGACCAACGATTTATTAATTAACCTCTTCGTTTATTCAGCCAG 1173  
Db 589 ValAspGlyAspArgIleIleGluThrAlaAsnThrAspTyrLeuAlaTrpGlyAla--- 607  
Qy 1174 GAAACAAATGTAAATATTTTCAGGGAATGGTGATGAAGGTTCAACAATTTATAGACGATAGC 1233  
Db 608 -----GlyProGlnAlaAsnAspArgPhe 615  
Qy 1234 ACAATAATTAAGTTTATAAGTTTGGAGATTAATCAAAATTTTCCAGATAGTAAACAAT 1293  
Db 616 IleHisValGluLeuValHisThrHisAspTyrAspSerPheAlaArgSer-----Ile 633  
Qy 1294 TATGATTACAGTGAATATGAAGATGTCACAATATGATGATTATGCCCAATTAGGAATAAT 1353  
Db 634 AsnAsnTyrAlaAspTyrAla---AlaThrAsnLeuGlnTyrTyrGlyLeuValProAsp 652  
Qy 1354 AATGATGTGAATATTAATTTTGGTAATATAGATTCACCATATATATTAAAGTTATTAGT 1413  
Db 653 -----SerAlaGluTyrAspGlyValGlyThrValThrHisGlnAlaValSer 669  
Qy 1414 AAATAT-----GACCTTAAT----- 1428  
Db 670 AsnTyrLeuGlyGlySerAspHisSerAspProHisGlyTyrLeuAlaAlaHisAsnTyr 689  
Qy 1429 -----AAGGATGATTACACGACTATACAGCAACTGTGACAAATCGACAGTACTATAAT 1482  
Db 690 SerTyrAspGluLeuTyrAspLeuIleTyrGluLysTyrLeuIleLysThrGly----- 707  
Qy 1483 GAGTATACCTGGTGGATTTAGAACACGATCTATGATAATAACAATTTCTCTCTACA--- 1539  
Db 708 -----GlnAlaAlaAlaTrpGlyThrThrSerSerGlySerThrGly 721  
Qy 1540 -----AGTTACAGTCAAGGACAA---GGTGACTTGCCTCTCTGAAAAA----- 1578  
Db 722 GlyThrGlyGlySerThrGlySerGlyAsnThrGlyThrThrProProSerLysSerGly 741  
Qy 1579 ACTTATAAATCGGAGATTTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAAATACA 1638  
Db 742 ThrValLysVal-----ThrGluAsnAsnGlyValGlyArgIle 754  
Qy 1639 AATGATAATGAACACCGCTTAGTAATATGTTGGTAACCTTTGACGCTATCTCTGATGAACT 1698  
Db 755 AsnSerLys-----AsnAspGlyLeuTyrThrThrValTyrAspGlnLysGly 770  
Qy 1699 TCAAAATCAGTCAGAACAGATGAAGAT-----GGGAAA 1731  
Db 771 LysLysThrAspArgValAsnGlnThrLeuLysValThrLysSerAlaThrLeuGlyLys 790  
Qy 1732 TATCAATTT 1740  
Db 791 GluGlnTyr 793

Search completed: August 12, 2006, 08:12:19  
Job time : 110.5 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 12, 2006, 07:41:50 ; Search time 106.6 Seconds  
(without alignments)  
4545.245 Million cell updates/sec

Title: US-10-806-288-12  
Perfect score: 3026  
Sequence: 1 tctagtgtatgaagaaagaa.....ggaatatcatattgatgga 1746

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+n2p.model -DEV=xlp  
-O=/abs/ABSSWEB/spool/US10806288/runat\_11082006\_163406\_21093/app\_query.fasta\_1  
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p  
-USER=US10806288 @CGN 1 1 891 @runat\_11082006\_163406\_21093 -NCPU=6 -ICPU=3  
-NO MAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3013	99.6	1056	2 Q8CQ72 STABS	Q8CQ72 staphylococ
2	3013	99.6	1092	2 Q70022 STAEQ	Q70022 staphylococ
3	2810.5	92.9	892	2 Q5HR16 STAEQ	Q5HR16 staphylococ
4	2810.5	92.9	931	2 Q9K113 STAEQ	Q9K113 staphylococ
5	1209.5	40.0	1137	2 Q6GJA6 STAAE	Q6GJA6 staphylococ
6	1185	39.2	1113	2 Q2YSA1 STAAE	Q2YSA1 staphylococ
7	1160.5	38.4	1171	2 Q9KWX6 STAAU	Q9KWX6 staphylococ
8	1144.5	37.8	1166	2 Q86489 STAAU	Q86489 staphylococ
9	1143.5	37.8	1141	2 Q6GBS4 STAAE	Q6GBS4 staphylococ
10	1143.5	37.8	1141	2 Q8NXX5 STAAW	Q8NXX5 staphylococ
11	1142.5	37.8	1166	2 Q5HIB2 STAAE	Q5HIB2 staphylococ
12	1137.5	37.6	1141	2 Q932F7 STAAE	Q932F7 staphylococ
13	1137.5	37.6	1141	2 Q99W46 STAAE	Q99W46 staphylococ
14	1018	33.6	444	2 Q2UW65 STAAU	Q2UW65 staphylococ
15	1018	33.6	444	2 Q2UW70 STAAU	Q2UW70 staphylococ
16	973	32.2	444	2 Q2UW91 STAAU	Q2UW91 staphylococ

17	969	32.0	444	2 Q2UW60 STAAU	Q2UW60 staphylococ
18	968	32.0	444	2 Q2UW93 STAAU	Q2UW93 staphylococ
19	966	31.9	444	2 Q2UW63 STAAU	Q2UW63 staphylococ
20	966	31.9	444	2 Q2UWA0 STAAU	Q2UWA0 staphylococ
21	965	31.9	444	2 Q2UW74 STAAU	Q2UW74 staphylococ
22	965	31.9	444	2 Q2UW96 STAAU	Q2UW96 staphylococ
23	962	31.8	444	2 Q2UW77 STAAU	Q2UW77 staphylococ
24	952	21.5	1563	2 Q4LAH6 STAHJ	Q4LAH6 staphylococ
25	576	19.0	1315	2 Q86488 STAAU	Q86488 staphylococ
26	576	19.0	1381	2 Q5HIB3 STAAC	Q5HIB3 staphylococ
27	567	18.7	1347	2 Q8NXX6 STAAW	Q8NXX6 staphylococ
28	567	18.7	1365	2 Q6GBS5 STAAE	Q6GBS5 staphylococ
29	559	18.5	1385	2 Q7A780 STAAE	Q7A780 staphylococ
30	559	18.5	1385	2 Q99W47 STAAE	Q99W47 staphylococ
31	499	16.5	1733	2 Q9KI14 STAEQ	Q9KI14 staphylococ
32	497	16.4	1633	2 Q8CMP4 STAES	Q8CMP4 staphylococ
33	489	16.2	953	2 Q7A781 STAAE	Q7A781 staphylococ
34	489	16.2	953	2 Q99W48 STAAE	Q99W48 staphylococ
35	485.5	16.0	1893	2 Q8KWM1 STASA	Q8KWM1 staphylococ
36	478.5	15.8	906	2 Q6GJA7 STAAE	Q6GJA7 staphylococ
37	470.5	15.5	928	1 CLFA STAAE	Q6GB45 staphylococ
38	470.5	15.5	946	1 CLFA STAAW	Q6GB45 staphylococ
39	465	15.4	955	2 Q8NXX7 STAAW	Q8NXX7 staphylococ
40	465	15.4	957	2 Q6GBS6 STAAE	Q6GBS6 staphylococ
41	460.5	15.2	881	2 Q93MH7 STALU	Q93MH7 staphylococ
42	458.5	15.2	566	2 Q8KR22 STAP	Q8KR22 staphylococ
43	456	15.1	1029	1 CLFA STAAE	Q6GJA7 staphylococ
44	455	15.0	933	1 CLFA STAAC	Q6GJA7 staphylococ
45	455	15.0	947	2 Q86487 STAAU	Q86487 staphylococ

## ALIGNMENTS

RESULT 1  
Q8CQ72 STABS  
ID Q8CQ72 STABS PRELIMINARY; PRT; 1056 AA.  
AC Q8CQ72;  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 22.  
DE Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein.  
GN OrderedLocNames=SE0331; ORFNames=SE 0331;  
OS Staphylococcus epidermidis (strain ATCC 12228).  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=176280;  
RN [1]\_\_  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=12950922; DOI=10.1046/j.1365-2958.2003.03671.x;  
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,  
RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,  
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;  
RT "Genome-based analysis of virulence genes in a non-biofilm-forming  
RT Staphylococcus epidermidis strain (ATCC 12228).";  
RL Mol. Microbiol. 49:1577-1593(2003).  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License

-----  
EMBL; AB015929; AA003928.1; -; Genomic\_DNA.  
DR HSSP; Q53653; IN67.  
DR SMR; Q8CQ72; 278-598.  
DR BioCyc; SEPI176280:SE0331-MONOMER; -.  
DR GO; GO:0009986; C:cell surface; IEA.  
DR GO; GO:0005618; C:cell wall; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR InterPro; IPR008454; Cna B.  
DR InterPro; IPR005877; Gpof\_Ysirk.  
DR InterPro; IPR001899; Gram\_pos\_anchor.  
DR Pfam; PF05738; CnaB; 2.  
DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
DR Pfam; PF02412; TSP\_3; 1.

DR Pfam: PF04650; YSIRK signal; 1.  
 DR TIGRPFAMs; TIGR01167; LPXTG anchor; 1.  
 DR TIGRPFAMs; TIGR01168; YSIRK signal; 1.  
 DR PROSITE; PS00847; GRAM\_POS ANCHORING; 1.  
 DR Cell wall; Complete proteome; Peptidoglycan-anchor.  
 SW SEQUENCE 1056 AA; 115728 MW; 015869A9E5CA2723 CRC64;

## Alignment Scores:

Pred. No.: 1.38e-138 Length: 1056  
 Score: 3013.00 Matches: 582  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 99.6% Indels: 0  
 DB: 2 Gaps: 0

US-10-806-288-12 (1-1746) x Q8CQ72\_STABs (1-1056)

QY 1 TCCTAGTGAAGAAAGAAATGATGTCATTAATAATCACTCAATATAACACACGACGAT 60  
 DB 75 SerSerAspGluGluLysAsnAspValIleAsnAsnGlnSerIleAsnThrAspAsp 94  
 QY 61 AATAACCAATTAATAAAGAAAGAAACGAATAACTACGATGGCATAGAAAAACGCTCA 120  
 DB 95 AsnAsnGlnIleIleLysLysGluGluThrAsnAsnTyrAspGlyIleGluLysArgSer 114  
 QY 121 GAAGATAGACAGACTCAACAACAATGTAGATGAAGAAAGCAACATTTTACAAAAG 180  
 DB 115 GluAspArgThrGluSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 134  
 QY 181 ACCCTCAAGATAATACCTCATACAGAAGAGAGTAAAGAAATCCTCATAGTCGAA 240  
 DB 135 ThrProGlnAspAsnThrHisLeuThrGluGluLysLysGluSerSerValGlu 154  
 QY 241 TCCTCAAAATTCATTAATGATCTGCCCAACCAACCATCTCAACAACAATAAATAGAGAA 300  
 DB 155 SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrThrIleAsnArgGlu 174  
 QY 301 GNACTGTTCACACAGTGATANTGTAGNAGTTACACGGTATCAGATTTTGTCACTCT 360  
 DB 175 GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer 194  
 QY 361 AAAATAAAGAGAGTAACACCTGTAAGTAAAGAGAGATCTATAGAGCAACCTAAT 420  
 DB 195 LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn 214  
 QY 421 AAGTAAAGAGATTCACAAACAAGTCAGCGCTCTGCTATACAAATATAGATGAAGAAA 480  
 DB 215 LysValLysGluAspSerThrThrSerGlnProSerGlyTyrThrAsnIleAspGluLys 234  
 QY 481 ATTTCAAAATCAGATGAGTTATTAATTTACCAATATGAATGAATAAGCTAGA 540  
 DB 235 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysAlaArg 254  
 QY 541 CCATTATCTACAACTCTGCCCAACCATCGATTAAACGTTAAACCGTAAATCAATTAGCG 600  
 DB 255 ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla 274  
 QY 601 GCGGAACAAGGTTGCAATGTTAAACCATTTAATAAAGTTACTGATCAAAAGTATTACTGAA 660  
 DB 275 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 294  
 QY 661 GGATATGATGATAGTGAAGGTGTTAATAAGCCACATGATGCTGAAAATCTTAATCTATGAT 720  
 DB 295 GlyTyrAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 314  
 QY 721 GTAACCTTTTGAAGTATAGATGAAGTGAATCTGCTGATACGATCAGATGGATATAGAT 780  
 DB 315 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAspIleAsp 334  
 QY 781 AAGAAATACAGTTCCATCAGATTAAACCGATAGCTTTTACAATACCAAAAAATAAAGATTAAT 840  
 DB 335 LysAsnThrValProSerAspLeuThrAspSerPheThrIleProLysIleLysAspAsn 354

QY 841 TCTGAGAAATCATCGCTACAGGTACTATTGATAACAAAATAAACAAATCACCTATACT 900  
 DB 355 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnLysAsnLysGlnIleThrTyrThr 374  
 QY 901 TTTACAGATTATGTAGATAAGTATGAAATATATAAGCACACCTTAAATTAACGTCATAC 960  
 DB 375 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 394  
 QY 961 ATTGATTAATCAAAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATATAAAGCGCC 1020  
 DB 395 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 414  
 QY 1021 CTTTCATCAGTAAATAAAACAATTTACGTTGCAATATCAAGACACCTAACGAAAAATCGGACT 1080  
 DB 415 LeuSerSerValAsnLysThrIleThrValGluTyrGlnArgProAsnGluAsnArgThr 434  
 QY 1081 GCTAACCTTCAAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTTGAGCAACG 1140  
 DB 435 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 454  
 QY 1141 ATTTATATTAACCTCTTCGTTATTACGCCAGGAAACAATGTAATATTTTCAGGGAAT 1200  
 DB 455 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 474  
 QY 1201 GGTGATGAAGGTTCAACAATTTATAGACGATAGCAACAATTAATAAGTTTATAAGCTTGA 1260  
 DB 475 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 494  
 QY 1261 GATAATCAAAATTTACAGATAGTAACAGAAATTTATGATTAACAGTGAATATGAAGATGC 1320  
 DB 495 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 514  
 QY 1321 ACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 DB 515 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 534  
 QY 1381 ATAGATTACCATATATTTATAAGTTATTAGTAAATATAGACCTTAATAAGGATGATTAC 1440  
 DB 535 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 554  
 QY 1441 ACGATATACAGCAAACTGTGACAATCGACAGCTATATAATGATGATGATGATGATGATGAT 1500  
 DB 555 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 574  
 QY 1501 AGACAGATCCTATGATATACAAATTCCTTCTCTACAGTTTCAGTTCAGTTCAGTTCAGTTCAGT 1560  
 DB 575 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 594  
 QY 1561 GACTTGCTCTCGAAAAAACTTATAAAATCGAGATTACGATGCGAAGATGTAGATAAA 1620  
 DB 595 AspLeuProGluLysThrTyrLysIleGlyAspTyrValTyrGluAspValAspLys 614  
 QY 1621 GATCGTATTCAAAATACAAATGATGATAAAGAAACCGCTTAGTATGATGATGATGATGATGAT 1680  
 DB 615 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 634  
 QY 1681 ACGTATCCTGATGAACTTCAAAATCAGTCAGACAGATGAGATGGGAATATCAATTT 1740  
 DB 635 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluAspGlyLysTyrGlnPhe 654  
 QY 1741 GATGGA 1746  
 DB 655 AspGly 656

## RESULT 2

O70022 STABP PRELIMINARY; PRT; 1092 AA.  
 ID O70022 STABP  
 AC O70022  
 DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.  
 DT 01-FEB-1998, sequence version 1.  
 DT 07-FEB-2006, entry version 28.  
 DE Fibrinogen-binding protein precursor.  
 OS Staphylococcus epidermidis.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1282;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=HB;  
 RA MEDLINE=98261511; PubMed=9596732;  
 RX Nilsson M., Frykberg L., Flock J.I., Pei L., Lindberg M., Guss B.;  
 RT "A fibrinogen-binding protein of Staphylococcus epidermidis";  
 RL Infect. Immun. 66:2666-2673(1998).  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; Y17116; CAA76638.1; -; Genomic\_DNA.  
 DR FIR; T30214; T30214.  
 DR HSP; Q53653; I167.  
 DR SMR; O70022; 278-598.  
 DR GO; GO:0003986; C:cell surface; IEA.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0007155; P:cell adhesion; IEA.  
 DR InterPro; IPR008454; Cna B.  
 DR InterPro; IPR005877; Gpos\_Ysirk.  
 DR InterPro; IPR001899; Gram\_pos\_anchor.  
 DR Pfam; PF05738; Cna B; 2.  
 DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
 DR Pfam; PF02412; TSP\_3; 1.  
 DR Pfam; PF04650; Ysirk\_signal; 1.  
 DR TIGRFAMs; TIGR01167; LPXG\_anchor; 1.  
 DR TIGRFAMs; TIGR01168; Ysirk\_signal; 1.  
 DR PROSITE; PS00847; GRAM\_POS\_ANCHORING; 1.  
 KW Cell wall; Peptidoglycan-anchor; Signal.  
 FT SIGNAL 1 51 potential.  
 FT CHAIN 52 1092 fibrinogen-binding protein.  
 SQ SEQUENCE 1092 AA; 119293 MW; 6542BC39AD8B984 CRC64;

Alignment Scores:  
 Pred. No.: 1.38e-138 Length: 1092  
 Score: 3013.00 Matches: 582  
 Percent Similarity: 100.0% Conservatives: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 99.6% Indels: 0  
 DB: 2 Gaps: 0

US-10-806-288-12 (1-1746) x O70022\_STAEP (1-1092)

QY 1 TCTAGTGATGAAGAAAGATGATGTGATCAATAATATCACTCAATAAACACCGCAT 60  
 DB 75 SerSerAspGluGluLysAsnAspValIleAsnAsnAsnGlnSerIleAsnThrAspAsp 94  
 QY 61 AATAACCAATATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120  
 DB 95 AsnAsnGlnIleIleLysLysGluGluThrAsnAsnThrAspGlyIleGluLysArgSer 114  
 QY 121 GAAGATAGACAGAGTCAACAAATAGTAGATGAAGAAAGAAAGAAAGAAAGAAAGAAAG 180  
 DB 115 GluAspArgThrGluSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 134  
 QY 181 ACCCTCTCAAGATAACTCTTACAGAAAGAGAGTAAAGAAATCCTCATCGTCA 240  
 DB 135 ThrProGlnAspAsnThrHisLeuThrGluGluValLysGluSerSerValGlu 154  
 QY 241 TCCTCAATTCATCAATTCATCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 300  
 DB 155 SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrThrIleAsnArgGlu 174  
 QY 301 GAATCTGTTCAACAAAGTGAATGTAGAAGATTCACAGTATCAGATTTCTCACTCT 360  
 DB 175 GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer 194  
 QY 361 AAAATAAAGAGAGTAACTCACTCGTAAAGAGAGAAATCTATAGACCACTAAT 420

Db 195 LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn 214  
 QY 421 AAAAGTAAAGAGATTCACAAACAAAGTTCAGCCGTCTGCTATACAAATATAGATGAAAAA 480  
 DB 215 LysValLysGluAspSerThrThrSerGlnProSerGlyThrAsnIleAspGluLys 234  
 QY 481 ATTTCAAATCAAGATGAGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540  
 DB 235 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrgluAsnLysAlaArg 254  
 QY 541 CCATTATCTACAACTCTGCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 600  
 DB 255 ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla 274  
 QY 601 GCGGAACAAAGTTCCGAATGTTAAACCATTTAAATTAAGTTACTGATCAAAAGTATTACTGA 660  
 DB 275 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 294  
 QY 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
 DB 295 GlyTyrAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 314  
 QY 721 GTAACTTTTGAAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 DB 315 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAspIleAsp 334  
 QY 781 AAGATAACAGTTCCATCAGATTACCGATTTACCAATGATCTTTACCAATGATCTTTACCA 840  
 DB 335 LysAsnThrValProSerAspLeuThrAspSerPheThrIleProLysIleLysAspAsn 354  
 QY 841 TCTGGAGAAATCATCGCTACAGGTACTTATGATGATGATGATGATGATGATGATGATGAT 900  
 DB 355 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnLysAsnLysGlnIleThrTyrThr 374  
 QY 901 TTTACAGATTATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 DB 375 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 394  
 QY 961 ATTGATAAATCAAGGTTCCAAATTAATAATACCAAGTTAGATGATGATGATGATGATGAT 1020  
 DB 395 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 414  
 QY 1021 CTTTCATCAGTAAATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080  
 DB 415 LeuSerSerValAsnLysThrIleThrValGluTyrGlnArgProAsnGluAsnArgThr 434  
 QY 1081 GCTAACCTTCAAGTATGTTTACAAATATAGATGATGATGATGATGATGATGATGATGAT 1140  
 DB 435 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 454  
 QY 1141 ATTTATATTAACCTCTCTTCGTTTATTCAGCAAGGAAACAAATGTAATATTTTTCAGG 1200  
 DB 455 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 474  
 QY 1201 GGTGATGAAGGTTCAACAAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1260  
 DB 475 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 494  
 QY 1261 GATTAATCAAAATTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
 DB 495 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 514  
 QY 1321 ACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
 DB 515 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 534  
 QY 1381 ATAGATTCCCATATATTATTAAAGTTATTAGTAAATATGACCCCTTAATAAGGATGATTAC 1440  
 DB 535 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 554  
 QY 1441 ACGACTATACAGCAACTGTGCAATGCAAGCAGCATTAATTAATGATGATGATGATGATGAT 1500  
 DB 555 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 574

```

QY 1501 AGAAGCATCTATGATAATACAAATGCTTTCTTACAAAGTTCAGGTCAAGGACAAGGT 1560
DB 575 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 594
QY 1561 GACTTGCTCTCTGAAAAAAGTATATAAATCGAGATTACGTATGGGAAGATGTAGATAAA 1620
DB 595 AspLeuProGluLysThrTyrLysIleGlyAspTyrValTTPGluAspValAspLys 614
QY 1621 GATGTATTCAAATACAAATGATATGAAAAACCGCTTAGTAAATGATTGTTGTTGTTG 1680
DB 615 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 634
QY 1681 ACGTATCTGATGGAACCTTCAAAATCAGTCAGACAGATGAAGATGGGAAATATCAATTT 1740
DB 635 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluAspGlyLysTyrGlnPhe 654
QY 1741 GATGGA 1746
DB 655 AspGly 656

RESULT 3
Q5HR16_STAEQ PRELIMINARY; PRT; 892 AA.
AC Q5HR16;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE SdrG protein.
GN OrderedLocNames=SRP0207;
OS Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=176279;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RA "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RL J. Bacteriol. 187:2426-2438(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DB EMBL; CP000029; AAW53571.1; -, Genomic_DNA.
DR TIGR; SRP0207; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008454; CnaB.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF05738; CnaB; 2.
DR Pfam; PF02412; TSP_3_1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
SQ Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 892 AA; 98747 MW; EC35C932B588F497 CRC64;

Alignment Scores:
Pred. No.: 9,59e-129 Length: 892
Score: 2810.50 Matches: 545
Percent Similarity: 96.2% Conservative: 15
Best Local Similarity: 93.6% Mismatches: 21
Query Match: 92.9% Indels: 1

```

```

DB: 2 Gaps: 1
US-10-806-288-12 (1-1746) x Q5HR16_STAEQ (1-892)
QY 1 TCTAGTGAAGAAAAAGAAATGATGTGATCAATTAATCAATCAATCAATCAATCAATCAATCAAT 60
DB 35 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 54
QY 61 AATACCAATTAATTAATAAAGAAAGAAACCAATTAACATGATGCGATGCAATGAAACCAAGCTCA 120
DB 55 AspAsnGln---IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer 73
QY 121 GAAGATGACAGAGTCAACAAACAAATGTAGATCAAAACGAAGCAACATTTTACAAAAG 180
DB 74 LysAspIleThrGlnSerThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 93
QY 181 ACCCTCAAGATATATCTCATCTTACAGAGAAGAGGTAAAGAATCCTCATAGTCAAA 240
DB 94 ThrProGlnAspAsnThrGlnLeuLysGluGluValValLysGluProSerSerValGlu 113
QY 241 TCCTCAATTCATCAATTTGATCTACTGCCCAACCAACCATCTCACACAATAAATAGAGAA 300
DB 114 SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu 133
QY 301 GAATCTGTTCAACCAAGTGAATGTAGAAGATTCAACAGTATCAGATTTTGTAACTCT 360
DB 134 AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer 153
QY 361 AAAATAAAGAGAGTAACACTGAATCTGGTAAAGAGAGAAATATCTATAGACAACTTAAT 420
DB 154 LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn 173
QY 421 AAAGTAAAGAGAGATTCAACCAACCAAGTCAGCCGCTCGCTATACAAATATATAGATGAAAA 480
DB 174 LysValArgGluAspSerIleThrSerGlnProSerSerTyrLysAsnIleAspGluLys 193
QY 481 ATTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAAATAAGGCTAGA 540
DB 194 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysValArg 213
QY 541 CCATTATCTCAACATCTGCCCAACCATTCGATTAAACGTGTAAACGTGTAAATCAATTAGCG 600
DB 214 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 233
QY 601 GCGCAACAAGSTTCGAATGTTAACCATTTAATTAAGTCTCTGATCAAGATTTACTGAA 660
DB 234 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 253
QY 661 GGATATGATGATGATGAAGGTGTTATTAAAGACATGATGCTGAAAACCTTAACTTATGAT 720
DB 254 GlyTyrAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 273
QY 721 GTAACCTTTGAAGATGATGATGAAGTGAATCTCGGTGATACGATGACAGTGGATATAGAT 780
DB 274 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 293
QY 781 AAGNATACAGTCTCCATCAGATTTTAACCGATAGCTTTTACAATACCAAAAATAAAGATATAT 840
DB 294 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 313
QY 841 TCTGAGAGAAATCATCGCTACAGGTACTTATGATTAACAAAATAAACAATAACCTTACTACT 900
DB 314 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr 333
QY 901 TTTCACAGATTATGTAGATAAGTATGAAAAATATTAAGCACACCTTAATTAACGTCTATAC 960
DB 334 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 353
QY 961 ATTGATTAATCAAGGTTCCAAAATAAATAATACCAAGTTAGATGTAGATATAAACAAGGCC 1020
DB 354 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 373
QY 1021 CTTTTCATCAGTAAATAAACAATTTACGGTTGAATATCAAGACCTCAAGAAATCGGACT 1080

```

Db 374 LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr 393  
 QY 1081 GCTAACCTCTCAAGTATGTTTACAAATATAGATACGAAATAATCATACAGTTGAGCAACG 1140  
 Db 394 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 413  
 QY 1141 ATTATATTAACTCTCTGTTATTCAGCAAGAAACAAATGTAATATTTTCAAGGAAT 1200  
 Db 414 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 433  
 QY 1201 GGTGATGAAGGTTCAACATTTAGACGATAGACACAAATTAATTAAGTTTATAGGTTGCA 1260  
 Db 434 GlyAspGluGlySerThrIleIleAspSerThrIleIleLysValTyrLysValGly 453  
 QY 1261 GATAATCAAAATTTACCATAGTATACAGAAATTTATGATTACAGTCAATATCAAGATGTC 1320  
 Db 454 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 473  
 QY 1321 ACAATGATGATATGCCCAATAGGAATAATATGATGTGAATATTTTGTGAAT 1380  
 Db 474 ThrAsnAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn 493  
 QY 1381 ATAGATTCCACATATATTAAAGTTATTAGTAATATGACCTTAATAGGATGATTAC 1440  
 Db 494 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 513  
 QY 1441 ACCACTATACAGCAAACTGTGCAATGTCAGACACTATAAATGAGTATATCTGTGAGTTT 1500  
 Db 514 ThrThrIleGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 533  
 QY 1501 AGAACAGCATCTTATGATTAATACAAATGCTTTCTCTACAGTTCAAGTCAAGCAAGGT 1560  
 Db 534 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 553  
 QY 1561 GACTTCCCTCTCGAAAAACTTATAAATCGGAGATTACGTATCGGAAGATGTAGATAAA 1620  
 Db 554 AspLeuProProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys 573  
 QY 1621 GATGGTATTCAAAATACAAATGATTAATGAAAAACCGCTTAGTAATGTTTGTGTACTTTG 1680  
 Db 574 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 593  
 QY 1681 ACGTATCTGTGAGAACTTCAAAATCAGTCAGAACAGATGAAGTGGGAAATATCAATTT 1740  
 Db 594 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyrGlnPhe 613  
 QY 1741 GATGCA 1746  
 Db 614 AspGly 615

RESULT 4  
 Q9K113 STAEF  
 ID Q9K113 STAEF PRELIMINARY; PRT; 931 AA.  
 AC Q9K113;  
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 23.  
 DE Fibrinogen-binding protein SdrG.  
 GN Name=sdrG;  
 OS Staphylococcus epidermidis.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1282;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K28;  
 RX MEDLINE=20340957; PubMed=10878118;  
 RA McCrea K.W., Hartford O., Davis S., Ni Eidhin D., Lina G.,  
 RA Speziale P., Foster T.J., Hook M.,  
 RT "The serine-aspartate repeat (Sdr) protein family in Staphylococcus  
 RT epidermidis.";  
 RL Microbiology 146:1535-1546(2000).  
 CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 CC EMBL; AF245042; AAF72510.1; -; Genomic\_DNA.  
 DR PDB; 1RL7; X-ray; A/B=274-598.  
 DR PDB; 1RL9; X-ray; A/B/C/D=274-598.  
 DR GO; GO:0009986; C:cell surface; IEA.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0007155; P:cell adhesion; IEA.  
 DR InterPro; IPR008454; Cna\_B.  
 DR InterPro; IPR005877; Gpos\_Y5IRK.  
 DR InterPro; IPR001899; Gram\_pos\_anchor.  
 DR Pfam; PF05738; Cna B; 2.  
 DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
 DR Pfam; PF02412; TSP\_3; 1.  
 DR Pfam; PF04650; Y5IRK\_signal; 1.  
 DR TIGRFAMs; TIGR01167; LPXTG\_anchor; 1.  
 DR TIGRFAMs; TIGR01168; Y5IRK\_signal; 1.  
 DR PROSITE; PS50847; GRAM\_POS\_ANCHORING; 1.  
 KW Cell wall; Peptidoglycan-anchor.  
 SQ SEQUENCE 931 AA; 102956 MW; 591E657D97027116 CRC64;

## Alignment Scores:

Pred. No.: 9,54e-129 Length: 931  
 Score: 2810.50 Matches: 545  
 Percent Similarity: 96.2% Conservative: 15  
 Best Local Similarity: 93.6% Mismatches: 21  
 Query Match: 92.8% Indels: 1  
 DB: 2 Gaps: 1

US-10-806-288-12 (1-1746) x Q9K113\_STAEF (1-931)

QY 1 TCTAGTGTGAGAAAGAAATGATGTGATCAATAATAATCATCAATAAATCAACACCGAGAT 60  
 Db 74 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 93  
 QY 61 AATAACCAATAATTAATAAAGAAAGAAAGAAATCACTACGATGGCATAGAAAAACGCTCA 120  
 Db 94 AspAsnGln---IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer 112  
 QY 121 GAAGTAGAAGACAGAGTCAACAAATGTAGATGAAACGAAGCAACATTTTACAAAAG 180  
 Db 113 LysAspIleThrGlnSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 132  
 QY 181 ACCCTCAAGATAATACTCATCTTACAGNAGAGAGTAAAGAAATCTCATCAGTCGAA 240  
 Db 133 ThrProGlnAspAsnThrGlnLysLysGluGluValLysGluProSerSerValGlu 152  
 QY 241 TCCTCAAAATTCATCAATTGATCTGCCCAACCAACCATCTCACACAACATAAATAGAGAA 300  
 Db 153 SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu 172  
 QY 301 GAATCTGTTCAACAAAGTGATAATGTAGAAGATTCCACGATCATCAGATTTTCTAACTCT 360  
 Db 173 AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer 192  
 QY 361 AAAATAAAGAGAGTAAACACTGAATCTGTGTAAGAAGAGAGATATCTATAGAGCAACTAAT 420  
 Db 193 LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn 212  
 QY 421 AAAGTAAAGAGAGATTCAACAAACAGTCAGCGCTCTGGCTATACAAATATAGATGAAAA 480  
 Db 213 LysValArgGluAspSerIleThrSerGlnProSerSerTyrLysAsnIleAspGluLys 232  
 QY 481 ATTTCAAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAAAAATAGGCTAGA 540  
 Db 233 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysValArg 252  
 QY 541 CCATATCTACAACTCTGCCCAACCATCGATTAAACGTGTAAACGTTAAATCAATAGCG 600  
 Db 253 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 272

```
QY 601 GCGNACAAAGGTTGGAATGTTAAACCACTTAATTAAGTTACTGATCAAGATTAATCTGAA 660
Db 273 AlaGluGlnGlySerAsnValAsnHisLeuLeuLeuValThrAspGlnSerIleThrGlu 292
QY 661 GGATATGATGATAGTGAAGGTGTTATTAAAGCACATGATGCTGMAAACTTAATCTATGAT 720
Db 293 GlyTyrAspAspSerAspGlyIleIleLeuValHisAspAlaGluAsnLeuIleTyrAsp 312
QY 721 GTAACCTTTGAAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAGTGGATATAGAT 780
Db 313 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 332
QY 781 AAGATACAGTTCAGTCAAGTTAAACCGATAGCTTTACAAATACCAAAATAAAGATTAAT 840
Db 333 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLeuAspAsn 352
QY 841 TCTGGAGAAATCATCGCTACAGGTACTTATGATACAAATAAACAATACACCTATACT 900
Db 353 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrTyrThr 372
QY 901 TTTACAGATTATGTAGATGATAAGTATGAAATATTAAGCACACCTTTAAATTAACGTATAC 960
Db 373 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLeuLeuThrSerTyr 392
QY 961 ATTGATTAATCAAGGTTCCAAATTAATTAACCAAGTTAGATGTAGATATATAAACGGCC 1020
Db 393 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 412
QY 1021 CTTTCATCAGTAAATAAACAATTAACGGTCAATCAAGACCTTAACGAAATTCGGACT 1080
Db 413 LeuSerSerValAsnLysThrIleThrValGluTyrGlnLysProAsnGluAsnArgThr 432
QY 1081 GCTAACCTTCAAGTATGTTCAAAATATAGATACGAAATAATCATACAGTTGAGCAACG 1140
Db 433 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 452
QY 1141 ATTTATATTAACCTCTTCGTTATTCAGCCAGGNAACAATGTAAATATTTTCAGGGAT 1200
Db 453 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 472
QY 1201 GGTGATGAAGGTTCAACAAATTATAGACGATAGCACAATAATTAAGTTTATAAGTTGGA 1260
Db 473 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 492
QY 1261 GATTAATCAAAATTTACAGATAGTAAACAAGATTTATGATTAACAGTGAATATGAAGATGC 1320
Db 493 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 512
QY 1321 ACAATGATGATTATGCCCATTAGGCAATATATGATGATGATGATTAATTAATTTTGGTAA 1380
Db 513 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 532
QY 1381 ATAGATTCCACATATATTATTAAGTTATTAGTAAATATGACCCCTTAATAAGATGATTAC 1440
Db 533 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 552
QY 1441 ACGACTATACAGCAAACTGTGACAAATGACAGCAGCTATATAATGATGATATCTGGTGAGTT 1500
Db 553 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 572
QY 1501 AGACAGCATCTATGATATATACATTTCTTCTACAGTTCCAGTTCAGGACAGGACAGGT 1560
Db 573 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 592
QY 1561 GACTTGCCTCTCGAAAAAATTTATAAAATCGAGATTACGATGCGAAGATGTAGATAAA 1620
Db 593 AspLeuProProGluLysThrTyrLysIleGlyAspTyrValTyrGluAspValAspLys 612
QY 1621 GATGTTATTTCAAAATACAAATGATTAATGAAAAACCGCTTAGTATGATTTGGTAACTTTG 1680
Db 613 AspGlyIleGlnAsnThrAsnAspAsnGlnLysProLeuSerAsnValLeuValThrLeu 632
```

```
QY 1681 ACGTATCTGATGCAACTTCAAAATCAGTCAGAACAGATGAAGTGGAAATATCAATTT 1740
Db 633 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyrGlnPhe 652
QY 1741 GATCGA 1746
Db 653 AspGly 654

RESULT 5
Q6GJA6_STAAR PRELIMINARY; PRT; 1137 AA.
ID Q6GJA6_STAAR
AC Q6GJA6
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Bone sialoprotein-binding protein.
GN Name=bbp; OrderedLocusNames=SA0567;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC EMBL; BX571856; CAG39588.1; -; Genomic_DNA.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; P:calcium ion binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003367; tsp_3.
DR Pfam; PF05738; Cna_B; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02412; TSP_3; 3.
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1137 AA; 123326 MW; 2C7DB7BABDC8FB81 CRC64;

Alignment Scores:
Pred. No.: 5,1e-51 Length: 1137
Score: 1209,50 Matches: 279
Percent Similarity: 60.2% Conservat: 98
Best Local Similarity: 44.8% Mismatches: 180
Query Match: 40.0% Indels: 69
DB: 2 Gaps: 20

US-10-806-288-12 (1-1746) x Q6GJA6_STAAR (1-1137)
```

QY 1 TCTAGTCAATGAGAAAGAATGAT-----GTGATCAATAATATATCAGTCAATAAAC 51

Db 57 SerThrGluAsnAlaLysGlnAspGluAlaSerAlaSerAspAsnLysGluValSer 76





Qy	829	ATAAAGATAATTTCTGGAGAAATCATCGCTACAGGTACTTATGNTACACAAAATAAACA	888
Db	344	IleThrAspProSerGlyGluValIleAlaLysGlyThrPheAspValAsnThrAsnThr	363
Qy	889	ATCACCTATATCTTTTACAGATTAATGTAGATAAGTATGAAAAATATTAAGACACACCTTAA	948
Db	364	IleThrTyrLysPheThrAspTyrValAspArgTyrGluAsnValAsnAlaLysLeuGlu	383
Qy	949	TTAACGTCATACATTGATAAATCAAAGTTTCCAAATAAATAATACCAAGTTAGATGTAGA	1008
Db	384	LeuAsnSerTyrIleAspLysLysThrValPro---AsnGluAlaAsnIleAsnLeuThr	402
Qy	1009	TATAAAGCGCTTTTCATCAGTAATAATAAAACAATACGTTCAAGTATCAAGACCTTAAC	1068
Db	403	PheGlyThrAlaAspLysGluThrSerLysAsnValAsnValGluTyrGlnLysProIle	422
Qy	1069	GAATAACGGACTGCTAACCTTCAAAGTATGTTTCAAAATATAGATACGAAAAATCATACA	1128
Db	423	ValLysAspGluSerAsnIleGlnSerIlePheSerHisLeuAspThrThrLysHisGlu	444
Qy	1129	GTTGAGCAAAAGCATTTATATAACCTCTTCGTTTTCAGCCAAAGGAAACAATGTAAAT	1188
Db	443	ValGluGlnThrIleTyrValSerProLeuLysLeuAsnAlaLysAsnThrAsnValThr	462
Qy	1189	ATT-----TCAGGGAATGGTGAT-----GAAGGTTTCAACAATT	1221
Db	463	IleLysSerGlyGlyValAlaAspAsnGlyAspTyrTyrThrGlyAspGlySerThrIle	482
Qy	1222	ATAGACATAGACAATAATATAAGTTTATAAGTTTGGAGATAATCAAAATTTACCAGAT	1281
Db	483	IleAspSerAsnThrGluIleLysValTyrLysValAlaSerGlyGlnGlnLeuProGln	502
Qy	1282	AGTAAACAGAAATTTATGATTCAGTGAATATGAAGATGTCACAAATGATGATTATGCCAA	1341
Db	503	SerAsnLysIleTyrAspTyrSerGlnTyrGluAspValThrAsnSer-----ValThr	520
Qy	1342	TTAGGAATAAT-----AATGATGTCAATATTAATTTTGTATAATATAGATTTACCA	1392
Db	521	IleAsnLysAsnTyrGlyThrAsnMetAlaAsnIleAsnPheGlyAspIleAspSerAla	540
Qy	1393	TATATTATAAAGTTATTAGTAAATATGACCTTAATAAGGATGATTACACGACTATACAG	1452
Db	541	TyrIleValLysValValSerLysTyrThrProGlyAlaGluAspAspLeuGluValGln	560
Qy	1453	CAAACTGTGCAATGCACAGCACTATAAATGAGTATATACTGGTGATTTAGNACAGCATCC	1512
Db	561	GlnGlyValArgMet---ThrThrThrAsnLysTyrAsnTyrSer---SerTyrAlaGly	578
Qy	1513	TATGATAATACAATTGCTTCTCTCAAGTTTCAGTCAAGGACAAGGTGACTTCG---CCT	1569
Db	579	TyrThrAsnThrIleLeuSerThrThrAspSerGlyGlyAspGlyThrAlaLysPro	598
Qy	1570	CCTGAAAAAATTTATAAAATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGTATT	1629
Db	599	GluGluLysLeuTyrLysIleGlyAspTyrValTyrGluAspValAspLysAspGlyVal	618
Qy	1630	CAAAATCAAAATGATATGAARACCGCTTAGTAATGTTTGGTAACTTTTGACCTATCCT	1689
Db	619	GlnGlyThrAspSerLysGluLysProMetAlaAsnValLeuValThrLeuThrTyrPro	638
Qy	1690	GATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATCGGAAATATCAATTTGATGGA	1746
Db	639	AspGlyThrThrLysSerValArgThrAspAspLysGlyHisTyrGluPheGlyGly	657
RESULT 7			
ID	Q9KWX6	STAAU	PRELIMINARY; PRT; 1171 AA.
AC	Q9KWX6		
DT	01-OCT-2000,		integrated into UniProtKB/TrEMBL.
DT	01-OCT-2000,		sequence version 1.
DT	07-FEB-2006,		entry version 23.
DE	Bone sialoprotein-binding protein.		



```

QY 1330 GATTATGCCCAATTAGGAATAAT-----AATGATGTGAATATTAATTTGGTAAAT 1380
Db 519 -----ValThrIleAsnLysAsnTyrGlyThrAsnMetAlaAsnIleAsnPheGlyAsp 536
QY 1381 ATAGATTCCACCATATATTATTAAGCTTATAGTAAATATGACCCCTAATAAGGATGATTAC 1440
Db 537 IleAspSerAlaTyrIleValLysValValSerLysTyrThrProGlyAlaGluAspAsp 556
QY 1441 ACGACTATACAGCAAACTGTGCAATGACAGACGACTATAAATGAGTATATCTGGTGAGTTT 1500
Db 557 LeuAlaValGlnGlnGlyValArgMetThrThr-----ThrAsnLysTyr 571
QY 1501 AGACAGCATCTATGATAAT-----ACAATTGCTTTC 1533
Db 572 AsnTyrSerSerTyrAlaGlyTyrThrIleLeuPheTyrGlnLeuLeuThrLeuValVal 591
QY 1534 TCTCAAGTTCAGGTCAAGGACACAGGTGACTTGCCTCTCGAATAAATCTTATAAATCGGA 1593
Db 592 ValThrValSerValLys-----ProGluGluLysLeuTyrLysIleGly 606
QY 1594 GATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAAATACAAATGATAATGAATAA 1653
Db 607 AspTyrValTyrGluAspValAspLysValGlyValGlnGlyThrAspSerLysGluLys 626
QY 1654 CCGCTTAGTATGTTTGGTAACTTTGACGTATCTGATGCGACTTCAAAATCAGTCAGA 1713
Db 627 ProMetAlaAsnValLeuValThrLeuThrTyrProAspGlyThrThrLysSerValArg 646
QY 1714 ACAGATGAAGATGGGAATATCAATTTGATGGA 1746
Db 647 ThrAspAlaAsnGlyHisTyrGluPheGlyGly 657

RESULT 8
ID O86489 STAAU PRELIMINARY; PRT; 1166 AA.
AC O86489.
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Sdr E protein.
GN Name=sdr E;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Newman;
RX MEDLINE=99098700; PubMed=9884231;
RA Josefsen E., McCrea K., Ni Eidhin D., O'Connell D., Cox J., Hook M.,
RA Foster T.J.;
RT "Three new members of the serine-aspartate repeat protein multigene
RT family of Staphylococcus aureus.";
RL Microbiology 144:3387-3395(1998).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AJ005647; CAA06652.1; -; Genomic_DNA.
DR PIR; T28680.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007155; F:cell adhesion; IEA.
DR InterPro; IPR008454; Cna B.
DR InterPro; IPR005877; Goos_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003367; tsp_3.
DR Pfam; PF05738; Cna B; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02412; TSP_3; 3.
DR Pfam; PF04650; Ysirk signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.

```

```

DR TIGRFAMs; TIGR01168; Ysirk signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchored.
SQ SEQUENCE 1166 AA; 126549 MW; 750A7B0135287D4A CRC64;

Alignment Scores:
Pred. No.: 7,29e-48 Length: 1166
Score: 1144.50 Matches: 263
Percent Similarity: 60.1% Conservative: 108
Best Local Similarity: 42.6% Mismatches: 191
Query Match: 37.8% Indels: 55
DB: 2 Gaps: 18

US-10-806-288-12 (1-1746) x O86489 STAAU (1-1166)
QY 1 TCTAGTGTGATGAAGAAAGAATGATGTGATCAATAATAATCAATCAATAAACAACCCGACGAT 60
Db 66 AlaThrThrSerAspAsnLysGluValValSerGluThrGluAsnAsnSerThrThrGlu 85
QY 61 AATAACCAATA-----ATTAAAAAGAACAAAGAAATAACTAGCATGGCATAGAAAAA 114
Db 86 AsnAsnSerThrAsnProIleLysLysGlu-----ThrAsnThrAspSerGlnProGlu 103
QY 115 CGCTCAGAAGATCAACAAGAGTCAACAACAAATCTAGATGAAACGAAGCAACATTTT 174
Db 104 AlaLysLysGluSerThrSerSerThrGlnLysGlnGlnAsnAsnValThrAlaThr 123
QY 175 CAAAGACCCCTCAAGATAATCTCATCTTACAGAAGAAGAGGTAAAGAATCC----- 228
Db 124 ThrGluThrLysProGlnAsn-----IleGluLysGluAsnValLysProSerThrAsp 141
QY 229 ---TCATCAGTCGAATCTCTCAATTCATCAATTCATCTGCTCCCAACACCATCTCACACA 285
Db 142 LysThrAlaThrGluAspThrSerValIleLysGluGluLysLysAlaProAsnAsnThr 161
QY 286 ACAATAAATAGAGAAGAAATCTGTTCAACAAGATGATAATGTAGAAGATTCACACGATCA 345
Db 162 -----AsnAsnAspValThrThrLysProSer-----ThrSer 172
QY 346 GATTTTGTCTAACTCTAAATAAAGAGAGAGTAACT-----GAATCTGGTAAAGAA 396
Db 173 GluProSerThrSerGluIleGlnThrLysProThrThrProGlnGluSerThrAsnIle 192
QY 397 GAGAACTACTAGAGCAACCTAATAAAGTAAAGAGATTCACACAAAGTCACGCCGCT 456
Db 193 GluAsnSerGlnProGlnProThrProSerLysValAsp-----AsnGlnValThr 209
QY 457 GGCTATACAAATATAGATGAAAAAATTTC-----AATCAAGATGAGTTATTAAATTTACCA 513
Db 210 AspAlaThrAsnProLysGluProValAsnValSerLysGluLysLysAsnAsnPro 229
QY 514 -----ATAAATGAATATGAAATAAGGCTAGACCATTA 546
Db 230 GluLysLeuLysGluLeuValArgAsnAspSerAsnThrAspHisSerThrLysProVal 249
QY 547 TCTCAACAATCTGCCCAACCATCGATTAAAGCTGTA-----ACCGTA 588
Db 250 AlaThrAlaProThrSerValAlaProLysArgValAsnAlaLysMetArgPheAlaVal 269
QY 589 AATCAATTTAGCGCGGAACAAGGTTTCGAATGTTAAACCATTTTAAATTAAGTTACTGATCAA 648
Db 270 AlaGlnProAlaAlaValAlaSerAsnAsnValAsnAspLeuIleLysValThrLysGln 289
QY 649 AGTATTACTGAAGATATGATGATGAGAGGTGTTATTAAAGCACATGATGCTGCTGCTGCTG 708
Db 290 ThrIleLysValGly---AspGlyLysAsnValAlaAlaAlaHisAspGlyLysAsp 308
QY 709 TTAATCTATGATGTAACCTTTTGAAGTAGATCATAGGTGAATCTGGTGATACCATGACACA 768
Db 309 IleGluTyrAspThrGluPheThrIleAspAsnLysValLysLysGlyAspThrMetThr 328
QY 769 GTGGATATAGATAAGAATAACAGTTCCCATGAGTTTAAACCGATGCTTTTCAATACCAAAA 828

```

Db 329 IleAsnTyrAspLysAsnValIleProSerAspLeuThrAspLysAsnAspProIleAsp 348  
 QY 829 ATAAAGAGATAATCTCGAGAAATCATCGCTACAGGTACTTATGATACAAAATAAACAA 888  
 Db 349 IleThrAspProSerGlyGluValIleAlaLysGlyThrPheAspLysAlaThrLysGln 368  
 QY 889 ATCACTATACATTTACAGATATGTAGATAGTATGAATAATTAACACACACCTTAA 948  
 Db 369 IleThrTyrThrPheThrAspTyrValAspLysTyrGluAspLysSerArgLeuThr 388  
 QY 949 TTAACGTCTACATTCATAAATCAAGGTTCCAAATAAATAATACCAAGTTAGATGAGAA 1008  
 Db 389 LeuTyrSerTyrIleAspLysThrValPro---AsnGluThrSerLeuAsnLeuThr 407  
 QY 1009 TATAAAGCCGCTTTCATCAGTAATAAATAAACAATACCGTTGCAATATCAAAAGACCTAAC 1068  
 Db 408 PheAlaThrAlaGlyLysGluThrSerGlnAsnValThrValAspTyrGlnAspProMet 427  
 QY 1069 GAAATCGGACTGCTTAACCTTCAAGATGTATTACAAATATAGATACGAAATAATCATACA 1128  
 Db 428 ValHisGlyAspSerAsnIleGlnSerIlePheThrLysLeuAspGluAspLysGlnThr 447  
 QY 1129 GTTGAGCAACGATTATATTACCTCTTCGTTTACAGCCAGCAAGAAACAATGTAAAT 1188  
 Db 448 IleGluGlnGlnIleTyrValAsnProLeuLysLysSerAlaThrAsnThrLysValAsp 467  
 QY 1189 ATTTGAGGAATGGT-----GATCAAGGTTCAACAATT 1221  
 Db 468 IleAlaGlySerGlnValAspAspTyrGlyAsnIleLysLeuGlyAsnGlySerThrIle 487  
 QY 1222 ATAGACGATGACCAATTAATAAGTTTAAAGTTGGAGATAATCAAAATTTACCAGAT 1281  
 Db 488 IleAspGlnAsnThrGluIleLysValTyrLysValAsnSerAspGlnGlnLeuProGln 507  
 QY 1282 AGTACAGATTTATGATACAGTCAATGATGAATGAAGTGTCAAAATGAT---GATTATGCC 1338  
 Db 508 SerAsnArgIleTyrAspPheSerGlnTyrGluAspValThrSerGlnPheAsnLys 527  
 QY 1339 CAATTAGGAAATAAATGATGATTAATTAATTTGGTAAATATAGATTCCACATATAT 1398  
 Db 528 LysSerPheSerAsnAsnValAlaThrLeuAspPheGlyAspIleAsnSerAlaTyrIle 547  
 QY 1399 ATTAAGATTATTAATATATGACCTTAATAGGATGATTACAGACTATATACGCAAACT 1458  
 Db 548 IleLysValValSerLysTyrThrProThrSerAspGlyGluLeuAspIleAlaGlnGly 567  
 QY 1459 GTGCAATGACAGACACTATAATGATATATCTGTTAGTATTAGAACAGCATCCTATGAT 1518  
 Db 568 ThrSerMetArgThrThr---AspLysTyr---GlyTyrTyrAsnTyrAlaGlyTyrSer 585  
 QY 1519 AATCAAAATTCCTTCTCTACAAGTTTCAGTCAAGCAAGGTCGCTTG---CCTCCTGAA 1575  
 Db 586 AsnPheIleValThrSerAsnAspThrGlyGlyAspGlyThrValLysProGluGlu 605  
 QY 1576 AAAAATTAATAATCGGAGATACGTATGCGAAGATGTAGATAAAGATGGTATTCAAAAT 1635  
 Db 606 LysLeuTyrLysIleGlyAspTyrValTrpGluAspValAspLysAspGlyValGlnGly 625  
 QY 1636 ACAATGATATAAAGAAACCGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1695  
 Db 626 ThrAspSerLysGluLysProMetAlaAsnValLeuValThrLeuThrTyrProAspGly 645  
 QY 1696 ACTTCAAATCAGTCAGACAGATGAAGTGGAAATATCAATTTGATGGA 1746  
 Db 646 ThrThrLysSerValArgThrAspAlaAsnGlyHisTyrGluPheGlyGly 662

## RESULT 9

Q6BS4 STAA5

ID Q6BS4 STAA5 PRELIMINARY; PRT; 1141 AA.

AC Q6BS4;

DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 19-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE Bone stialoprotein-binding protein.  
 GN OrderedLocusNames=SAS0521;  
 OS Staphylococcus aureus (strain MSSA476).  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=282459;  
 RN [1]  
 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;  
 RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,  
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,  
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,  
 RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,  
 RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,  
 RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,  
 RA Ormond D., Quail M.A., Rabinowitz E., Rutherford K.M., Sanders M.,  
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,  
 RA Spratt B.G., Parkhill J.;  
 RT "Complete genomes of two clinical Staphylococcus aureus strains:  
 RT evidence for the rapid evolution of virulence and drug resistance.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; BX571857; CAG42296.1; -; Genomic\_DNA.  
 DR GO; GO:0009986; C:cell surface; IEA.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 DR GO; GO:0036020; C:membrane; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0007155; P:cell adhesion; IEA.  
 DR InterPro; IPR008454; Cna B.  
 DR InterPro; IPR005877; GpoB\_YsIRK.  
 DR InterPro; IPR001899; Gram\_pos\_anchor.  
 DR InterPro; IPR003367; tsp\_3.  
 DR Pfam; PF05738; Cna B; 3.  
 DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
 DR Pfam; PF02412; TSP\_3; 3.  
 DR Pfam; PF04650; YsIRK signal; 1.  
 DR TIGRPFAMs; TIGR01167; LPXTG anchor; 1.  
 DR TIGRPFAMs; TIGR01168; YsIRK signal; 1.  
 DR TIGRPFAMs; TIGR01168; YsIRK signal; 1.  
 DR PROSITE; PS50847; GRAM\_POS\_ANCHORING; 1.  
 KW Cell wall; Complete proteome; Peptidoglycan-anchor.  
 SQ SEQUENCE 1141 AA; 123998 MW; 372E5860850A332C CRC64;

## Alignment Scores:

Pred. No.:	8.17e-48	Length:	1141
Score:	1143.50	Matches:	266
Percent Similarity:	59.2%	Conservative:	98
Best Local Similarity:	43.3%	Mismatches:	192
Query Match:	37.8%	Indels:	59
DB:	2	Gaps:	18

US-10-806-288-12 (1-1746) x Q6BS4\_STAA5 (1-1141)

QY 1 TCTAGTGATGAAGAAACAATGATGATCAATAATAATCACTCAATAAACCACGACGAT 60  
 Db 69 SerAspAsnLysGluValSerGluAlaGluAsnAsnSerThrThrGluAsnAspSer 88  
 QY 61 AATAACCAATAATTTAAAAAGAAAGAAACGAAATACGATGCGATGAGAAACGCTCA 120  
 Db 89 ThrAsnProIle-----LysLysGluThrAsnThr---AspSerGlnProGluAlaLys 105  
 QY 121 GAAGATGAACAGAGTCAACACAAATGTAGATGAAGAAACGAAAGCAACATTTTACAAAG 180  
 Db 106 GluGluSerThrLysSerSerThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 125  
 QY 181 ACCCTCTCAAGATAATCTCATCTTACAGAAAGAGGTAAGAAAGATCC-----TCA 231  
 Db 126 ThrLysProGlnAsn-----IleGluLysGluAsnValLysProSerThrAspLysThr 143  
 QY 232 TCAGTCGAATCCTCAAAATTCATCAATTCATGCTACTGCCCAACCAACCATCTCACACAATA 291  
 Db 144 AlaThrGluAspThrSerValIleLeuGluGluLysLysAlaProAsnAsnThr----- 161

Qy	292	AATAGAGAAGAAATCTGTTCAACAACAAAGTATAATGTAGAAGATTACACAGTATCAGATTTT	351
Db	162	AsnAenAepValThrThrLysProSer-----	170
Qy	352	GCTAACTCTAAATAATAAAGAGAGATAACACT-----GAATCTGTTAAAGAGAAGAAT	402
Db	171	--ThrSerGluIleGlnThrLysProThrThrProGlnGluSerThrAenIleGluAen	189
Qy	403	ACTATAGAGCAACCTTAATAAGTATAAAGAGAGATTCAACAACAGCTACGCGTCTGGCTAT	462
Db	190	SerGlnProGlnProThrProSerLysValAep-----AenGlnValThrAepAla	206
Qy	463	ACAATAATAGATGAAAAAATTTTCA---AATCAAGATGAGTTATTAAATTTTACCA-----	513
Db	207	ThrAenProLysGluProValAenValSerLysGluLeuLysAenAenProGluLys	226
Qy	514	-----ATAAATGAATATGAAATAAAGGTAGCGTAGACCATTTATCTTACA	552
Db	227	LeuLysGluLeuValArgAenAepSerAenThrAepHisSerThrLysProValAlaThr	246
Qy	553	ACATCTGCCCAACCATCGATTAAACGGTGA-----ACCGTAAATCAAA	594
Db	247	AlaProThrSerValAlaProLysArgValAenAlaLysMetArgPheAlaValAlaGln	266
Qy	595	TTAGCGCGGGAACAAGGTTGCAATGTTAAACCATTTAATTAAGTTACTGTCAAGATATT	654
Db	267	ProAlaAlaValAlaSerAenAenValAenAenProLeuLysValThrLysGlnThrIle	286
Qy	655	ACTGAAGGATATGATGATGATGAGTGAAGGTGTTATTAAAGCACATGATGCTGAAGAACTTAAATC	714
Db	287	LysValGly---AepGlyLysAepAenValAlaAlaHisAepGlyLysAepIleGlu	305
Qy	715	TATGATGTAACTTTTGAAGTAGATGAAGTGAAGTCTGGTGATACGATGACAGATGGAT	774
Db	306	TyrAepThrGluPheThrIleAepAenLysValLysLysGlyAepThrMetThrIleAen	325
Qy	775	ATAGATAAGAAATACAGTTCCATCAGATTTTAAACCGATAGCTTTTCAATACCAAAATAAAA	834
Db	326	TyrAepLysAenValIleProSerAepLeuThrAepLysAenAepProIleAepIleThr	345
Qy	835	GATAATTTCTGGAGAAATCATCGCTACAGGTACTTATGATATACAAAAATAACAATCACC	894
Db	346	AepProSerGlyGluValIleAlaLysGlyThrPheAepLysAlaThrLysGlnIleThr	365
Qy	895	TATACTTTTACAGATTATGTAGATAAGTATGAAAAATATTAAAGCACACCTTAAATTAACG	954
Db	366	TyrThrPheThrAepTyrValAepLysTyrGluAepIleLysSerArgLeuThrLeuTyr	385
Qy	955	TCATACATGTATAATCAAAAGGTTCCAAATAATATCAAGTTAGATGTAGATATAAA	1014
Db	386	SerTyrIleAepLysLysThrValPro---AenGluThrSerLeuAenLeuThrPheAla	404
Qy	1015	ACGCGCCCTTTTCATCAGTAAATAAAACAATTACCGTTGAATATCAAGACCTTAACGAAAT	1074
Db	405	ThrAlaGlyLysGluThrSerGlnAenValThrValAepTyrGlnAepProMetValHis	424
Qy	1075	CGGACTGCTAACTTCAAGATGATGTTTACAAATATAGATACGAAAAATCATACAGTTGAG	1134
Db	425	GlyAepSerAenIleGlnSerIlePheThrLysLeuAepGluAepLysGlnThrIleGlu	444
Qy	1135	CAAAACGATTATATTAACCCCTCTCGTTATTTCAGCCAAAGGAAAAACAATGTAAATTTTCA	1194
Db	445	GlnGlnIleTyrValAenProLeuLysLysSerAlaThrAenThrLysValAepIleAla	464
Qy	1195	GGGAATGGT-----GATGAAGGTTTCAACAATTTATAGAC	1227
Db	465	GlySerGlnValAepAepTyrGlyAenIleLysLeuGlyAenGlySerThrIleIleAep	484
Qy	1228	GATAGCACAAATAATTAAGTTTATAGGTTGGAGATAATCAAAATTTTACCGATGATTAAC	1287
Db	485	GlnAenThrGluIleLysValTyrLysValAenSerAepGlnGlnLeuProGlnSerAen	504

[illegible]

DT 07-FEB-2006, entry version 11.



SdrE protein.  
GN Name=edrE; OrderedLocusNames=SACOL0610;  
OS Staphylococcus aureus (strain COL);  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=93062;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;  
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,  
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,  
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,  
RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,  
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,  
RA Hance I.R., Nelson K.E., Fraser C.M.;  
RT "Insights on evolution of virulence and resistance from the complete  
RT genome analysis of an early methicillin-resistant Staphylococcus  
RT aureus strain and a biofilm-producing methicillin-resistant  
RT Staphylococcus epidermidis strain";  
RL J. Bacteriol. 187:2426-2438(2005).  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC -----  
DR EMBL; CP000046; AAW37719.1; -; Genomic DNA.  
DR TIGR; SACOL0610; -;  
DR GO; GO:000986; C:cell surface; IEA.  
DR GO; GO:0005618; C:cell wall; IEA.  
DR GO; GO:0046020; C:membrane; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR InterPro; IPR008454; Cna\_B.  
DR InterPro; IPR005877; GpoB\_YSIK.  
DR InterPro; IPR001899; Gram\_pos\_anchor.  
DR Pfam; PF05738; Cna\_B; 3.  
DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
DR Pfam; PF02412; TSP\_3; 3.  
DR TIGRPFAMs; TIGR01167; LPXTG\_signal; 1.  
DR TIGRPFAMs; TIGR01168; YSIK\_signal; 1.  
DR PROSITE; PS50847; GRAM\_POS\_ANCHORING; 1.  
KW Cell wall; Complete proteome; Peptidoglycan-anchor.  
SQ SEQUENCE 1166 AA; 126563 MW; 92DFC023B75AB8F CRC64;

Alignment Scores:  
Pred. No.: 9,11e-48 Length: 1166  
Score: 1142.50 Matches: 262  
Percent Similarity: 60.1% Conservative: 107  
Best Local Similarity: 42.7% Mismatches: 196  
Query Match: 37.8% Indels: 49  
DB: 2 Gaps: 18

US-10-806-288-12 (1-1746) x Q5HIB2\_STAAC (1-1166)

QY 1 TCTAGTGATGAAGAAGAAAGTGTGATCAATAATAATCAAGTCAATAAACAACGACGAT 60  
Db 66 AlathrThrSerAspAsnLysGluValSerGluThrGluAsnAsnSerThrThrGlu 85  
QY 61 AATACCAATA-----ATTAAGAAAGAAACGAATAACTACGATGGCATAGAAAA 114  
Db 86 AsnAsnSerThrAsnProIleLysLysGlu-----ThrAsnThrAspSerGlnProGlu 103  
QY 115 CGCTCAGAGATAGACAGAGTCAACAATAATGTAGATGAAGAAACGACGACATTTTA 174  
Db 104 AlaLysLysGluSerThrSerSerThrGlnLysGlnGlnAsnAsnValThrAlaThr 123  
QY 175 CAAAGACCCCTCAAGATAAATACTCATCTTACAGAAAGAGGTAAGAAAGATCC----- 228  
Db 124 ThrGluThrLysProGlnAsn-----IleGluLysGluAsnValLysProSerThrAsp 141  
QY 229 ---TCATCAGTCGAATCTCAATTCATCAATTGATCTGCCCAACACCATCTCACACA 285  
Db 142 LysThrAlaThrGluAspThr-SerValIleLeuGluLysLysAlaProAsnAsnThr 161

QY 286 ACAATAATAGAGAAGAAATCTGTTCAAACAGTGTATAATGTAGAAGATTTCACACGTATCA 345  
Db 162 -----AsnAsnAspValThrThrLysProSer-----ThrSer 172  
QY 346 GATTTTGCTAACTCTAAATAAAAGAGAGTAACACT-----GAATCTGGTAAGAA 396  
Db 173 GluProSerThrSerGluIleGlnThrLysProThrProGlnGlnSerThrAsnIle 192  
QY 397 GAGAAATCTATAGAGCAACCTTAATAAGTAAGAAAGAT-----TCACAAACAAGT 447  
Db 193 GluAsnSerGlnProGlnProThrProSerLysValAspAsnGlnValThrAspAlaThr 212  
QY 448 CAGCGCTCTGCTATACAAATATA-----GATCAAAAAAATTCCAATCAAGATGAGTTA 501  
Db 213 AsnProLysGluProValAsnValSerLysGluLeuLysLysAsnProGluLysLeu 232  
QY 502 TTAATTTTACCATAAAATGAA-----TATGAAATTAAGGCTAGACCATTTATCAACA 555  
Db 233 LysGluLeuValArgAsnAspSerAsnThrAspHisSerThrLysProValAlaThrAla 252  
QY 556 TCTGCCCAACCATCGATTAAACGTGTA-----ACCGTAAATCAATTA 597  
Db 253 ProThrSerValAlaProLysArgValAsnAlaLysMetArgPheAlaValAlaGlnPro 272  
QY 598 GCGCGGCAACAAGGTTTGAATGTTAAACCATTTAATTAAGTTTACTGATCAAGTATTACT 657  
Db 273 AlaAlaValAlaSerAsnAsnValAsnAspLeuIleLysValThrLysGlnThrIleLys 292  
QY 658 GAAGGATATGATGATAGTAGGAAGGTGTTATTAAAGCACATGATGCTGAAAACCTTAATCTAT 717  
Db 293 ValGly--AspGlyLysAspAsnValAlaAlaAlaHisAspGlyLysAspIleGluThr 311  
QY 718 GATGTAATCTTTGAAGTAGATGATAGGTGAATCTCGTGTAGTACGATGACAGTGGATATA 777  
Db 312 AspThrGluPheThrIleAspAsnLysValLysLysGlyAspThrMetThrIleAsnThr 331  
QY 778 GATGAAGATACAGTTCATCAGATTAAACCGATAGCTTTACAATACCAAAAAATAAAGAT 837  
Db 332 AspLysAsnValIleProSerAspLeuThrAspLysAsnAspProIleAspIleThrAsp 351  
QY 838 AATTCTCGAGAAATCATCGCTACAGGTACTTATGATTAACAAAAATAAACAATCACCTAT 897  
Db 352 ProSerGlyGluValIleAlaLysGlyThrPheAspLysAlaThrLysGlnIleThrThr 371  
QY 898 ACTTTTACAGATTATGTAGATAGTAAATGAAATATTAAAGCACACACCTTTAAATTAACGTCA 957  
Db 372 ThrPheThrAspThrValAspLysLysGlyAspIleLysSerArgLeuThrLeuThrSer 391  
QY 958 TACATTGATAAATCAAAAGGTTTCCAAATAATAATACCAAGTTAGATGTAGATAATAAAGC 1017  
Db 392 TyrlleAspLysLysThrValPro---AsnGluThrSerLeuAsnLeuThrPheAlaThr 410  
QY 1018 GCCCTTTTCATCAGTAAATAAAACAATTAACGTTTGAATATCAAGACCTTAACGAAATCGG 1077  
Db 411 AlaGlyLysGluThrSerGlnAsnValThrValAspThrGlnAspProMetValHisGly 430  
QY 1078 ACTGCTAACCTTCAAAGTATGTTTACAAATATAGATAGCAAAAAATCATACAGTTGAGCAA 1137  
Db 431 AspSerAsnIleGlnSerIlePheThrLysLeuAspGluAspLysGlnThrIleGluGln 450  
QY 1138 ACGATTTTATTAACCTCTTCTGTTATTTCAGCCCAAGGAAACAAATGTAATAATTTCAGGG 1197  
Db 451 GlnIleThrValAsnProLeuLysSerAlaThrAsnThrLysValAspIleAlaGly 470  
QY 1198 AATGGT-----GATGAAGGTTCAACAATATATAGACGAT 1230  
Db 471 SerGlnValAspAspThrGlyAsnIleLysLeuGlyAsnGlySerThrIleIleAspGln 490  
QY 1231 AGCAATAATTAAGTTTATAGTTTGGAGATTAATCAAAATTTTACCAGATAGTACAGACA 1290  
Db 491 AsnThrGluIleLysValThrLysValAsnSerAspGlnGlnLeuProGlnSerAsnArg 510





```
Db      306 TyrAspThrGluPheThrIleAspAsnLysValLysLysGlyAspThrMetThrIleAsn 325
Qy      775 ATAGATAAGATACAGTTCCATCAGATTAAACCGATAGCTTTACAAATACCAAAATAAAA 834
Db      326 TyrAspLysAsnValIleProSerAspLeuThrAspLysAsnAspProIleAspIleThr 345
Qy      835 GATAATCTCGAGAAATCATCGCTACAGTGTACTTATGATACAAATAAATAACAATACCC 894
Db      346 AspProSerGlyGluValIleAlaLysGlyThrPheAspLysAlaThrLysGlnIleThr 365
Qy      895 TATACCTTTTACAGATTATGTAGATAAGTATGAAATATTAAGACACACTTAAATTAACG 954
Db      366 TyrThrPheThrAspTyrValAspLysTyrGluAspIleLysAlaAaGLeuThrLeuTyr 385
Qy      955 TCATACATTGATAATCAAGGTTCCAAATATATATACCAAGTGTAGATGATAGATATAA 1014
Db      386 SerTyrIleAspLysGlnAlaValPro---AenGluThrSerLeuAsnLeuThrPheAla 404
Qy      1015 ACGGCCCTTTCATCAGTAAATAAACAATTAACGTTGAATATCAAGACCTAACGAAAT 1074
Db      405 ThrAlaGlyLysGluThrSerGlnAsnValSerValAspTyrGlnAspProMetValHis 424
Qy      1075 CGGACTGCTACCTTCAAGTATGTTTACAAATATATAGATACGAAATAATCATACAGTTGAG 1134
Db      425 GlyAspSerAsnIleGlnSerIlePheThrLysLeuAspGluAsnLysGlnThrIleGlu 444
Qy      1135 CAACGATTATATTAACCTCTTCGTTATTTCAGCCAAAGGAACAATAATGTTAAATTTTCA 1194
Db      445 GlnGlnIleTyrValAsnProLeuLysLysThrAlaThrAsnThrLysValAspIleAla 464
Qy      1195 GGGATGCT-----GATGAAGTTCACCAATTTATGAC 1227
Db      465 GlySerGlnValAspAspTyrGlyAsnIleLysLeuGlyAsnGlySerThrIleIleAsp 484
Qy      1228 GATAGCAACAATAATTAAGTTTATAAGCTTCGAGATATCAAAATTTTACCAAGATGTAAC 1287
Db      485 GlnAsnThrGluIleLysValTyrLysValAsnProAsnGlnGlnLeuProGlnSerAsn 504
Qy      1288 AGAATTTATGATTACAGTGAATATGAAGATGTCACAAATGAT---GATTATGCCCAATTA 1344
Db      505 ArgIleTyrAspPheSerGlnTyrGluAspValThrSerGlnPheAsnLysLysSer 524
Qy      1345 GGAAATATATATGATGTAATATTAATTTTGGTATATAGATTACCATATATATTATAA 1404
Db      525 PheSerAsnAsnValAlaThrLeuAspPheGlyAspIleAsnSerAlaTyrIleIleLys 544
Qy      1405 GTTATTAGTAATATGACCTTAATAAGCATGATTACACGACTATACACAACTGTGACA 1464
Db      545 ValValSerLysTyrThrProThrSerAspGlyGluLeuAspIleAlaGlnGlyThrSer 564
Qy      1465 ATGCAGACGACTATAATAGTATCTACTGCTGAGTTTAGAACAGCATCTATGATAATACA 1524
Db      565 MetArgThrThr---AspLysTyr---GlyTyrTyrAsnTyrAlaGlyTyrSerAsnPhe 582
Qy      1525 ATTGCTTCTCTACAAGTTTCAAGTCAAGCAAGTGTGCTG---CCTCCTGAAAAAACT 1581
Db      583 IleValThrSerAsnAspThrGlyGlyAspGlyThrValLysProGluGluLysLeu 602
Qy      1582 TATAAAATCGGAGATTACGTATGGGAAGATGTAGATAAGATGGTATTTCAAAATACAAAT 1641
Db      603 TyrLysIleGlyAspTyrValTyrGluAspValAspLysAspGlyValGlnGlyThrAsp 622
Qy      1642 GATAATGAAAACCGCTTAGTAATGTATGTTGTAATCTTGGTACTTGGTATCTCTGATGGA 1701
Db      623 SerLysGluLysProMetAlaAsnValLeuValThrLeuThrTyrProAspGlyThrThr 642
Qy      1702 AAATCAGTCAGACAGATGAGATGGGAATATCAATTTGATGA 1746
Db      643 LysSerValArgThrAspAlaAsnGlyHisTyrGluPheGlyGly 657
```

RESULT 13

Q99W46\_STAAN

ID Q99W46\_STAAN PRELIMINARY; PRT; 1141 AA.

```
AC      Q99W46;
DT      01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT      01-JUN-2001, sequence version 1.
DT      07-FEB-2006, entry version 23.
DB      Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein.
GN      Name=sdr8; OrderedLocusNames=SA0521;
OS      Staphylococcus aureus (strain N315).
OC      Bacteria; Firmicutes; Bacillales; Staphylococcus.
CC      NCBI_TaxID=158879;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      MEDLINE=21311953; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA      Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA      Cui L., Oguchi A., Aoki K., Nagai K., Nagai Y., Lian J.-Q., Ito T., Kanamori M.,
RA      Matsunaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA      Takahashi N.K., Sawano T., Inoue R., Kaito C., Sekimizu K.,
RA      Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA      Yamashita A., Oshina K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA      Ogasawara N., Hayaashi H., Hiramatsu K.;
RT      "Whole genome sequencing of methicillin-resistant Staphylococcus
RT      aureus.";
RL      Lancet 357:1225-1240 (2001).
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      EMBL; BA000018; BAB41752.1; -; Genomic_DNA.
DR      PTR; E89824; E89824.
DR      BIOCYC; SAURI58879:SA0521-MONOMER; -.
DR      GO; GO:0009986; C:cell surface; IEA.
DR      GO; GO:0005618; C:cell wall; IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0005509; F:calcium ion binding; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      InterPro; IPR008454; Cna_B.
DR      InterPro; IPR005877; Gpos_Ysirk.
DR      InterPro; IPR001899; Gram_pos_anchor.
DR      InterPro; IPR003367; tsp_3.
DR      Pfam; PF05738; Cna_B_3.
DR      Pfam; PF00746; Gram_pos_anchor; 1.
DR      Pfam; PF02412; TSP_3; 3.
DR      Pfam; PF04650; Ysirk_signal; 1.
DR      TIGRPFAMs; TIGR01167; LPXTG_anchor; 1.
DR      TIGRPFAMs; TIGR01168; Ysirk_signal; 1.
DR      PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
KW      Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ      SEQUENCE 1141 AA; 124027 MW; 445419D0B8C5A4F8 CRC64;
Alignment Scores:
Pred. No.: 1.6e-47 Length: 1141
Score: 1137.50 Matches: 266
Percent Similarity: 59.0% Conservative: 97
Best Local Similarity: 43.3% Mismatches: 193
Query Match: 37.6% Indels: 59
DB: Gaps: 2
US-10-806-288-12 (1-1746) x Q99W46_STAAN (1-1141)
Qy      1 TCTAGTGTGATGAAGAAAGAATGTGTCATCAATTAATATCAATCAATAAACCCGACGAT 60
Db      69 SerAspAsnLysGluValSerGluThrGluAsnAsnSerThrThrGluAsnAspSer 88
Qy      61 AATACCAATAATTAATAAAGAAAGAACGATTAACGATGCGATGCGATAGAAAACGCTCA 120
Db      89 ThrAsnProIle-----LysLysGluThrAsnThr---AspSerGlnProGluAlaLys 105
Qy      121 GAAGATAGACAGAGTCAACCAACAAATGTAGATGAACCAAGCAAGCAACATTTTACAAAAG 180
Db      106 GluGluSerThrThrSerSerThrGlnGlnGlnAsnAsnValThrAlaThrThrGlu 125
Qy      181 ACCCTCTCAAGATATACTCATCTTACAGAAAGAGAGGTAAAGAAATCC-----TCA 231
Db      126 ThrLysProGlnAsn-----IleGluLysGluAsnValLysProSerThrAspLysThr 143
```

```
QY 232 TCAGTCGAATCCTCAAAATTCATCAATTTGATCTGCCCCAACCAACCACTCTCACCAACAATA 291
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
144 AlaThrGluAspThrSerValIleLeuGluGluLysAlaProAsnTyrThr-----161
QY 292 AATAGAGAGAACTCTCTTCAACACAGTGATATGTAGAGATTACACGCTATCAGATTTT 351
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
162 AsnAsnAspValThrLysProSer-----170
QY 352 GCTAACTCTAAATAAAGAGAGTAACACT-----GAATCTGGTAAAGAGAGAAAT 402
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
171 ---ThrSerGluIleGlnThrLysProThrThrProGlnGluSerThrAsnIleGluAsn 189
QY 403 ACTATAGACACACTTAATAAGTAAAGAAAGATTCAACAAAGTCAGCGCTCTGCTAT 462
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
190 SerGlnProGlnProThrProSerLysValAsp-----AsnGlnValThrAspAla 206
QY 463 ACAAAATATAGACAAAATTTC-----AATCAAGATGAGTTTAAATTTTACCA-----513
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
207 ThrAsnProLysGluProValAsnValSerLysGluGluLeuLysAsnAsnProGluLys 226
QY 514 -----ATAATGAATATGAAATAAGGCTAGACCATTTATCTACA 552
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
227 LeuLysGluLeuValArgAsnAsnAsnThrAspArgSerThrLysProValAlaThr 246
QY 553 -----ACATCTGCCCAACCA-----TCGATTTAAACGTGTAAACCGTAAATCAA 594
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
247 AlaProThrSerValAlaProLysArgLeuAsnAlaLysMetArgPheAlaValAlaGln 266
QY 595 TTAGCGGGACACAGGTTGCAATGTATTAACATTTTAAATTAAGTTACTGATCAAGATT 654
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
267 ProAlaAlaValAlaSerAsnAsnValAsnAspLeuIleThrValThrLysGlnThrIle 286
QY 655 ACTGAAGGATATGATGATAGTCAAGGTGTTATTAAAGCACATGATGCTCAAAACTTAATC 714
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
287 LysValGly---AspGlyLysAspAsnValAlaAlaAlaHisAspGlyLysAspIleGlu 305
QY 715 TATGATGTAACTTTTGAAGTAGATGATAGGTGAAATCTGGTGACATGACAGTGGAT 774
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
306 TyrAspThrGluPheThrIleAspAsnLysValLysLysGlyAspThrMetThrIleAsn 325
QY 775 ATAGATAGAAATACAGTTCATCAGATTAAACCGTAGCTTTACAAATACCAAAATAAAA 834
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
326 TyrAspLysAsnValIleProSerAspLeuThrAspLysAsnAspProIleAspIleThr 345
QY 835 GATAATTTCTGGAGAATCATCTACAGTACTTATGATAACAAAAATAAACAATCACC 894
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
346 AspProSerGlyGluValIleAlaLysGlyThrPheAspLysAlaThrLysGlnIleThr 365
QY 895 TATACCTTTTACAGATTATGTAGATGATGAAATATTTAAAGCACACCTTAAATTAACG 954
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
366 TyrThrPheThrAspTyrValAspLysTyrGluAspIleLysAlaArgLeuThrLeuTyr 385
QY 955 TCATACATGATAAATCAAGGTTCCAAATATATATACCAATGATGATGATGATGATGATA 1014
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
386 SerTyrIleAspLysGlnAlaValPro---AsnGluThrSerLeuAsnLeuThrPheAla 404
QY 1015 ACGGCCCTTTTCATCAGTAAATAAAACAATTCAGTTGATATCAAGACCTTAAACGAAAT 1074
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
405 ThrAlaGlyLysGluThrSerGlnAsnValSerValAspTyrGlnAspProMetValHis 424
QY 1075 CGGACTGCTAACCTTCAAGATGATGTTTACAAATATATAGATACGAAATAATCATACGTTGAG 1134
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
425 GlyAspSerAsnIleGlnSerIlePheThrLysLeuAspGluAsnLysGlnThrIleGlu 444
QY 1135 CAAACGATTTATTAATCAACCTCTCTGTTATTCAGGCAAGGAAACAAATGTAAATTTTCA 1194
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
445 GlnGlnIleTyrValAsnProLeuLysLysThrAlaThrAsnThrLysValAspIleAla 464
QY 1195 GGGATGCT-----GATGAGGTTCAACATTTATGAC 1227
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
465 GlySerGlnValAspAspTyrGlyAsnIleLysLeuGlyAsnGlySerThrIleIleAsp 484
```

```
QY 1228 GATACACACAATAATTAAAGTTTATTAAGGTTGGAGATAATCAAAATTTTACCAGATAGTAAC 1287
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
485 GlnAsnThrGluIleLysValTyrLysValAsnProAsnGlnGlnLeuProGlnSerAsn 504
QY 1288 AGAATTTATGATACAGTGAATATGAGATGTCACAAATGAT---GATTATGCCCAATTA 1344
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
505 ArgIleTyrAspPheSerGlnTyrGluAspValThrSerGlnPheAspAsnLysLysSer 524
QY 1345 GGAAATAATAATGATGTGAATATTAATTTTGTGTATATATAGATTCACCATATATATTAAA 1404
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
525 PheSerAsnAsnValAlaThrLeuAspPheGlyAspIleAsnSerAlaTyrIleIleLys 544
QY 1405 GTTATTAGTAAATATGACCTTAATAGGATGATTACAGACTATATACAGCAAACTGTGACA 1464
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
545 ValValSerLysTyrThrProThrSerAspGlyGluLeuAspIleAlaGlnGlyThrSer 564
QY 1465 ATGCAGACGACTATAAATGAGTATCTACTGGTGGATTGTAGAACAGCATCCTCATGATATA 1524
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
565 MetArgThrThr---AspLysTyr---GlyTyrTyrAsnTyrAlaGlyTyrSerAsnPhe 582
QY 1525 ATTGCTTTCTCTACAAAGTTCAGGTCAGGCAAGCAAGGTGACTTG---CCTCCTGAAAAA 1581
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
583 IleValThrSerAsnAspThrGlyGlyAspGlyThrValLysProGluGluLysLeu 602
QY 1582 TATAAAATCGGAGATTACGTATGCGAAGATGTAGATAAAGATGGTATTCAAAATACAAAT 1641
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
603 TyrLysIleGlyAspTyrValTyrGluAspValAspLysAspGlyValGlnGlyThrAsp 622
QY 1642 GATAATGAAAAACCGCTTAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1701
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
623 SerLysGluLysProMetAlaAsnValLeuValThrLeuThrTyrProAspGlyThrThr 642
QY 1702 AAATCAGTCAGACAGATGAGATGCGAAATATCAATTTGATGGA 1746
Db   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
643 LysSerValArgThrAspAlaAsnGlyHisTyrGluPheGlyGly 657

RESULT 14
Q2UM65 STAAU PRELIMINARY; PRT; 444 AA.
AC Q2UM65-
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein
DE (Fragment).
GN Name=sdrE;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GE149;
RX PubMed=16352833; DOI=10.1128/JB.188.1.169-178.2006;
RA Kuhn G., Francioli P., Blanc D.S.;
RT "Evidence for clonal evolution among highly polymorphic genes in
RT methicillin resistant Staphylococcus aureus.";
RL J. Bacteriol. 188:169-178(2006).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AM076279; CAJ27916.1; -; Genomic_DNA.
FT NON_TER 1.
FT NON_TER 444.
SQ SEQUENCE 444 AA; 49117 MW; 8086D6B66F994224 CRC64;

Alignment Scores:
Pred. No.: 1.13e-41 Length: 444
Score: 1018.00 Matches: 205
Percent Similarity: 70.3% Conservative: 51
Best Local Similarity: 56.3% Mismatches: 90
Query Match: 33.6% Indels: 18
DB: 2
```

[illegible]

Db 120 TyrGlnLysProIleValLysAspGluSerAsnIleGlnSerIlePheSerHisLeuAsp 139  
QY 1114 ACGAAAAATCATACAGTTCAGCAACAGATTATATTAACCTCTTCGTTATTTCAGCCAAG 1173  
Db 140 ThrThrLysHisGluValGluGlnThrIleTyrValAsnProLeuLysLeuAsnAlaLys 159  
QY 1174 GAAACAATGTAAATATT-----TCAGGGAATGGTGAT----- 1206  
Db 160 AsnThrAsnValThrIleLysSerGlyGlyValAlaAspAsnGlyAspTyrTyrThrGly 179  
QY 1207 GAAGGTTCAACAAATTATACAGCATAGCACAAATAATTAAGTTTATAAGGTTGGAGATAAT 1266  
Db 180 AspGlySerThrIleLeuAspSerAsnThrGluIleLysValTyrLysValAlaSerGly 199  
QY 1267 CAAATTTTACCAGATAGTAAACAGAAATTTATGATTACAGTGAATATGACAGATGTCACAAAT 1326  
Db 200 GlnGlnLeuProGlnSerAsnLysIleTyrAspTyrSerGlnTyrGluAspValThrAsn 219  
QY 1327 GATGATTATGCCCAATTAGGAATATAT-----AATGATGTGAATATTAATTTGGT 1377  
Db 220 Ser-----ValThrIleAsnLysAsnTyrGlyThrAsnMetAlaAsnIleAsnPheGly 237  
QY 1378 ATATAGATTCCACCATATATTATTAAGTTATTAGTAAATATGACCCCTAATAAGGATGAT 1437  
Db 238 AspIleAspSerAlaTyrIleValLysValSerLysTyrThrProGlyAlaGluAsp 257  
QY 1438 TACACGACTATACAGCAAACTGTGACAAATGACAGCAGCTATAAATGAGTATACTGGTGAG 1497  
Db 258 AspLeuAlaValGlnGlnGlyValArgMet---ThrThrThrAsnLysTyrAsnTyrSer 276  
QY 1498 TTTAGAACAGCATCCTATGATTAATCAATTGGTTCTTCTTCAAGTTCAAGGTCAGGCAAGCAA 1557  
Db 277 ---SerTyrAlaGlyTyrThrAsnThrIleLeuSerThrThrAspSerGlyGlyAsp 295  
QY 1558 GGTGACTTG---CCTCCTGAAAAAACTTATAAAATCGAGATACGATATGGGAAGATGTA 1614  
Db 296 GlyThrValLysProGluGluLysLeuTyrLysIleGlyAspTyrValTrpGluAspVal 315  
QY 1615 GATAAGATGGTATTCAAAATACAAATGATAATGAAAAACCGCTTAGTAATGTATTGGTA 1674  
Db 316 AspLysAspGlyValGlnGlyThrAspSerLysGluLysProMetAlaAsnValLeuVal 335  
QY 1675 ACTTTGACGTATCCTGATGGAACTTCAAAATCAGTCAGAACAGATGAAGATGGAAATAT 1734  
Db 336 ThrLeuThrTyrProAspGlyThrThrLysSerValArgThrAspAlaAsnGlyHisTyr 355  
QY 1735 CAATTTGATGGA 1746  
Db 356 GluPheGlyGly 359

Search completed: August 12, 2006, 08:10:02  
Job time : 579 secs

**This Page Blank (uspto)**

GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: August 12, 2006, 08:55:26 ; Search time 194 Seconds  
 (without alignments)  
 1371.649 Million cell updates/sec

Title: US-10-806-288-13  
 Perfect score: 3013  
 Sequence: 1 SDESKNDVINNNQSDTDD.....PDGTSKSVRTDEGKYQFDG 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_8.\*  
 1: Geneseqp1980s.\*  
 2: Geneseqp1990s.\*  
 3: Geneseqp2000s.\*  
 4: Geneseqp2001s.\*  
 5: Geneseqp2002s.\*  
 6: Geneseqp2003as.\*  
 7: Geneseqp2003bs.\*  
 8: Geneseqp2004s.\*  
 9: Geneseqp2005s.\*  
 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3013	100.0	1092	2 AAW41602	AAW41602 Staphyloc
2	3013	100.0	1092	7 ABM79019	ABM79019 Staphyloc
3	2810.5	93.3	892	6 ABU42557	ABU42557 Protein e
4	2810.5	93.3	892	8 ADO84849	ADO84849 S epiderm
5	2810.5	93.3	892	8 ADS20651	ADS20651 S. epider
6	2810.5	93.3	930	5 ABP40469	ABP40469 Staphyloc
7	2810.5	93.3	930	8 ADS06014	ADS06014 Staphyloc
8	2810.5	93.3	991	3 AAY83171	AAY83171 Cell wall
9	2810.5	93.3	991	3 AAY70120	AAY70120 Staph. ep
10	2670	88.6	549	7 ABM79020	ABM79020 Staphyloc
11	2510.5	83.3	560	7 ABM79015	ABM79015 Staphyloc
12	1702	56.5	331	9 AEB23146	AEB23146 Ligand bi
13	1672	55.5	343	7 ABM79016	ABM79016 Staphyloc
14	1562	51.8	316	7 ABM79017	ABM79017 Staphyloc
15	1144.5	38.0	1166	2 AAY08643	AAY08643 S. aureus
16	1142.5	37.9	1166	6 ABU18982	ABU18982 Pathogen
17	1137.5	37.8	1141	6 ABU42327	ABU42327 Protein e
18	1116.5	37.1	670	6 ABU42520	ABU42520 Protein e
19	857	28.4	278	4 AAG82803	AAG82803 S. epider
20	795.5	26.4	338	9 AEB23147	AEB23147 Ligand bi
21	576	19.1	1315	2 AAY08642	AAY08642 S. aureus
22	576	19.1	1315	6 ABJ18969	ABJ18969 Pathogen
23	576	19.1	1349	4 AAU37544	AAU37544 Staphyloc

## ALIGNMENTS

RESULT 1  
 AAW41602  
 ID AAW41602 standard; protein; 1092 AA.  
 XX  
 AC AAW41602;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 22-JUN-1998 (first entry)  
 XX  
 DE Staphylococcus epidermidis fibrinogen binding protein FIG.  
 XX  
 KW Fibrinogen binding protein; FIG; aggregation; infection;  
 KW coagulase-negative Staphylococcus; therapy; diagnosis; immunisation;  
 KW immunogen; vaccine.  
 XX  
 OS Staphylococcus epidermidis; strain HB.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..51  
 FT Protein /label= Sig\_peptide  
 FT /label= Mat\_protein  
 FT Region 52..824  
 FT /note= "non-repetitive region, harbouring fibrinogen binding activity"  
 FT Region 825..1040  
 FT /note= "App-Ser dipeptide repeat region"  
 FT Region 1053..1057  
 FT /note= "cell wall anchoring motif"  
 XX  
 WO9748727-A1.  
 XX  
 PD 24-DEC-1997.  
 XX  
 PF 18-JUN-1997; 97WO-SE001091.  
 XX  
 PR 20-JUN-1996; 96SE-00002496.  
 XX  
 (GUSS/) GUSS B.  
 PA (NILS/) NILSSON M.  
 PA (FRYK/) FRYKBERG L.  
 PA (FLOCK/) FLOCK J.  
 PA (LIND/) LINDBERG M.  
 XX  
 Guss B, Nilsson M, Frykberg L, Flock J, Lindberg M;  
 PI  
 XX

24 576 19.1 1349 4 AAU34402 Aau34402 Staphyloc  
 25 576 19.1 1349 6 ABM72436 Abm72436 Staphyloc  
 26 559 18.6 1385 6 ABU16400 Abu16400 Protein e  
 27 499.5 16.6 932 4 AAU36845 Aau36845 Staphyloc  
 28 499.5 16.6 932 4 AAU34082 Aau34082 Staphyloc  
 29 499 16.6 1802 3 AAY83170 Aay83170 Cell wall  
 30 499 16.6 1802 3 AAY70119 Aay70119 Staph. ep  
 31 497 16.5 1155 4 AAG82343 Aag82343 S. epider  
 32 493 16.4 1633 6 ABU42513 Abu42513 Protein e  
 33 489 16.2 953 6 ABU16533 Abu16533 Protein e  
 34 486.5 16.1 1920 6 ABU43489 Abu43489 Protein e  
 35 476 15.8 408 9 AEB23148 Aeb23148 Ligand bi  
 36 455 15.1 841 4 AAU37158 Aau37158 Staphyloc  
 37 455 15.1 841 4 AAU34283 Aau34283 Staphyloc  
 38 455 15.1 930 2 AAY08641 Aay08641 S. aureus  
 39 455 15.1 933 6 ABJ18947 Abj18947 Pathogen  
 40 455 15.1 947 6 ABJ18940 Abj18940 Pathogen  
 41 455 15.1 995 6 ABM72437 Abm72437 Staphyloc  
 42 454 15.1 927 6 ABM72221 Abm72221 Staphyloc  
 43 454 15.1 936 2 AAW89801 Aaw89801 Staphyloc  
 44 452 15.0 933 3 AAY58435 Aay58435 Staphyloc  
 45 452 15.0 933 4 AAB569508 Aab569508 Staphyloc

DR WPI, 1998-063079/06.  
XX N-ESDB; AAV04279.  
XX Fibrinogen-binding protein from coagulase-negative Staphylococcus - used  
PT for prevention, treatment and diagnosis of Staphylococcus infection.  
XX  
XX Example 3; Fig 6; 45pp; English.  
XX  
XX The protein comprises the fibrinogen binding protein (FIG) of coagulase-  
CC negative Staphylococcus epidermidis HB. Its amino acid sequence was  
CC deduced from the isolated fig gene (see AAV04279). The closest known  
CC analogue of FIG is the clumping factor of *S. aureus* which also binds  
CC fibrinogen and promotes bacterial aggregation in serum. Recombinant FIG  
CC polypeptides can be expressed in host cells. They are used as immunogens,  
CC particularly in vaccines (which may be expressed in vivo) to protect  
CC humans and animals against coagulase-negative Staphylococcus infection.  
CC Antibodies raised against FIG can be used for passive immunisation. They  
CC block the adherence of bacteria) and for diagnosis. (Updated on 17-OCT-  
CC 2003 to standardise OS field)  
XX  
XX Sequence 1092 AA;

Query Match 100.0%; Score 3013; DB 2; Length 1092;  
Best Local Similarity 100.0%; Pred. No. 2.3e-156;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENEAFLQK 60  
DB 75 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENEAFLQK 134  
QY 61 TPQDNTHLTEREVKSSVESNSSIDTAQOPSHTTINREESVQTSNDVESHVSDFANS 120  
DB 135 TPQDNTHLTEREVKSSVESNSSIDTAQOPSHTTINREESVQTSNDVESHVSDFANS 194  
QY 121 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPINEYENKAR 180  
DB 195 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPINEYENKAR 254  
QY 181 PLSTTSAQPSIKRVTNVQALAEQGSNNVHLIKVTDQSITEGYDDSEGVIKAHDAENLIYD 240  
DB 255 PLSTTSAQPSIKRVTNVQALAEQGSNNVHLIKVTDQSITEGYDDSEGVIKAHDAENLIYD 314  
QY 241 VTFEVDKVKSGDWTVDIDKNTVPSDLTDSFTIPKIDNSGEIITATGYDNKNKIITYT 300  
DB 315 VTFEVDKVKSGDWTVDIDKNTVPSDLTDSFTIPKIDNSGEIITATGYDNKNKIITYT 374  
QY 301 FTDYVDKYENIKAHKLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNNKTIITVEYQRPENRT 360  
DB 375 FTDYVDKYENIKAHKLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNNKTIITVEYQRPENRT 434  
QY 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSGTIIDDSIIKVKYKG 420  
DB 435 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSGTIIDDSIIKVKYKG 494  
QY 421 DNQNLPSNRIRYDYSEYEDVNDYDQAOLGNNDVNNINFGNIDSPYIIKVISKYPNKDDY 480  
DB 495 DNQNLPSNRIRYDYSEYEDVNDYDQAOLGNNDVNNINFGNIDSPYIIKVISKYPNKDDY 554  
QY 481 TTIOQTVMQTTINEYTGFEFTASVDNTIAFTSSGQGGDLPPPEKTKIGDYVWEDVDK 540  
DB 555 TTIOQTVMQTTINEYTGFEFTASVDNTIAFTSSGQGGDLPPPEKTKIGDYVWEDVDK 614  
QY 541 DGIQNTNDNEKPLSNVLVTLYTPDCTSKSVRTDEGKYQFDG 582  
DB 615 DGIQNTNDNEKPLSNVLVTLYTPDCTSKSVRTDEGKYQFDG 656

RESULT 2  
ABM79019  
ID ABM79019 standard; protein; 1092 AA.  
XX  
AC ABM79019;  
XX

DT 15-JAN-2004 (first entry)  
XX Staphylococcus epidermidis polypeptide.  
DE Infection; antibacterial; vaccine.  
XX  
XX Staphylococcus epidermidis.  
OS  
XX WO2003076470-A1.  
PN  
XX 18-SEP-2003.  
PD  
XX  
XX 05-MAR-2003; 2003WO-US006415.  
PP  
XX 05-MAR-2002; 2002US-0361324P.  
PR  
XX (INHI-) INHIBITEX INC.  
PA (TEXA ) UNIV TEXAS A & M SYSTEM.  
XX  
XX Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;  
PI Robbins J, Vernachio J, Bowden MG;  
FI  
XX WPI; 2003-722324/68.  
DR  
XX New antibody recognizing a Staphylococcus epidermidis protein comprising  
PT SdrG NIN2N3, SdrG N2N3 or SdrGIR2 useful for preparing a composition for  
PT treating or preventing a coagulase-negative Staphylococcus infection.  
XX  
XX Claim 16; Page 36-37; 78pp; English.  
PS  
XX The present sequence comprises the protein sequence of a polypeptide of a  
CC coagulase-negative Staphylococcus epidermidis. A claimed monoclonal  
CC antibody recognises this protein and is used in a claimed method of  
CC treating or preventing a coagulase-negative staphylococcus infection in a  
CC human or animal, e.g. a nosocomial coagulase-negative staphylococcus  
CC infection in low birth weight infants  
XX  
XX Sequence 1092 AA;

Query Match 100.0%; Score 3013; DB 7; Length 1092;  
Best Local Similarity 100.0%; Pred. No. 2.3e-156;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENEAFLQK 60  
DB 75 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENEAFLQK 134  
QY 61 TPQDNTHLTEREVKSSVESNSSIDTAQOPSHTTINREESVQTSNDVESHVSDFANS 120  
DB 135 TPQDNTHLTEREVKSSVESNSSIDTAQOPSHTTINREESVQTSNDVESHVSDFANS 194  
QY 121 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPINEYENKAR 180  
DB 195 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPINEYENKAR 254  
QY 181 PLSTTSAQPSIKRVTNVQALAEQGSNNVHLIKVTDQSITEGYDDSEGVIKAHDAENLIYD 240  
DB 255 PLSTTSAQPSIKRVTNVQALAEQGSNNVHLIKVTDQSITEGYDDSEGVIKAHDAENLIYD 314  
QY 241 VTFEVDKVKSGDWTVDIDKNTVPSDLTDSFTIPKIDNSGEIITATGYDNKNKIITYT 300  
DB 315 VTFEVDKVKSGDWTVDIDKNTVPSDLTDSFTIPKIDNSGEIITATGYDNKNKIITYT 374  
QY 301 FTDYVDKYENIKAHKLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNNKTIITVEYQRPENRT 360  
DB 375 FTDYVDKYENIKAHKLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNNKTIITVEYQRPENRT 434  
QY 421 DNQNLPSNRIRYDYSEYEDVNDYDQAOLGNNDVNNINFGNIDSPYIIKVISKYPNKDDY 480  
DB 495 DNQNLPSNRIRYDYSEYEDVNDYDQAOLGNNDVNNINFGNIDSPYIIKVISKYPNKDDY 554  
QY 481 TTIOQTVMQTTINEYTGFEFTASVDNTIAFTSSGQGGDLPPPEKTKIGDYVWEDVDK 540  
DB 555 TTIOQTVMQTTINEYTGFEFTASVDNTIAFTSSGQGGDLPPPEKTKIGDYVWEDVDK 614  
QY 541 DGIQNTNDNEKPLSNVLVTLYTPDCTSKSVRTDEGKYQFDG 582  
DB 615 DGIQNTNDNEKPLSNVLVTLYTPDCTSKSVRTDEGKYQFDG 656





OS Staphylococcus epidermidis.  
 XX WO2004025416-A2.  
 PN 25-MAR-2004.  
 PD 15-SEP-2003; 2003WO-US028789.  
 PP 13-SEP-2002; 2002US-0410303P.  
 PR (TEXA ) UNIV TEXAS A & M SYSTEM.  
 PA (INHI-) INHIBITEX INC.  
 PA (UABR-) UAB RES FOUND.  
 XX Hook M, Xu Y, Sillanpaa JV, Sthanam N, Ponnuraj K, Patti JM;  
 PI Hutchins JT, Hall A;  
 XX WPI; 2004-315684/29.  
 XX Identifying LPXTG-containing cell wall-anchored surface proteins from  
 PT Gram positive bacteria, for treating infection caused by the bacteria,  
 PT comprises searching sequence information database for the sequence having  
 PT LPXTG-motif.  
 XX Claim 16; SEQ ID NO 21; 96pp; English.  
 PS This invention relates to a novel method of identifying LPXTG-containing  
 XX cell wall-anchored surface proteins from Gram positive bacteria that bind  
 CC to an extracellular matrix molecule which comprises searching a database  
 CC of sequence information for a putative protein sequence having the LPXTG-  
 CC motif in its C-terminal region and analysing the sequence for the  
 CC presence of one or more Immunoglobulin (Ig)-like fold regions. The  
 CC invention may be useful for the production of compounds with an  
 CC antibacterial activity or for production of a vaccine. In addition the  
 CC disclosed sequences may be useful for gene therapy. The antibody is  
 CC useful for treating or preventing an infection of Gram-positive bacteria  
 CC in a human or animal patient. The method and the proteins are useful in  
 CC generating antibodies for treating and preventing the spread of  
 CC infections of Gram positive bacteria, for interfering with, or inhibiting  
 CC binding interactions by Gram positive bacteria, for monitoring the level  
 CC of gram positive bacterial antigens, or antibodies recognising the  
 CC antigens in a human or animal patients suspected of containing the  
 CC antigens or antibodies, in preventing or reducing infection of medical  
 CC devices and prosthesis caused by such organisms, and in treating or  
 CC preventing infections in highly susceptible groups such as premature  
 CC newborns, AIDS and debilitated cancer patients, and bone marrow  
 CC transplantation. The present sequence is that of a surface anchored LPXTG  
 CC protein identified using the method of the invention.  
 XX Sequence 892 AA;  
 SQ

Query Match 93.3%; Score 2810.5; DB 8; Length 892;  
 Best Local Similarity 93.6%; Pred. No. 2.1e-145;  
 Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;  
 1 SSDEKNDVINNQSIINTDDNQ-IKKEETNNYDGIKRSSEDRFESTTNVDENAEATFLQK 60  
 35 SSNEKNDVINNQSIINTDDNQ-IKKEETNSDAIENRSKDITQSTNVNVDENAEATFLQK 93  
 61 TPQDNTHLTREVEKSSVESNSSIDTAQOPSHTTINREESVQTSNDVDSHVSDFANS 120  
 94 TPQDNTHLTREVEKSSVESNSSIDTAQOPSHTTINSEASIQTSNDNEERSVDFANS 153  
 121 KIKESNTSGKEENTIEQPNKVEDSTTSQPSGYTNIDEKISNQDELLNLPINYEKAR 180  
 154 KIKESNTSGKEENTIEQPNKVEDSTTSQPSGYTNIDEKISNQDELLNLPINYEKAR 213  
 181 PLSTTSQAQPSKRVTVNQLAEOGSNVNHLIKVTDQSTIEGYDDSEGVKAHDAENLIYD 240  
 214 PLSTTSQAQPSKRVTVNQLAEOGSNVNHLIKVTDQSTIEGYDDSEGVKAHDAENLIYD 273  
 241 VTFEVDKVKSGDWTMTVDIKNTVPSDLTDSFTPIPKIDNSGEIATQTYNKNKQIYTT 300

Db 274 VTFEVDKVKSGDWTMTVDIKNTVPSDLTDSFAIPKIDNSGEIATQTYNKNKQIYTT 333  
 Qy 301 PTDYVDKYENIKAHCLKLTSYIDKSKVPNNNTKLDVEYKLTALSSVNKTITVYQRPNEVRT 360  
 Db 334 PTDYVDKYENIKAHCLKLTSYIDKSKVPNNNTKLDVEYKLTALSSVNKTITVYQRPNEVRT 393  
 Qy 361 ANLOSMFTNIDTKNHTVEQTIYINPLYSABETNWNISGNGDEGSTIIDDSSTIIKVKVG 420  
 Db 394 ANLOSMFTNIDTKNHTVEQTIYINPLYSABETNWNISGNGDEGSTIIDDSSTIIKVKVG 453  
 Qy 421 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDNVNINFGNIDSPYIIKVISKYDPNKDDY 480  
 Db 454 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDNVNINFGNIDSPYIIKVISKYDPNKDDY 513  
 Qy 481 TTIQOTVTMOTTINEYTGEPRTASYDNTIAFSTSSGQGGDLPPKTYKIGDYVWEDVDK 540  
 Db 514 TTIQOTVTMOTTINEYTGEPRTASYDNTIAFSTSSGQGGDLPPKTYKIGDYVWEDVDK 573  
 Qy 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDDEGKYQPDG 582  
 Db 574 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDDEGKYQPDG 615

RESULT 5  
 ADS20651  
 ID ADS20651 standard; protein; 892 AA.  
 XX AC ADS20651;  
 XX DT 30-DEC-2004 (first entry)  
 XX DE S. epidermidis hyperimmune serum reactive antigen protein - SEQ ID 52.  
 XX KW antigen; antibiotic resistance; antibacterial; vaccine; gene therapy.  
 XX OS Staphylococcus epidermidis.  
 XX PN WO2004087746-A2.  
 XX PD 14-OCT-2004.  
 XX PF 31-MAR-2004; 2004WO-EP003398.  
 XX PR 31-MAR-2003; 2003EP-00450078.  
 XX PA (INTE-) INTERCELL AG.  
 XX PI Meinke A, Min Bui D, Nagy E;  
 XX WPI; 2004-729219/71.  
 XX N-ESDB; ADS20620.  
 XX New nucleic acid molecules encoding hyperimmune serum reactive antigens  
 PT from Staphylococcus epidermidis, useful for diagnosing, preventing or  
 PT treating S. epidermidis infections.  
 XX Claim 11; SEQ ID NO 52; 196pp; English.  
 XX The invention relates to a novel isolated nucleic acid molecule encoding  
 CC a hyperimmune serum reactive antigen or its fragment. Staphylococcus  
 CC commonly associated with human disease. Both Staphylococcus epidermidis  
 CC and Staphylococcus aureus have become resistant to many commonly used  
 CC antibiotics, most importantly methicillin (MRSA) and vancomycin (VISA).  
 CC drug resistance is an increasingly important public health concern and  
 CC novel therapies to combat staphylococci infection must be developed in  
 CC preparation for a time when such infections may be untreatable by  
 CC antibiotics. The molecules of the invention demonstrate antibacterial  
 CC activity and may be useful for manufacturing a medicament, such as a  
 CC vaccine, for treating or preventing S. epidermidis infections, possibly  
 CC via gene therapy. The antigen or its fragment may also be used for  
 CC generating an anticaline peptide binding to the hyperimmune serum  
 CC reactive antigen or fragment, for manufacturing a functional nucleic  
 CC acid, such as an aptamer or spiegelmer and for manufacturing a functional

CC ribonucleic acid, such as a ribozyme, antisense nucleic acid or siRNA  
CC (short interfering RNA). The current sequence is that of a Staphylococcus  
CC epidermidis hyperimmune serum reactive antigen protein of the invention.  
XX  
SQ Sequence 892 AA;

Query Match 93.3%; Score 2810.5; DB 8; Length 892;  
Best Local Similarity 93.6%; Pred. No. 2.1e-145;  
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;  
QY 1 SSDEEKNDVNNQSIINTDDNNQIIKKEETNNYDGIKESRDETSSTNNVDNEATFLOK 60  
DB 35 SSNEEKNDVINNSQSINTDDNQ- IKKEETNSDNLNENSKDITQSTNNVDNEATFLOK 93  
QY 61 TPQDNTHLTTEEVKSSSVSSSSIDTAQPSHTTINREESVQTSNDVSDSHVSPANS 120  
DB 94 TPQDNTHLTTEEVKSSSVSSSSMDTAQPSHTTINSEASITQSDNEENSRSVPANS 153  
QY 121 KIKESNTSGKENTIEQPNKVEDSTTSQPSGYTNIDKISNQDELLNLPINEYENKAR 180  
DB 154 KIKESNTSGKENTIEQPNKVEDSITQPSGYTKNIDKISNQDELLNLPINEYENKVR 213  
QY 181 PLSTTSAQPSIKRVTNQLAAEQGSNNVHLIKVTDQSITGVDSDSGVIKAHDAENLIYD 240  
DB 214 PLSTTSAQPSIKRVTNQLAAEQGSNNVHLIKVTDQSITGVDSDSGVIKAHDAENLIYD 273  
QY 241 VTFEVDKVKSGDVTMDIDKNTVPSDLTDSFTPIKIDNSGEIATGYDKNKQITVT 300  
DB 274 VTFEVDKVKSGDVTMDIDKNTVPSDLTDSFPAIKIDNSGEIATGYDNTNKQITVT 333  
QY 301 FTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKLDVEYKTALSSVNTITVEYQRPNEKT 360  
DB 334 FTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKLDVEYKTALSSVNTITVEYQRPNEKT 393  
QY 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNDEGSTIIDSTIIKVKYVG 420  
DB 394 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNDEGSTIIDSTIIKVKYVG 453  
QY 421 DNQNLPSNRIYDYSEYEDVTNDYDQAQLGNNDVNFNFGNIDSPYIIKVISKYPNKODY 480  
DB 454 DNQNLPSNRIYDYSEYEDVTNDYDQAQLGNNDVNFNFGNIDSPYIIKVISKYPNKODY 513  
QY 481 TTIQQTVMQTTINEYTGFBRTASYDNTIAFSTSSGQGGDLPPKTKYKIGYVWEDVDK 540  
DB 514 TTIQQTVMQTTINEYTGFBRTASYDNTIAFSTSSGQGGDLPPKTKYKIGYVWEDVDK 573  
QY 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 582  
DB 574 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 615

RESULT 6  
ABP40469  
ID ABP40469 standard; protein; 930 AA.  
XX  
AC ABP40469;  
XX  
DT 24-JUL-2002 (first entry)  
XX  
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5314.  
XX  
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;  
XX antibacterial; gene therapy.  
XX  
OS Staphylococcus epidermidis.  
XX  
PN US6380370-B1.  
XX  
PD 30-APR-2002.  
XX  
PF 13-AUG-1998; 98US-00134001.  
XX  
PR 14-AUG-1997; 97US-0055779P.

PR 08-NOV-1997; 97US-0064964P.  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Doucette-Stamm LA, Bush D;  
XX  
DR WPI; 2002-381255/41.  
DR N-PSDB; ABN93014.  
XX  
PT Novel isolated nucleic acid encoding a Staphylococcus epidermis  
XX polypeptide, useful for diagnosing and treating bacterial infections.  
PS Disclosure; SEQ ID NO 5314; 267pp; English.  
XX  
CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading  
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences  
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have  
CC antibacterial activity and can be used in gene therapy. The sequences can  
CC also be used in the diagnosis and treatment of bacterial infections,  
CC particularly S. epidermidis infections. The sequences can be used to  
CC screen for compounds able to interfere with the S. epidermidis life cycle  
CC or inhibit S. epidermidis infection. N.B. The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from the USPTO web site

SQ Sequence 930 AA;

Query Match 93.3%; Score 2810.5; DB 5; Length 930;  
Best Local Similarity 93.6%; Pred. No. 2.3e-145;  
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;  
QY 1 SSDEEKNDVNNQSIINTDDNNQIIKKEETNNYDGIKESRDETSSTNNVDNEATFLOK 60  
DB 73 SSNEEKNDVINNSQSINTDDNQ- IKKEETNSDNLNENSKDITQSTNNVDNEATFLOK 131  
QY 61 TPQDNTHLTTEEVKSSSVSSSSIDTAQPSHTTINREESVQTSNDVSDSHVSPANS 120  
DB 132 TPQDNTHLTTEEVKSSSVSSSSMDTAQPSHTTINSEASITQSDNEENSRSVPANS 191  
QY 121 KIKESNTSGKENTIEQPNKVEDSTTSQPSGYTNIDKISNQDELLNLPINEYENKAR 180  
DB 192 KIKESNTSGKENTIEQPNKVEDSITQPSGYTKNIDKISNQDELLNLPINEYENKVR 251  
QY 181 PLSTTSAQPSIKRVTNQLAAEQGSNNVHLIKVTDQSITGVDSDSGVIKAHDAENLIYD 240  
DB 252 PLSTTSAQPSIKRVTNQLAAEQGSNNVHLIKVTDQSITGVDSDSGVIKAHDAENLIYD 311  
QY 241 VTFEVDKVKSGDVTMDIDKNTVPSDLTDSFTPIKIDNSGEIATGYDKNKQITVT 300  
DB 312 VTFEVDKVKSGDVTMDIDKNTVPSDLTDSFPAIKIDNSGEIATGYDNTNKQITVT 371  
QY 301 FTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKLDVEYKTALSSVNTITVEYQRPNEKT 360  
DB 372 FTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKLDVEYKTALSSVNTITVEYQRPNEKT 431  
QY 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNDEGSTIIDSTIIKVKYVG 420  
DB 432 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNDEGSTIIDSTIIKVKYVG 491  
QY 421 DNQNLPSNRIYDYSEYEDVTNDYDQAQLGNNDVNFNFGNIDSPYIIKVISKYPNKODY 480  
DB 492 DNQNLPSNRIYDYSEYEDVTNDYDQAQLGNNDVNFNFGNIDSPYIIKVISKYPNKODY 551  
QY 481 TTIQQTVMQTTINEYTGFBRTASYDNTIAFSTSSGQGGDLPPKTKYKIGYVWEDVDK 540  
DB 552 TTIQQTVMQTTINEYTGFBRTASYDNTIAFSTSSGQGGDLPPKTKYKIGYVWEDVDK 611  
QY 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 582  
DB 612 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 653

RESULT 7



XX 31-AUG-1998; 98US-0098443P.  
PR 25-JAN-1999; 99US-0117119P.  
XX  
XX (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.  
PA (TEXA ) UNIV TEXAS A & M SYSTEM.  
XX  
XX Foster TJ, Hook M, Davis S, Hartford O, Mccrea K, Ni Eidhin D;  
PI  
XX WPI; 2000-256637/22.  
DR N-PSDB; AA293534.  
XX  
XX Recombinant or synthetic proteins from coagulase-negative staphylococci  
PT useful for prevention, treatment and diagnosis of staphylococcal  
PT infections bind soluble and immobilized fibrinogen.  
XX  
XX Claim 8; Fig 3; 104pp; English.  
XX  
XX Isolated Staphylococcus Sdr cell wall proteins which bind both soluble  
CC and immobilized fibrinogen are useful for treating or preventing  
CC coagulase-negative staphylococcal infection such as septicemia,  
CC osteomyelitis or endocarditis, and for inducing immune responses in  
CC patients. The cell wall proteins are also useful for reducing coagulase-  
CC negative staphylococci infection of indwelling medical devices such as  
CC vascular grafts, vascular stents, intravenous catheters, artificial heart  
CC valves and cardiac assist devices. The cell wall associated proteins are  
CC able to inhibit staphylococcal adhesion to immobilised extracellular  
CC matrix or host cells present on the surface of implanted biomaterials  
XX  
XX Sequence 991 AA;  
SQ  
Query Match 93.3%; Score 2810.5; DB 3; Length 991;  
Best Local Similarity 93.6%; Pred. No. 2.5e-145;  
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;  
QY 1 SDEEKNVNNQSTINTDNNQIIKKEETNNYDGIKESRDETRSTTNNVDNEATFLOK 60  
DB 106 SNEEKNVNNQSTINTDNNQ- I KKEETNNDAIENRSKDTOSTTNNVDNEATFLOK 164  
QY 61 TPQDNTHTLTEEVKSSSVESNSSIDTAQPSHTTINREESVQTSNDVDSHVSDFANS 120  
DB 165 TPQDNTQLKEEVKSPSSVESNSSMDTAQPSHTTINSEASIQTSNDNEERSVDFANS 224  
QY 121 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISQDELLMLPINEYENKAR 180  
DB 225 KIIESNTESKEENTIEQPNKVKEDSITSPQSYKNIDEKISQDELLMLPINEYENKVR 284  
QY 181 PLSTTSAQPSIKRVTNQLAAGQSGNVNHLIKVTQSIITEGYDDSEGVIKAHDAENLIYD 240  
DB 285 PLSTTSAQPSKRVTVNQLAAGQSGNVNHLIKVTQSIITEGYDDSDGIKAHDAENLIYD 344  
QY 241 VTFEVDDKVKSGDTMTVDIDKNTVPSDLTDSFTPIKIDNSGEIATGYDNKNKOITVT 300  
DB 345 VTFEVDDKVKSGDTMTVDIDKNTVPSDLTDSFAIPKIDNSGEIATGYDNKNKOITVT 404  
QY 301 FTDYVDKVENIKAHKLKLSYIDSKSVNNNTKLDVEYKLTALSSVNTKITVEYQENRNT 360  
DB 405 FTDYVDKVENIKAHKLKLSYIDSKSVNNNTKLDVEYKLTALSSVNTKITVEYQENRNT 464  
QY 361 ANLQSMFTNIDPKNTVETQTIYNPLRYSAKETNNVNSGNGEGSTIIDSTIIKVKYVG 420  
DB 465 ANLQSMFTNIDPKNTVETQTIYNPLRYSAKETNNVNSGNGEGSTIIDSTIIKVKYVG 524  
QY 421 DNQNLPSDSNRIYDYSEYEDVTNDVDAQLGNNDNVNFGNIDSPYIIKVISKYDNKDDY 480  
DB 525 DNQNLPSDSNRIYDYSEYEDVTNDVDAQLGNNDNVNFGNIDSPYIIKVISKYDNKDDY 584  
QY 481 TTIIQQTVMQTITNEYTGFEFTASVDNTIAFTSSGQGGDLPPKPKTKIGYVWEDVDK 540  
DB 585 TTIIQQTVMQTITNEYTGFEFTASVDNTIAFTSSGQGGDLPPKPKTKIGYVWEDVDK 644  
QY 541 DGIQNTDNEKPLSNVLTLYTPDGTGTSKSVRTDEGKYQFDG 582  
|||||

Db 645 DGIQNTDNEKPLSNVLTLYTPDGTGTSKSVRTDEGKYQFDG 686

## RESULT 9

AY70120  
ID AAY70120 standard; protein; 991 AA.  
XX  
XX AC AAY70120;  
XX  
XX 06-JUN-2000 (first entry)  
XX  
XX Staph. epidermidis serine-aspartate repeat region protein SdrG.  
XX  
XX Multicomponent vaccine; immunostimulatory; antibacterial; MSCRAMM;  
KW microbial surface components recognising adhesive matrix molecules;  
KW collagen binding protein; CBP; CNA; fibrinogen binding protein;  
KW Clumping factor A; ClfA; Clumping factor B; ClfB; FnBP;  
KW fibronectin binding protein; Staphylococcus infection;  
KW serine-aspartate repeat region protein; SDR protein; SdrG.  
XX  
XX Staphylococcus epidermidis.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 14  
FT /note= "Encoded by in-frame stop codon TAG"  
FT Misc-difference 33  
FT /note= "Encoded by in-frame stop codon TGA"  
FT Misc-difference 964  
FT /note= "Encoded by in-frame stop codon TAA"  
FT Misc-difference 980  
FT /note= "Encoded by in-frame stop codon TAG"  
FT Misc-difference 989  
FT /note= "Encoded by in-frame stop codon TAA"  
XX  
XX WO200012131-A1.  
XX  
XX 09-MAR-2000.  
XX  
XX 31-AUG-1999; 99WO-US019727.  
XX  
XX 31-AUG-1998; 98US-0098439P.  
XX  
XX (INHI-) INHIBITEX INC.  
PA (TEXA ) UNIV TEXAS A & M SYSTEM.  
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.  
XX  
XX Patti JM, Foster TJ, Hook M;  
PI  
XX WPI; 2000-237781/20.  
DR N-PSDB; AA251202.  
XX  
XX Composition used for generating immune response or for inhibiting  
PT microbial colonization in an animal comprises antibodies that bind  
PT collagen binding protein, fibrinogen binding protein and, optionally,  
PT fibronectin binding protein.  
XX  
XX Claim 8; Fig 4; 115pp; English.  
XX  
XX The patent discloses multicomponent vaccines containing selected  
CC combinations of bacterial binding proteins termed MSCRAMM (microbial  
CC surface components recognising adhesive matrix molecules) or their  
CC antibodies. A vaccine composition is provided that includes collagen  
CC binding protein or peptide, e.g. CNA, a fibrinogen binding protein  
CC preferably Clumping factor A (ClfA) or Clumping factor B (ClfB), and  
CC optionally a fibronectin binding protein e.g. FnBP-A. The vaccines are  
CC useful for imparting protection against a broad spectrum of  
CC Staphylococcal strains and for inhibiting microbial colonisation,  
CC especially of Staphylococcus aureus, in an animal. The combinations  
CC also be used to select donor blood pools for the preparation of purified  
CC blood products for passive immunisation. The present sequence is a serine  
CC aspartate repeat region protein, SdrG from Staphylococcus epidermidis.  
CC The Sdr protein is useful in vaccine preparation in combination with  
CC specific bacterial binding proteins. These vaccines can be used to treat

CC a broad spectrum of bacterial infections, including those arising from  
 CC both coagulase-positive and coagulase-negative bacteria  
 XX  
 SQ Sequence 991 AA;

Query Match 93.3%; Score 2810.5; DB 3; Length 991;  
 Best Local Similarity 93.6%; Pred. No. 2.5e-145;  
 Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;  
 Qy 1 SSDEKNDVINNNQSIINTDDNQ-IKKEETNSDAIENKSDITQSTTNVDENEATFLQK 164  
 Db SSDEKNDVINNNQSIINTDDNQ-IKKEETNSDAIENKSDITQSTTNVDENEATFLQK 164  
 Qy 61 TPQDNTHLTREEVKSESSVSSNSIDTAQPSHTTINREESVQTSNDVESHVSDPANS 120  
 Db TPQDNTHLTREEVKSESSVSSNSIDTAQPSHTTINREESVQTSNDVESHVSDPANS 120  
 Qy 121 KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNOBELNLPLINEYENKAR 180  
 Db KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNOBELNLPLINEYENKAR 180  
 Qy 225 KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNOBELNLPLINEYENKAR 284  
 Db KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNOBELNLPLINEYENKAR 284  
 Qy 181 PLSTTSQAQPSIKRVTVNQLAAEQSGSNVNLHLYKVTDSITQSGYDSEGVKAHAENLIYD 240  
 Db PLSTTSQAQPSIKRVTVNQLAAEQSGSNVNLHLYKVTDSITQSGYDSEGVKAHAENLIYD 240  
 Qy 241 VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIATGYDNKNKQIYTT 300  
 Db VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIATGYDNKNKQIYTT 300  
 Qy 301 FTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKLDVEYKLTALSSVNTKTITVEYQRPENRT 360  
 Db FTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKLDVEYKLTALSSVNTKTITVEYQRPENRT 360  
 Qy 361 ANLOSMTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSIIDDDSTIIKVKYKG 420  
 Db ANLOSMTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSIIDDDSTIIKVKYKG 420  
 Qy 421 DNQNLPSNRIYDYSEYEDVNDYDVAQLGNNDVNIINFGNIDSPYIIKVISKYDPNKDDY 480  
 Db DNQNLPSNRIYDYSEYEDVNDYDVAQLGNNDVNIINFGNIDSPYIIKVISKYDPNKDDY 480  
 Qy 481 TTIOQTVMQTINEYTGFEPTASVDNTIAFSTSGQGQGLPPEKTYKIGDYVWEDVDK 540  
 Db TTIOQTVMQTINEYTGFEPTASVDNTIAFSTSGQGQGLPPEKTYKIGDYVWEDVDK 540  
 Qy 541 DGIQNTNDEKPLSNVLVTLYPDGTSKSVRTDEGKYQFDG 582  
 Db DGIQNTNDEKPLSNVLVTLYPDGTSKSVRTDEGKYQFDG 582

RESULT 10  
 ABM79020  
 ID ABM79020 standard; protein; 549 AA.

XX AC ABM79020;

XX DT 15-JAN-2004 (first entry)

XX Staphylococcus epidermidis polypeptide.

XX Infection; antibacterial; vaccine.

XX Staphylococcus epidermidis.

XX WO2003076470-A1.

XX 18-SEP-2003.

XX 05-MAR-2003; 2003WO-US006415.

XX 05-MAR-2002; 2002US-0361324P.

XX (INH1-) INHIBITEX INC.

(TEXA ) UNIV TEXAS A & M SYSTEM.

XX Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;  
 PI Robbins J, Vernachio J, Bowden MG;

XX WPI; 2003-722324/68.

XX New antibody recognizing a Staphylococcus epidermidis protein comprising  
 PT SdrG N1N2N3, SdrG N2N3 or SdrG R2 useful for preparing a composition for  
 PT treating or preventing a coagulase-negative Staphylococcal infection.

XX Claim 20; Page 37; 78pp; English.

XX The present sequence comprises the protein sequence of a polypeptide of a  
 CC coagulase-negative Staphylococcus epidermidis. A claimed monoclonal  
 CC antibody recognizes this protein and is used in a claimed method of  
 CC treating or preventing a coagulase-negative staphylococcal infection in a  
 CC human or animal, e.g. a nosocomial coagulase-negative staphylococcal  
 CC infection in low birth weight infants

XX Sequence 549 AA;

Query Match 88.6%; Score 2670; DB 7; Length 549;  
 Best Local Similarity 98.7%; Pred. No. 5.5e-138;  
 Matches 519; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SSDEKNDVINNNQSIINTDDNQ-IKKEETNNYOGIEKRSSEDRTESTTNVDENEATFLQK 60  
 Db SSDEKNDVINNNQSIINTDDNQ-IKKEETNNYOGIEKRSSEDRTESTTNVDENEATFLQK 60  
 Qy 61 TPQDNTHLTREEVKSESSVSSNSIDTAQPSHTTINREESVQTSNDVESHVSDPANS 120  
 Db TPQDNTHLTREEVKSESSVSSNSIDTAQPSHTTINREESVQTSNDVESHVSDPANS 120  
 Qy 84 SPQDNTHLTREEVKSESSVSSNSIDTAQPSHTTINREESVQTSNDVESHVSDPANS 143  
 Db SPQDNTHLTREEVKSESSVSSNSIDTAQPSHTTINREESVQTSNDVESHVSDPANS 143  
 Qy 121 KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNOBELNLPLINEYENKAR 180  
 Db KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNOBELNLPLINEYENKAR 180  
 Qy 181 PLSTTSQAQPSIKRVTVNQLAAEQSGSNVNLHLYKVTDSITQSGYDSEGVKAHAENLIYD 240  
 Db PLSTTSQAQPSIKRVTVNQLAAEQSGSNVNLHLYKVTDSITQSGYDSEGVKAHAENLIYD 240  
 Qy 241 VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIATGYDNKNKQIYTT 300  
 Db VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIATGYDNKNKQIYTT 300  
 Qy 264 VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIATGYDNKNKQIYTT 323  
 Db VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIATGYDNKNKQIYTT 323  
 Qy 301 FTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKLDVEYKLTALSSVNTKTITVEYQRPENRT 360  
 Db FTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKLDVEYKLTALSSVNTKTITVEYQRPENRT 360  
 Qy 324 FTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKLDVEYKLTALSSVNTKTITVEYQRPENRT 383  
 Db FTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKLDVEYKLTALSSVNTKTITVEYQRPENRT 383  
 Qy 361 ANLOSMTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSIIDDDSTIIKVKYKG 420  
 Db ANLOSMTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSIIDDDSTIIKVKYKG 420  
 Qy 384 ANLOSMTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSIIDDDSTIIKVKYKG 443  
 Db ANLOSMTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSIIDDDSTIIKVKYKG 443  
 Qy 421 DNQNLPSNRIYDYSEYEDVNDYDVAQLGNNDVNIINFGNIDSPYIIKVISKYDPNKDDY 480  
 Db DNQNLPSNRIYDYSEYEDVNDYDVAQLGNNDVNIINFGNIDSPYIIKVISKYDPNKDDY 480  
 Qy 444 DNQNLPSNRIYDYSEYEDVNDYDVAQLGNNDVNIINFGNIDSPYIIKVISKYDPNKDDY 503  
 Db DNQNLPSNRIYDYSEYEDVNDYDVAQLGNNDVNIINFGNIDSPYIIKVISKYDPNKDDY 503  
 Qy 481 TTIOQTVMQTINEYTGFEPTASVDNTIAFSTSGQGQGLPPEK 526  
 Db TTIOQTVMQTINEYTGFEPTASVDNTIAFSTSGQGQGLPPEK 526

RESULT 11  
 ABM79015  
 ID ABM79015 standard; protein; 560 AA.

XX AC ABM79015;

XX DT 15-JAN-2004 (first entry)

XX Staphylococcus epidermidis SdrG N1N2N3 domain.

KW SdrG; surface protein; infection; antibacterial; vaccine.

OS Staphylococcus epidermidis.

XX WO2003076470-A1.

XX 18-SEP-2003.

XX 05-MAR-2003; 2003WO-US006415.

XX 05-MAR-2002; 2002US-0361324P.

XX (INHI-) INHIBITEX INC.

XX (TEXA ) UNIV TEXAS A & M SYSTEM.

XX Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;

XX Robbins J, Vernachio J, Bowden MG;

XX WPI; 2003-722324/68.

XX N-PSDB; ACF80624.

XX New antibody recognizing a Staphylococcus epidermidis protein comprising SdrG N1N2N3, SdrG N2N3 or SdrGTR2 useful for preparing a composition for treating or preventing a coagulase-negative Staphylococcal infection.

XX Claim 27; Page 24-25; 78pp; English.

XX The present sequence comprises the protein sequence of the N1N2N3 region (amino acids 50-597), or putative A domain, of the SdrG surface protein of coagulase-negative Staphylococcus epidermidis. A claimed antibody recognises a protein selected from SdrG N1N2N3, N2N3 and TR2. The antibody may be a monoclonal antibody, including a chimeric, murine, humanized, human or single chain monoclonal antibody, which prevents a coagulase-negative staphylococcal infection in a human or animal by inhibiting binding of staphylococcus bacteria to fibrinogen. Such antibodies can be used to treat or prevent staphylococcal infections including nosocomial coagulase-negative staphylococcal infections in low birth weight infants. A claimed vaccine comprises the isolated SdrG N1N2N3, N2N3 or TR2 protein

XX Sequence 560 AA;

Query Match 83.3%; Score 2510.5; DB 7; Length 560;

Best Local Similarity 93.2%; Pred. No. 3e-129;

Matches 490; Conservative 14; Mismatches 21; Indels 1; Gaps 1;

QY 1 SSDEKNDVNNQSIINTDDNNQIKKETNNYDGTGKESEDRSTSTNNVDENEATFLOK 60

DB 36 SNEERNDVNNQSINTDDNNQ- IKKETNSDAIENRSKIDTOSTNNVDENEATFLOK 94

QY 61 TPQDNTLHTEERVKESSSVSSNSSIDTAQPSHTTINREESVQTSNDVDSHVSDFANS 120

DB 95 TPQDNTQLKEVVKEPSSVSSNSSMDTAQPSHTTINSEASIQSDNEERSVDSDFANS 154

QY 121 KIKESNTSGKENTIEQKNVKESSTTSQPSGYTNIDKISQDELNLPLINEYENKAR 180

DB 155 KIKESNTSGKENTIEQKNVKESSTTSQPSGYTNIDKISQDELNLPLINEYENKVR 214

QY 181 PLSTTSAPQSIKRVTVNQLAAEGSNVNLIKVTQSIQTEGYDDSEGVIKAHDAENLYD 240

DB 215 PLSTTSAPQSSKRVTVNQLAAEGSNVNLIKVTQSIQTEGYDDSEGVIKAHDAENLYD 274

QY 241 VTFEVDKVKSGDVTVDIDKNTVPSDLTDSFTPIKIDKNSGEIATGYDNKNKQITVT 300

DB 275 VTFEVDKVKSGDVTVDIDKNTVPSDLTDSFAPKIDKNSGEIATGYDNKNKQITVT 334

QY 301 FTDYVDKVENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKTALSSVNTITVEYQRPENRT 360

DB 335 FTDYVDKVENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKTALSSVNTITVEYQKPNENRT 394

QY 361 ANLQSMFTNIDPKNTVEQTIYINPLRYSAKETNNISGNGEGSTIIDSIIKVKYVG 420

DB 395 ANLQSMFTNIDPKNTVEQTIYINPLRYSAKETNNISGNGEGSTIIDSIIKVKYVG 454

QY 421 DNQNLPSNRIYDYSEYEDVTNDYVAQLGNNDVNINFGNNDVNIPIIKVSKYDPNKDDY 480  
DB 455 DNQNLPSNRIYDYSEYEDVTNDYVAQLGNNDVNINFGNNDVNIPIIKVSKYDPNKDDY 514  
QY 481 TTIIQQTVMQTTINETYGTGFRTASVDNTIAFSTSSGQGGDLPEK 526  
DB 515 TTIIQQTVMQTTINETYGTGFRTASVDNTIAFSTSSGQGGDLPEK 560

RESULT 12

AEB23146

ID AEB23146 standard; protein; 331 AA.

XX AEB23146;

XX 08-SEP-2005 (first entry)

XX DE Ligand binding region of bacterial adhesin, SdrG.

KW candida infection; candida albicans infection; infection;

KW antibody therapy; antigen; diagnosis; immunotherapy;

KW serine-aspartate repeat G; SdrG; adhesin; fungicide.

XX Staphylococcus epidermidis.

XX WO2005060713-A2.

XX 07-JUL-2005.

XX 20-DEC-2004; 2004WO-US043276.

XX 19-DEC-2003; 2003US-0530654P.

XX 13-APR-2004; 2004US-0561540P.

XX 29-APR-2004; 2004US-0566082P.

XX (INHI-) INHIBITEX INC.

XX (TEXA ) UNIV TEXAS A & M SYSTEM.

XX Patti J, Vernachio J, Liu Y, Hook M, Bowden M, Singvall JK;

XX WPI; 2005-479410/48.

XX Inhibiting a Candidal infection for preventing or treating such infections by administering a purified human donor immunoglobulin composition having antibody titer to S. aureus Clfa protein and/or S. epidermidis SdrG protein.

XX Example 7; Fig 4; 42pp; English.

XX The invention relates to a method of inhibiting a Candidal infection. The method comprises administering to a patient a purified human donor immunoglobulin composition having an antibody titer to a Staphylococcus aureus Clumping Factor A (Clfa) protein in combination with an antibody titer to a Staphylococcus epidermidis serine-aspartate repeat G (SdrG) protein where both antibody titers are higher than that found in pooled intravenous immunoglobulin obtained from unselected human donors in an amount effective to inhibit a Candidal infection. Also described are: (1) a method of diagnosing a Candidal infection comprising introducing the immunoglobulin composition to a sample suspected of containing antigens from Candida yeast for a time sufficient to allow the Candida antigens to bind to the antibodies in the immunoglobulin composition, and diagnosing a Candidal infection by determining if Candida antigens in the sample have bound to the antibodies in the immunoglobulin composition; (2) a method of identifying a Candidal surface antigen comprising obtaining a cell wall extract from a culture of Candida yeast cells, introducing into the extract the immunoglobulin composition, and detecting Candida antigens that have bound to the antibodies in the immunoglobulin composition; (3) a probe for identifying Candidal surface antigens comprising the immunoglobulin composition, and a means for detecting binding of the antibodies in the immunoglobulin composition with Candidal surface antigens; and (4) a method of inhibiting an infection caused by Candida albicans comprising administering to a

CC patient a purified human donor immunoglobulin composition as cited above  
 CC in an amount effective to inhibit an infection caused by *Candida*  
 CC albicans. The methods and compositions are useful for treating or  
 CC preventing infections caused by *Candida albicans*. This sequence  
 CC represents the ligand binding region of a bacterial adhesin.  
 XX  
 SQ Sequence 331 AA;

Query Match 56.5%; Score 1702; DB 9; Length 331;  
 Best Local Similarity 98.2%; Pred. No. 2.8e-85;  
 Matches 325; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 201 AEQGSNVNHLIKVTDQSITGEYDDSEGVKKAHDAENLIYDVFVDDKVKSGDTMTVDID 260  
 Db 1 AEQGSNVNHLIKVTDQSITGEYDDSGIHKAHDAENLIYDVFVDDKVKSGDTMTVDID 60  
 Qy 261 KNTVPSDLTDSFTIPKIKDNGSEIIATGTYDNKNKQIITYTFTDYVDKYENIKAKHLKLSY 320  
 Db 61 KNTVPSDLTDSFAIPKIKDNGSEIIATGTYDNKNKQIITYTFTDYVDKYENIKAKHLKLSY 120  
 Qy 321 IDKSKVPNNNTKLDVEYKTALSSVKNKTIIVYQRPENRNTANLQSMFTNIDTKNHTVEQT 380  
 Db 121 IDKSKVPNNNTKLDVEYKTALSSVKNKTIIVYQRPENRNTANLQSMFTNIDTKNHTVEQT 180  
 Qy 381 IYINPLRYSAKETNVNISGNGDEGSIIDDSIIKVKYKVGDNQNLPSNRIYDYSEYEDV 440  
 Db 181 IYINPLRYSAKETNVNISGNGDEGSIIDDSIIKVKYKVGDNQNLPSNRIYDYSEYEDV 240  
 Qy 441 TNDDYAQLGNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIOQVTMTQTINEYTGFEF 500  
 Db 241 TNDDYAQLGNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIOQVTMTQTINEYTGFEF 300  
 Qy 501 RTASYDNTIAFSTSSGQGGDLPPKTYKIG 531  
 Db 301 RTASYDNTIAFSTSSGQGGDLPPKTYKIG 331

RESULT 13  
 ABM79016  
 ID ABM79016 standard; protein; 343 AA.  
 XX  
 AC ABM79016;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Staphylococcus epidermidis SdrG N2N3 domain.  
 XX  
 KW SdrG; surface protein; infection; antibacterial; vaccine.  
 XX  
 OS Staphylococcus epidermidis.  
 XX  
 PN WO2003076470-A1.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PF 05-MAR-2003; 2003WO-US006415.  
 XX  
 PR 05-MAR-2002; 2002US-0361324P.  
 XX  
 PA (INHI-) INHIBITEX INC.  
 XX  
 PA (TEXA) UNIV TEXAS A & M SYSTEM.  
 XX  
 PI Patti JM, Hutchins JT, Hall A, Domaneki P, Patel P, Hook M;  
 PI Robbins J, Vernachio J, Bowden MG;  
 XX  
 DR WPI; 2003-722324/68.  
 DR N-PSDB; ACF80625.  
 XX  
 PT New antibody recognizing a *Staphylococcus epidermidis* protein comprising  
 PT SdrG N1N2N3, SdrG N2N3 or SdrGTR2 useful for preparing a composition for  
 PT treating or preventing a coagulase-negative *Staphylococcus* infection.  
 XX  
 PS Claim 27; Page 25; 78pp; English.

XX The present sequence comprises the protein sequence of the N2N3 region  
 CC (amino acids 273-597) of the SdrG surface protein of coagulase-negative  
 CC *Staphylococcus epidermidis*. A claimed antibody recognises a protein  
 CC selected from SdrG N1N2N3, N2N3 and TR2. The antibody may be a monoclonal  
 CC antibody, including a chimeric, murine, humanized, human or single chain  
 CC monoclonal antibody, which prevents a coagulase-negative *staphylococcus*  
 CC infection in a human or animal by inhibiting binding of *staphylococcus*  
 CC bacteria to fibrinogen. Such antibodies can be used to treat or prevent  
 CC staphylococcal infections including nosocomial coagulase-negative  
 CC staphylococcal infections in low birth weight infants. A claimed vaccine  
 CC comprises the isolated SdrG N1N2N3, N2N3 or TR2 protein  
 XX  
 SQ Sequence 343 AA;

Query Match 55.5%; Score 1672; DB 7; Length 343;  
 Best Local Similarity 97.9%; Pred. No. 1.3e-83;  
 Matches 319; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 201 AEQGSNVNHLIKVTDQSITGEYDDSEGVKKAHDAENLIYDVFVDDKVKSGDTMTVDID 260  
 Db 18 SEQGSNVNHLIKVTDQSITGEYDDSGIHKAHDAENLIYDVFVDDKVKSGDTMTVDID 77  
 Qy 261 KNTVPSDLTDSFTIPKIKDNGSEIIATGTYDNKNKQIITYTFTDYVDKYENIKAKHLKLSY 320  
 Db 78 KNTVPSDLTDSFAIPKIKDNGSEIIATGTYDNKNKQIITYTFTDYVDKYENIKAKHLKLSY 137  
 Qy 321 IDKSKVPNNNTKLDVEYKTALSSVKNKTIIVYQRPENRNTANLQSMFTNIDTKNHTVEQT 380  
 Db 138 IDKSKVPNNNTKLDVEYKTALSSVKNKTIIVYQRPENRNTANLQSMFTNIDTKNHTVEQT 197  
 Qy 381 IYINPLRYSAKETNVNISGNGDEGSIIDDSIIKVKYKVGDNQNLPSNRIYDYSEYEDV 440  
 Db 198 IYINPLRYSAKETNVNISGNGDEGSIIDDSIIKVKYKVGDNQNLPSNRIYDYSEYEDV 257  
 Qy 441 TNDDYAQLGNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIOQVTMTQTINEYTGFEF 500  
 Db 258 TNDDYAQLGNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIOQVTMTQTINEYTGFEF 317  
 Qy 501 RTASYDNTIAFSTSSGQGGDLPPK 526  
 Db 318 RTASYDNTIAFSTSSGQGGDLPPK 343

RESULT 14  
 ABM79017  
 ID ABM79017 standard; protein; 316 AA.  
 XX  
 AC ABM79017;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Staphylococcus epidermidis SdrG TR2 protein.  
 XX  
 KW SdrG; surface protein; infection; antibacterial; vaccine.  
 XX  
 OS Staphylococcus epidermidis.  
 XX  
 PN WO2003076470-A1.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PF 05-MAR-2003; 2003WO-US006415.  
 XX  
 PR 05-MAR-2002; 2002US-0361324P.  
 XX  
 PA (INHI-) INHIBITEX INC.  
 XX  
 PA (TEXA) UNIV TEXAS A & M SYSTEM.  
 XX  
 PI Patti JM, Hutchins JT, Hall A, Domaneki P, Patel P, Hook M;  
 PI Robbins J, Vernachio J, Bowden MG;  
 XX  
 DR WPI; 2003-722324/68.





Qy	217	SITEGYDDSEGVIIKAHDAENLIYDVTFEVDDKXSGDTMTVDIDIKNTVPSDLTDSFTIPK	276
Db	290	TIKVG-DGKDNVAAAHDKDIEYDTEFTIDNKKVKGDTWTINYDKNVIPSDLTDKNDDPID	348
Qy	277	IKDMSGELIATGYDNKNKQIITYFTFDYVDKYENIKAHKLKLTSYIDKSKVPNNNTKLDVE	336
Db	349	ITDPSGEVIAKGTFDKATKQIITYFTFDYVDKYEDIKSRLLTLYSIDKKTVP-NETSLNLT	407
Qy	337	YKTALSSVNTTITVEYQRPENRRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVN	396
Db	408	FATAGKETSONVTVDYQDPMVHGDNSIQSIETKLDEDKQTEQQIYVNPPLKKSATNTKVD	467
Qy	397	ISGNG-----DEGSTIIDSTIIKVKYKGNQNLPSNRIYDYSEYEDVTND-DYA	446
Db	468	IAGSQVDDYGNIKLNGSTIIDQNTETIKVKYKNSDQQLPQSNRIYDFSQYEDVTSQFDNK	527
Qy	447	QLGNNDVNINFGNIDSPYIIKVISKYDPNKDDYTTIOQTVMQTTINEYTGEPRTASYD	506
Db	528	KSFNNVATLDFGDINSAYIIKWSKSYTPTSDGELDIAQGTSMRTT-DKY-GYNYAGYS	585
Qy	507	NTIAFSTSSGOGQDGL-PPEKTYKIGDYVWEDVDKDGIQNTNDNEKPLSNVLVLTLYPDG	565
Db	586	NPIVTSNDTGGDGTVPKEEKLYKIGDYVWEDVDKDGVGQTDSDSKEKPMANVLVLTLYPDG	645
Qy	566	TSKSVRTDEDEKYPFDG	582
Db	646	TTKSVRTDANGHYEFGG	662

Search completed: August 12, 2006, 08:59:40  
Job time : 195 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2006, 09:05:06 ; Search time 50 Seconds  
(without alignments)  
1018.857 Million cell updates/sec

Title: US-10-806-288-13  
Perfect score: 3013  
Sequence: 1 SSDEKNDVINNNQSIINTDD.....PDGTSKVRTEDEGKYQFDG 582

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pcp.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pcp.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pcp.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB.pcp.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCUTS COMB.pcp.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pcp.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3013	100.0	582	2	US-09-147-405B-13
2	3013	100.0	593	2	US-09-147-405B-11
3	3013	100.0	1092	2	US-09-147-405B-15
4	2810.5	93.3	930	2	US-09-134-001C-5314
5	2810.5	93.3	930	2	US-09-386-962C-10
6	1144.5	38.0	1166	2	US-09-200-650E-7
7	857	28.4	278	2	US-09-710-279-2700
8	576	19.1	1315	2	US-09-200-650E-5
9	499	16.6	1742	2	US-09-386-962C-4
10	499	16.6	1742	2	US-09-386-959-4
11	497	16.5	1155	2	US-09-710-279-1780
12	455	15.1	930	2	US-09-200-650E-3
13	454	15.1	936	2	US-08-956-171E-5249
14	454	15.1	936	2	US-08-781-986A-5249
15	452	15.0	933	2	US-08-293-728-2
16	452	15.0	933	2	US-09-421-868-2
17	452	15.0	933	2	US-09-679-643-2
18	443.5	14.7	520	2	US-10-056-052A-2
19	396	13.1	918	2	US-09-200-650E-1
20	349	11.6	331	2	US-10-056-052A-4
21	349	11.6	345	2	US-08-856-253-7
22	300.5	10.0	1027	2	US-08-956-171E-5254
23	300.5	10.0	1027	2	US-08-781-986A-5254
24	259.5	8.6	1112	1	US-08-714-402-2
25	259.5	8.6	1161	2	US-09-327-536-2
26	220.5	7.3	3696	2	US-09-134-001C-5080

ALIGNMENTS

RESULT 1

US-09-147-405B-13

; Sequence 13, Application US/09147405B

; Patent No. 6733758

; GENERAL INFORMATION:

; APPLICANT: Guss, Bengt

; APPLICANT: Nilsson, Martin

; APPLICANT: Frykberg, Lars

; APPLICANT: Flock, Jan-Ingmar

; APPLICANT: Lindberg, Martin

; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from

; TITLE OF INVENTION: Coagulase-Negative Staphylococcus

; FILE REFERENCE: guss 09/147405

; CURRENT APPLICATION NUMBER: US/09/147,405B

; PRIOR FILING DATE: 1999-04-11

; PRIOR APPLICATION NUMBER: PCT/SE97/10191

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: SE 9602496-3

; PRIOR FILING DATE: 1996-06-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 13

; LENGTH: 582

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-147-405B-13

Query Match	100.0%;	Score 3013;	DB 2;	Length 582;
Best Local Similarity	100.0%;	Pred. No. 4.6e-171;		
Matches 582;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SSDEKNDVINNNQSIINTDDNNQIIKKGETNNYDGIKESDRTSTTNVDNEATFLOK	60	
Db	1	SSDEKNDVINNNQSIINTDDNNQIIKKGETNNYDGIKESDRTSTTNVDNEATFLOK	60	
QY	61	TPQDNTHLTEERVKSSSVSSNSSIDTAQPSHTTINREESVQTSNDVSDHVSDFANS	120	
Db	61	TPQDNTHLTEERVKSSSVSSNSSIDTAQPSHTTINREESVQTSNDVSDHVSDFANS	120	
QY	121	KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYNNIDEKISNOQDELLNLPINEYENKAR	180	
Db	121	KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYNNIDEKISNOQDELLNLPINEYENKAR	180	
QY	181	PLSTTSAPSKRVTVNQLAAEQGSNVNHLIKVTQSQITEGYDDSEGVIKAHDAENLIYD	240	
Db	181	PLSTTSAPSKRVTVNQLAAEQGSNVNHLIKVTQSQITEGYDDSEGVIKAHDAENLIYD	240	
QY	241	VTFEVDKVKSGDWTVDIDKNTVPSDLTSTFIPKIDNSGEIATGTIDYDKNKQIYTT	300	
Db	241	VTFEVDKVKSGDWTVDIDKNTVPSDLTSTFIPKIDNSGEIATGTIDYDKNKQIYTT	300	

Db 241 VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIIATGTVDNKNKQIYTT 300  
Qy 301 FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKLTALSSVNKTITVEYQRENRT 360  
Db 301 FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKLTALSSVNKTITVEYQRENRT 360  
Qy 361 ANLOSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSTIIDDDSTIIKVKYVG 420  
Db 361 ANLOSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSTIIDDDSTIIKVKYVG 420  
Qy 421 DNQNLPSNRIRYDYSEYEDVNDYDQAQLGNNNDVNFNGNIDSPYIIKVIKSKYDPNKDDY 480  
Db 421 DNQNLPSNRIRYDYSEYEDVNDYDQAQLGNNNDVNFNGNIDSPYIIKVIKSKYDPNKDDY 480  
Qy 481 TTIQOTVTMQTTINEYTGFEFTASVDNTIAFSTSSGQGGDLPPBKTKYIGDYVWEDVDK 540  
Db 481 TTIQOTVTMQTTINEYTGFEFTASVDNTIAFSTSSGQGGDLPPBKTKYIGDYVWEDVDK 540  
Qy 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 582  
Db 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 582

## RESULT 2

US-09-147-405B-11

; Sequence 11, Application US/09147405B

; Patent No. 6733758

; GENERAL INFORMATION:

; APPLICANT: Guss, Bengt

; APPLICANT: Nilesen, Martin

; APPLICANT: Frykberg, Lars

; APPLICANT: Flock, Jan-Ingmar

; APPLICANT: Lindberg, Martin

; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from

; FILE REFERENCE: Guss 09/147405

; CURRENT APPLICATION NUMBER: US/09/147,405B

; PRIOR FILING DATE: 1999-04-11

; PRIOR APPLICATION NUMBER: PCT/SE97/10191

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: SE 9602496-3

; PRIOR FILING DATE: 1996-06-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 11

; LENGTH: 593

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-147-405B-11

Query Match 100.0%; Score 3013; DB 2; Length 593;

Best Local Similarity 100.0%; Pred. No. 4.7e-171;

Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSDEKNDVINNNOSINTDDNNQIIKKEETNNYDGIKRSERDTESTTNVDENEATFLQK 60  
Db 8 SSDEKNDVINNNOSINTDDNNQIIKKEETNNYDGIKRSERDTESTTNVDENEATFLQK 67  
Qy 61 TPQDNTHLTHEEVKSSSVSSSSIDTAQPSHTTINREESVQTSNDVEDSHVSDFANS 120  
Db 68 TPQDNTHLTHEEVKSSSVSSSSIDTAQPSHTTINREESVQTSNDVEDSHVSDFANS 127  
Qy 121 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPINEYENKAR 180  
Db 128 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPINEYENKAR 187  
Qy 181 PLSTTSAQPSIKRVTVNQLAAEQGSNNVHLLIKVTDQSITEGYDDSEGVIIKAHDAENLIYD 240  
Db 188 PLSTTSAQPSIKRVTVNQLAAEQGSNNVHLLIKVTDQSITEGYDDSEGVIIKAHDAENLIYD 247  
Qy 241 VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIIATGTVDNKNKQIYTT 300  
Db 248 VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIIATGTVDNKNKQIYTT 307

Qy 301 FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKLTALSSVNKTITVEYQRENRT 360  
Db 308 FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKLTALSSVNKTITVEYQRENRT 367  
Qy 361 ANLOSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSTIIDDDSTIIKVKYVG 420  
Db 368 ANLOSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSTIIDDDSTIIKVKYVG 427  
Qy 421 DNQNLPSNRIRYDYSEYEDVNDYDQAQLGNNNDVNFNGNIDSPYIIKVIKSKYDPNKDDY 480  
Db 428 DNQNLPSNRIRYDYSEYEDVNDYDQAQLGNNNDVNFNGNIDSPYIIKVIKSKYDPNKDDY 487  
Qy 481 TTIQOTVTMQTTINEYTGFEFTASVDNTIAFSTSSGQGGDLPPBKTKYIGDYVWEDVDK 540  
Db 488 TTIQOTVTMQTTINEYTGFEFTASVDNTIAFSTSSGQGGDLPPBKTKYIGDYVWEDVDK 547  
Qy 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 582  
Db 548 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 589

## RESULT 3

US-09-147-405B-15

; Sequence 15, Application US/09147405B

; Patent No. 6733758

; GENERAL INFORMATION:

; APPLICANT: Guss, Bengt

; APPLICANT: Nilesen, Martin

; APPLICANT: Frykberg, Lars

; APPLICANT: Flock, Jan-Ingmar

; APPLICANT: Lindberg, Martin

; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from

; FILE REFERENCE: Coagulase-Negative Staphylococcus

; CURRENT APPLICATION NUMBER: US/09/147,405B

; PRIOR FILING DATE: 1999-04-11

; PRIOR APPLICATION NUMBER: PCT/SE97/10191

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: SE 9602496-3

; PRIOR FILING DATE: 1996-06-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 15

; LENGTH: 1092

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-147-405B-15

Query Match 100.0%; Score 3013; DB 2; Length 1092;

Best Local Similarity 100.0%; Pred. No. 1e-170;

Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSDEKNDVINNNOSINTDDNNQIIKKEETNNYDGIKRSERDTESTTNVDENEATFLQK 60  
Db 75 SSDEKNDVINNNOSINTDDNNQIIKKEETNNYDGIKRSERDTESTTNVDENEATFLQK 134  
Qy 61 TPQDNTHLTHEEVKSSSVSSSSIDTAQPSHTTINREESVQTSNDVEDSHVSDFANS 120  
Db 135 TPQDNTHLTHEEVKSSSVSSSSIDTAQPSHTTINREESVQTSNDVEDSHVSDFANS 194  
Qy 121 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPINEYENKAR 180  
Db 195 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPINEYENKAR 254  
Qy 181 PLSTTSAQPSIKRVTVNQLAAEQGSNNVHLLIKVTDQSITEGYDDSEGVIIKAHDAENLIYD 240  
Db 255 PLSTTSAQPSIKRVTVNQLAAEQGSNNVHLLIKVTDQSITEGYDDSEGVIIKAHDAENLIYD 314  
Qy 241 VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIIATGTVDNKNKQIYTT 300  
Db 315 VTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIIATGTVDNKNKQIYTT 374

QY 301 FTDYVDKYENIKAHKLTSTYIDKSKVPNNNTKLDVEYKTALSSVNTTIIVYORPNEKRT 360  
DB 375 FTDYVDKYENIKAHKLTSTYIDKSKVPNNNTKLDVEYKTALSSVNTTIIVYORPNEKRT 434  
QY 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNDEGSTIIDSTIIKVKYKG 420  
DB 435 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNDEGSTIIDSTIIKVKYKG 494  
QY 421 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDVNFNFGNIDSPYIIKVISKYDPNKDDY 480  
DB 495 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDVNFNFGNIDSPYIIKVISKYDPNKDDY 554  
QY 481 TTIOQTVMQTTINBYTGEFRITASVDNTIAFSTSSGQGGDLPPPEKTYKIGDYVWEDVDK 540  
DB 555 TTIOQTVMQTTINBYTGEFRITASVDNTIAFSTSSGQGGDLPPPEKTYKIGDYVWEDVDK 614  
QY 541 DGIQNTNDNEKPLSNVLVTLTPDGTGSKSVRTDEDKGYQFDG 582  
DB 615 DGIQNTNDNEKPLSNVLVTLTPDGTGSKSVRTDEDKGYQFDG 656

RESULT 4  
US-09-134-001C-5314  
; Sequence 5314, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 5314  
; LENGTH: 930  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5314

Query Match 93.3%; Score 2810.5; DB 2; Length 930;  
Best Local Similarity 93.6%; Pred. No. 8.5e-159;  
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

QY 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKESDRTSTTNVDENEATFLQK 60  
DB 73 SSNEEKNDVINNSQSINTDDNQ-IKKEETNSDAIENRSKIDITQSTTNVDENEATFLQK 131  
QY 61 TPQDNTHLTEREEVKSSSVESNSSSIDTAQPSHTTINREESVOTSDNVDSHVSDPANS 120  
DB 132 TPQDNTHLTEREEVKSSSVESNSSSIDTAQPSHTTINREESVOTSDNVDSHVSDPANS 191  
QY 121 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDKISNQDELLNLPINEYENKAR 180  
DB 192 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDKISNQDELLNLPINEYENKAR 251  
QY 181 PLSTTSAQPSIKRVTVNQLAAEQSGNVNHLIKVTDQSTIEGVDYDSEGVIKAHAENLIYD 240  
DB 252 PLSTTSAQPSIKRVTVNQLAAEQSGNVNHLIKVTDQSTIEGVDYDSEGVIKAHAENLIYD 311  
QY 241 VTFFVDDKVKSGDVTMVDIDKNTVPSDLTDSFTPIKIKNSGEIATGTIDYKNKQIYTT 300  
DB 312 VTFFVDDKVKSGDVTMVDIDKNTVPSDLTDSFTPIKIKNSGEIATGTIDYKNKQIYTT 371  
QY 301 FTDYVDKYENIKAHKLTSTYIDKSKVPNNNTKLDVEYKTALSSVNTTIIVYORPNEKRT 360  
DB 372 FTDYVDKYENIKAHKLTSTYIDKSKVPNNNTKLDVEYKTALSSVNTTIIVYORPNEKRT 431  
QY 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNDEGSTIIDSTIIKVKYKG 420

DB 432 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNDEGSTIIDSTIIKVKYKG 491  
QY 421 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDVNFNFGNIDSPYIIKVISKYDPNKDDY 480  
DB 492 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDVNFNFGNIDSPYIIKVISKYDPNKDDY 551  
QY 481 TTIOQTVMQTTINBYTGEFRITASVDNTIAFSTSSGQGGDLPPPEKTYKIGDYVWEDVDK 540  
DB 552 TTIOQTVMQTTINBYTGEFRITASVDNTIAFSTSSGQGGDLPPPEKTYKIGDYVWEDVDK 611  
QY 541 DGIQNTNDNEKPLSNVLVTLTPDGTGSKSVRTDEDKGYQFDG 582  
DB 612 DGIQNTNDNEKPLSNVLVTLTPDGTGSKSVRTDEDKGYQFDG 653

RESULT 5  
US-09-386-962C-10  
; Sequence 10, Application US/09386962C  
; Patent No. 6635473  
; GENERAL INFORMATION:  
; APPLICANT: FOSTER, Timothy  
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCUS  
; FILE REFERENCE: P06335US2/BAS  
; CURRENT APPLICATION NUMBER: US/09/386,962C  
; CURRENT FILING DATE: 1999-08-31  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: 60/117,119  
; PRIOR FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 930  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-386-962C-10

Query Match 93.3%; Score 2810.5; DB 2; Length 930;  
Best Local Similarity 93.6%; Pred. No. 8.5e-159;  
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

QY 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKESDRTSTTNVDENEATFLQK 60  
DB 73 SSNEEKNDVINNSQSINTDDNQ-IKKEETNSDAIENRSKIDITQSTTNVDENEATFLQK 131  
QY 61 TPQDNTHLTEREEVKSSSVESNSSSIDTAQPSHTTINREESVOTSDNVDSHVSDPANS 120  
DB 132 TPQDNTHLTEREEVKSSSVESNSSSIDTAQPSHTTINSEASIQTSDEENSRVSDPANS 191  
QY 121 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDKISNQDELLNLPINEYENKAR 180  
DB 192 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDKISNQDELLNLPINEYENKAR 251  
QY 181 PLSTTSAQPSIKRVTVNQLAAEQSGNVNHLIKVTDQSTIEGVDYDSEGVIKAHAENLIYD 240  
DB 252 PLSTTSAQPSIKRVTVNQLAAEQSGNVNHLIKVTDQSTIEGVDYDSEGVIKAHAENLIYD 311  
QY 241 VTFFVDDKVKSGDVTMVDIDKNTVPSDLTDSFTPIKIKNSGEIATGTIDYKNKQIYTT 300  
DB 312 VTFFVDDKVKSGDVTMVDIDKNTVPSDLTDSFTPIKIKNSGEIATGTIDYKNKQIYTT 371  
QY 301 FTDYVDKYENIKAHKLTSTYIDKSKVPNNNTKLDVEYKTALSSVNTTIIVYORPNEKRT 360  
DB 372 FTDYVDKYENIKAHKLTSTYIDKSKVPNNNTKLDVEYKTALSSVNTTIIVYORPNEKRT 431  
QY 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNDEGSTIIDSTIIKVKYKG 420  
DB 432 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNDEGSTIIDSTIIKVKYKG 491  
QY 421 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDVNFNFGNIDSPYIIKVISKYDPNKDDY 480  
DB 492 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDVNFNFGNIDSPYIIKVISKYDPNKDDY 551











RESULT 14  
US-08-781-986A-5249  
; Sequence 5249, Application US/08781986A  
; Patent No. 6737248  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781.986A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Benson, Bob  
; REGISTRATION NUMBER: 30,446  
; REFERENCE/DOCKET NUMBER: PB248PP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 5249:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 936 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-781-986A-5249

Query Match 15.1%; Score 454; DB 2; Length 936;  
Best Local Similarity 26.6%; Pred. No. 5.3e-19;  
Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;  
Qy 1 SSDEKNDVINNNOSINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENBEATFLOK 60  
Db 60 SNEKSNDSVSAAPKTDITNV-----SDTKSSNTN---NGETSVAQ 100  
Qy 61 TPQDNTHLTBEVEKSSVSSNSIDTAQOPSHHTINREESVQTSNDVDSHVSDFANS 120  
Db 61 TPQDNTHLTBEVEKSSVSSNSIDTAQOPSHHTINREESVQTSNDVDSHVSDFANS 120  
Qy 101 NP-----AQETQSSSTNATTEPTVTGEATTTTNTQANTPATQOS-SNTNABELVN- 152  
Db 101 NP-----AQETQSSSTNATTEPTVTGEATTTTNTQANTPATQOS-SNTNABELVN- 152  
Qy 121 KIKESNTSGKEENTIEQPNKVKEDSTTSPQSGVYNIDEKISNODELLN-LPINEYENKA 179  
Db 121 KIKESNTSGKEENTIEQPNKVKEDSTTSPQSGVYNIDEKISNODELLN-LPINEYENKA 179  
Qy 153 --QTSNETTNDTNTV-----SSVNSPQNSTNAENVSTTQDTSTEATPSN---NES 198  
Db 153 --QTSNETTNDTNTV-----SSVNSPQNSTNAENVSTTQDTSTEATPSN---NES 198  
Qy 180 RPLSTTSAQPSIKRVTVN-----QLAAEQGSNNVHLIKVTDQ--SITEGYDDSEGV 228  
Db 180 RPLSTTSAQPSIKRVTVN-----QLAAEQGSNNVHLIKVTDQ--SITEGYDDSEGV 228  
Qy 199 APOSTDASNDKDVNQAVNTSAPRMAFSLAAVAADAPVAGTDITNQLTNVTVG1-DSGTT 257  
Db 199 APOSTDASNDKDVNQAVNTSAPRMAFSLAAVAADAPVAGTDITNQLTNVTVG1-DSGTT 257  
Qy 229 IKAHDAENLIYDVTFEVDKVKSGDWTVDIKNTVPSDLTSDFTIPKIDNSGGEIATG 288  
Db 229 IKAHDAENLIYDVTFEVDKVKSGDWTVDIKNTVPSDLTSDFTIPKIDNSGGEIATG 288  
Qy 258 VYPHQAGVYKLVGFSVPNSAVKGDTFKITVPKELNLNGVTSTAKVPPIMAGD-QVLANG 316  
Db 258 VYPHQAGVYKLVGFSVPNSAVKGDTFKITVPKELNLNGVTSTAKVPPIMAGD-QVLANG 316  
Qy 289 TYDNKKNKOITFTYTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKL-DVEYKTLASS--VN 345  
Db 289 TYDNKKNKOITFTYTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKL-DVEYKTLASS--VN 345  
Qy 317 VIDS--DGNVIYFTFDYVNTKDDVKATLTMPAYID----PENVKKTGNVTLATGIGSTAN 371  
Db 317 VIDS--DGNVIYFTFDYVNTKDDVKATLTMPAYID----PENVKKTGNVTLATGIGSTAN 371  
Qy 346 KTIITVEQRNENRTANLQSMFTNIDTKNHTVEQTIYINPL--RYSAKETNNVNSGNGDE 403  
Db 346 KTIITVEQRNENRTANLQSMFTNIDTKNHTVEQTIYINPL--RYSAKETNNVNSGNGDE 403

Db 372 KTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYVNPSGDNVIAVLTLGNLKPNTDS 431  
Qy 404 GSTIIDSTIIKYKVGDNQNLPSNRIDYSEYEDVTNDYAOLGNNNDVNIWVNF- 459  
Db 432 NALIDQOQNTSIKYKVDNAADLSSEYFV-NPENFEDVTNSVNIITFPNPQYKVFNTPDD 490  
Qy 460 NIDSPYIIKVISKYDNP-KDDYTTIQOQVTVMQTTINEYTG-PRTSYDNTNTIAFSTSSG 516  
Db 491 QITTPYIIVVNGHIDPNSKGD-----LALRSTLYGYNISNIIWRSMWDNEVAFNNGSG 543  
Qy 517 QGQG-DLP--PEKTYKIGDY--VMEDVDKO-GIQNTNDN 549  
Db 544 SGDGIKPVVPEQDPDEGEIEPIEDSDSDPGSDSGSDS 582  
RESULT 15  
US-08-293-728-2  
; Sequence 2, Application US/08293728D  
; Patent No. 6008341  
; GENERAL INFORMATION:  
; APPLICANT: Foster, Timothy J.  
; APPLICANT: McDevitt, Damien L.  
; TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene  
; FILE REFERENCE: 05344.105011  
; CURRENT APPLICATION NUMBER: US/08/293,728D  
; CURRENT FILING DATE: 1994-08-22  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 933  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-08-293-728-2

Query Match 15.0%; Score 452; DB 2; Length 933;  
Best Local Similarity 26.6%; Pred. No. 7e-19;  
Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;  
Qy 1 SSDEKNDVINNNOSINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENBEATFLOK 60  
Db 51 SNEKSNDSVSAAPKTDITNV-----SDTKSSNTN---NGETSVAQ 91  
Qy 61 TPQDNTHLTBEVEKSSVSSNSIDTAQOPSHHTINREESVQTSNDVDSHVSDFANS 120  
Db 92 NP-----AQETQSSSTNATTEPTVTGEATTTTNTQANTPATQOS-SNTNABELVN- 143  
Qy 121 KIKESNTSGKEENTIEQPNKVKEDSTTSPQSGVYNIDEKISNODELLN-LPINEYENKA 179  
Db 144 --QTSNETTNDTNTV-----SSVNSPQNSTNAENVSTTQDTSTEATPSN---NES 189  
Qy 180 RPLSTTSAQPSIKRVTVN-----QLAAEQGSNNVHLIKVTDQ--SITEGYDDSEGV 228  
Db 190 APOSTDASNDKDVNQAVNTSAPRMAFSLAAVAADAPVAGTDITNQLTNVTVG1-DSGTT 248  
Qy 229 IKAHDAENLIYDVTFEVDKVKSGDWTVDIKNTVPSDLTSDFTIPKIDNSGGEIATG 288  
Db 249 VYPHQAGVYKLVGFSVPNSAVKGDTFKITVPKELNLNGVTSTAKVPPIMAGD-QVLANG 307  
Qy 289 TYDNKKNKOITFTYTDYVDKYENIKAHKLKTSYIDKSKVPNNNTKL-DVEYKTLASS--VN 345  
Db 308 VIDS--DGNVIYFTFDYVNTKDDVKATLTMPAYID----PENVKKTGNVTLATGIGSTAN 362  
Qy 346 KTIITVEQRNENRTANLQSMFTNIDTKNHTVEQTIYINPL--RYSAKETNNVNSGNGDE 403  
Db 363 KTVLVDEYKYGKFNLSIKGTIDQIDKTNNTYRQTIYVNPFGDNVIAVLTLGNLKPNTDS 422  
Qy 404 GSTIIDSTIIKYKVGDNQNLPSNRIDYSEYEDVTNDYAOLGNNNDVNIWVNF- 459  
Db 423 NALIDQOQNTSIKYKVDNAADLSSEYFV-NPENFEDVTNSVNIITFPNPQYKVFNTPDD 481  
Qy 460 NIDSPYIIKVISKYDNP-KDDYTTIQOQVTVMQTTINEYTG-PRTSYDNTNTIAFSTSSG 516  
Db 482 QITTPYIIVVNGHIDPNSKGD-----LALRSTLYGYNISNIIWRSMWDNEVAFNNGSG 534

Qy 517 QGQG-DLP--PEKTYKIGDY--VWEDVDKD-GIQTNDN 549  
Db 535 SGDGIDKPVVPEQDEPGEIEPIPEDSDSDPGSDSGSDS 573

Search completed: August 12, 2006, 09:06:34  
Job time : 52 secs

**This Page Blank (uspto)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2006, 09:17:06 ; Search time 184 Seconds  
(without alignments)  
1465.169 Million cell updates/sec

Title: US-10-806-288-13  
Perfect score: 3013  
Sequence: 1 SDEKNDVINNNQSIINTDD.....PDGTSKSVRTDEGKYQFDG 582

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3013	100.0	582	4	US-10-806-288-13
2	3013	100.0	593	4	US-10-806-288-11
3	3013	100.0	1092	4	US-10-378-674-8
4	2810.5	93.3	892	4	US-10-806-288-15
5	2810.5	93.3	892	4	US-10-282-122A-70481
6	2810.5	93.3	892	4	US-10-661-809-21
7	2810.5	93.3	930	4	US-10-615-383-10
8	2810.5	93.3	930	4	US-10-690-184-10
9	2810.5	93.3	930	4	US-10-689-082-10
10	2810.5	93.3	930	4	US-10-724-972A-5309
11	2670	88.6	549	4	US-10-378-674-9
12	2510.5	83.3	560	4	US-10-378-674-2
13	1702	56.5	331	6	US-11-016-564-3
14	1672	55.5	343	4	US-10-378-674-4
15	1562	51.8	316	4	US-10-378-674-6
16	1144.5	38.0	1166	5	US-10-744-672-7
17	1144.5	38.0	1166	5	US-10-744-616-7
18	1142.5	37.9	1166	5	US-10-470-0488-153
19	1137.5	37.8	1141	4	US-10-282-122A-70251
20	1116.5	37.1	670	4	US-10-282-122A-70444
21	857	28.4	278	5	US-10-793-626-2700
22	795.5	26.4	338	6	US-11-016-564-4
23	576	19.1	1315	5	US-10-744-672-5
24	576	19.1	1315	5	US-10-744-616-5
25	576	19.1	1315	5	US-10-470-0488-124
26	576	19.1	1349	3	US-09-815-242-5898
27	576	19.1	1349	3	US-09-815-242-13137

28	559	18.6	1385	4	US-10-282-122A-44324	Sequence 44324, A
29	499.5	16.6	932	3	US-09-815-242-5578	Sequence 5578, Ap
30	499.5	16.6	932	3	US-09-815-242-12438	Sequence 12438, A
31	499	16.6	1742	4	US-10-615-383-4	Sequence 4, Appli
32	499	16.6	1742	4	US-10-690-184-4	Sequence 4, Appli
33	499	16.6	1742	4	US-10-689-082-4	Sequence 4, Appli
34	497	16.5	1155	5	US-10-793-626-1780	Sequence 1780, Ap
35	493	16.4	1633	4	US-10-282-122A-70437	Sequence 70437, A
36	489	16.2	953	4	US-10-282-122A-44457	Sequence 44457, A
37	486.5	16.1	1920	4	US-10-282-122A-71413	Sequence 71413, A
38	476	15.8	408	6	US-11-016-564-5	Sequence 5, Appli
39	455	15.1	841	3	US-09-815-242-5779	Sequence 5779, Ap
40	455	15.1	841	3	US-09-815-242-12751	Sequence 12751, A
41	455	15.1	930	5	US-10-744-672-3	Sequence 3, Appli
42	455	15.1	930	5	US-10-744-616-3	Sequence 3, Appli
43	455	15.1	933	5	US-10-470-0488-93	Sequence 93, Appli
44	455	15.1	947	5	US-10-470-0488-86	Sequence 86, Appli
45	454	15.1	936	2	US-08-781-986A-5249	Sequence 5249, Ap

ALIGNMENTS

RESULT 1  
US-10-806-288-13  
; Sequence 13, Application US/10806288  
; Publication No. US20040209326A1  
; GENERAL INFORMATION:  
; APPLICANT: Guss, Bengt  
; APPLICANT: Nilsson, Martin  
; APPLICANT: Frykberg, Lars  
; APPLICANT: Flock, Jan-Ingmar  
; APPLICANT: Lindberg, Martin  
; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from  
; TITLE OF INVENTION: Coagulase-Negative Staphylococcus  
; FILE REFERENCE: guss 09/147405  
; CURRENT APPLICATION NUMBER: US/10/806,288  
; CURRENT FILING DATE: 2004-03-23  
; PRIOR APPLICATION NUMBER: US/09/147,405  
; PRIOR FILING DATE: 1999-04-11  
; PRIOR APPLICATION NUMBER: PCT/SE97/10191  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: SE 9602496-3  
; PRIOR FILING DATE: 1996-06-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 582  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-10-806-288-13

Query Match	100.0%;	Score 3013;	DB 4;	Length 582;
Best Local Similarity	100.0%;	Pred. No. 2.6e-150;	Mismatches 0;	Indels 0;
Matches 582;	Conservative 0;			Gaps 0;
Qy	1	SSDEKNDVINNNQSIINTDDNNQIIKGBETNNYDGIKRSEDRTESTTNVDNEATFLOK 60		
Db	1	SSDEKNDVINNNQSIINTDDNNQIIKGBETNNYDGIKRSEDRTESTTNVDNEATFLOK 60		
Qy	61	TPQDNTHLTHEBEVKESSESSVSSNSSIDTAQPSHTTINREESVQTSQDNVEDSHVSDFANS 120		
Db	61	TPQDNTHLTHEBEVKESSESSVSSNSSIDTAQPSHTTINREESVQTSQDNVEDSHVSDFANS 120		
Qy	121	KIKESNTSGKEENTIEQPNVKEDSTTSQPSGYNNIDEKISNOQDELLNPLINEYENKAR 180		
Db	121	KIKESNTSGKEENTIEQPNVKEDSTTSQPSGYNNIDEKISNOQDELLNPLINEYENKAR 180		
Qy	181	PLSTTSAQPSIKRVTVNQLAAEQGSNNVHLIKVTDQSITEGVDDSEGVIKAHDAENLIYD 240		
Db	181	PLSTTSAQPSIKRVTVNQLAAEQGSNNVHLIKVTDQSITEGVDDSEGVIKAHDAENLIYD 240		
Qy	241	VTFEYDDKVKSGDWTVDIDKNVTVPDLSFTPIKIDNSGEIATGTIDNKNKQITVT 300		

Db 241 VTFFVDDKVKSGDWTMTVDIDKNTVPSDLTDSFTIPKIKDNGSGEIIATGTYDNKNKQIITYT 300  
Qy 301 FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKTALSSVNKTTITVEYQRPENRNT 360  
Db 301 FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKTALSSVNKTTITVEYQRPENRNT 360  
Qy 361 ANLQSMFTNIDTKNHTVQGTIYINPLRYSAKETNNVNSGNGDEGSTIIDSTIIKVKYKVG 420  
Db 361 ANLQSMFTNIDTKNHTVQGTIYINPLRYSAKETNNVNSGNGDEGSTIIDSTIIKVKYKVG 420  
Qy 421 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKVKISYDPNKDDY 480  
Db 421 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKVKISYDPNKDDY 480  
Qy 481 TTIOQVTVMQTTINEYTGFEFTASVDNTIAFSTSSGQGGDLPPPEKTYKIGDYVWEDVDK 540  
Db 481 TTIOQVTVMQTTINEYTGFEFTASVDNTIAFSTSSGQGGDLPPPEKTYKIGDYVWEDVDK 540  
Qy 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 582  
Db 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 582

RESULT 2

US-10-806-288-11  
; Sequence 11, Application US/10806288  
; Publication No. US20040209326A1  
; GENERAL INFORMATION:  
; APPLICANT: Guss, Bengt  
; APPLICANT: Nilsson, Martin  
; APPLICANT: Frykberg, Lars  
; APPLICANT: Flock, Jan-Ingmar  
; APPLICANT: Lindberg, Martin  
; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from  
; FILE REFERENCE: Coagulase-Negative Staphylococcus  
; CURRENT APPLICATION NUMBER: US/10/806,288  
; CURRENT FILING DATE: 2004-03-23  
; PRIOR APPLICATION NUMBER: US/09/147,405  
; PRIOR FILING DATE: 1999-04-11  
; PRIOR APPLICATION NUMBER: PCT/SE97/10191  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: SE 9602496-3  
; PRIOR FILING DATE: 1996-06-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-10-806-288-11

Query Match 100.0%; Score 3013; DB 4; Length 593;  
Best Local Similarity 100.0%; Pred. No. 2.6e-150;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SSDEEKNDVINNQSINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENBEATFLQK 60  
Db 8 SSDEEKNDVINNQSINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENBEATFLQK 67  
Qy 61 TPQDNTHLTHEEVKSESSVSSNSIDTAQOPSHTTINREESVQTSNVDESHVSDFANS 120  
Db 68 TPQDNTHLTHEEVKSESSVSSNSIDTAQOPSHTTINREESVQTSNVDESHVSDFANS 127  
Qy 121 KIKESNTESGKEENTIEOPNKVKEDSTTSQPSGYTNIDEKISNQDELINLPINEYENKAR 180  
Db 128 KIKESNTESGKEENTIEOPNKVKEDSTTSQPSGYTNIDEKISNQDELINLPINEYENKAR 187  
Qy 181 PLSTTSAQPSIKRVTNQLAAEQGSNNVHLLIKVTDQSITEGYDDSEGVKAHAENLIYD 240  
Db 188 PLSTTSAQPSIKRVTNQLAAEQGSNNVHLLIKVTDQSITEGYDDSEGVKAHAENLIYD 247

Qy 241 VTFFVDDKVKSGDWTMTVDIDKNTVPSDLTDSFTIPKIKDNGSGEIIATGTYDNKNKQIITYT 300  
Db 248 VTFFVDDKVKSGDWTMTVDIDKNTVPSDLTDSFTIPKIKDNGSGEIIATGTYDNKNKQIITYT 307  
Qy 301 FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKTALSSVNKTTITVEYQRPENRNT 360  
Db 308 FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKTALSSVNKTTITVEYQRPENRNT 367  
Qy 361 ANLQSMFTNIDTKNHTVQGTIYINPLRYSAKETNNVNSGNGDEGSTIIDSTIIKVKYKVG 420  
Db 368 ANLQSMFTNIDTKNHTVQGTIYINPLRYSAKETNNVNSGNGDEGSTIIDSTIIKVKYKVG 427  
Qy 421 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKVKISYDPNKDDY 480  
Db 428 DNQNLPSNRIDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKVKISYDPNKDDY 487  
Qy 481 TTIOQVTVMQTTINEYTGFEFTASVDNTIAFSTSSGQGGDLPPPEKTYKIGDYVWEDVDK 540  
Db 488 TTIOQVTVMQTTINEYTGFEFTASVDNTIAFSTSSGQGGDLPPPEKTYKIGDYVWEDVDK 547  
Qy 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 582  
Db 548 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 589

RESULT 3

US-10-378-674-8  
; Sequence 8, Application US/10378674  
; Publication No. US20040006209A1  
; GENERAL INFORMATION:  
; APPLICANT: PATTI, Joseph M.  
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATI  
; FILE REFERENCE: P07556US01/BAS  
; CURRENT APPLICATION NUMBER: US/10/378,674  
; CURRENT FILING DATE: 2003-03-05  
; PRIOR APPLICATION NUMBER: 60/361,324  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 1092  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-10-378-674-8

Query Match 100.0%; Score 3013; DB 4; Length 1092;  
Best Local Similarity 100.0%; Pred. No. 5.4e-150;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SSDEEKNDVINNQSINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENBEATFLQK 60  
Db 75 SSDEEKNDVINNQSINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENBEATFLQK 134  
Qy 61 TPQDNTHLTHEEVKSESSVSSNSIDTAQOPSHTTINREESVQTSNVDESHVSDFANS 120  
Db 135 TPQDNTHLTHEEVKSESSVSSNSIDTAQOPSHTTINREESVQTSNVDESHVSDFANS 194  
Qy 121 KIKESNTESGKEENTIEOPNKVKEDSTTSQPSGYTNIDEKISNQDELINLPINEYENKAR 180  
Db 195 KIKESNTESGKEENTIEOPNKVKEDSTTSQPSGYTNIDEKISNQDELINLPINEYENKAR 254  
Qy 181 PLSTTSAQPSIKRVTNQLAAEQGSNNVHLLIKVTDQSITEGYDDSEGVKAHAENLIYD 240  
Db 255 PLSTTSAQPSIKRVTNQLAAEQGSNNVHLLIKVTDQSITEGYDDSEGVKAHAENLIYD 314  
Qy 241 VTFFVDDKVKSGDWTMTVDIDKNTVPSDLTDSFTIPKIKDNGSGEIIATGTYDNKNKQIITYT 300  
Db 315 VTFFVDDKVKSGDWTMTVDIDKNTVPSDLTDSFTIPKIKDNGSGEIIATGTYDNKNKQIITYT 374  
Qy 301 FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKTALSSVNKTTITVEYQRPENRNT 360  
Db 375 FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKTALSSVNKTTITVEYQRPENRNT 434

QY 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSISGDEGSGTIIDSTIIKVKYKG 420  
DB 435 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSISGDEGSGTIIDSTIIKVKYKG 494  
QY 421 DNQNLPSNRIDYSEYEDVTNDYDVAQLGNNDVNFNFGNIDSPYIIKVISKYDPNKDDY 480  
DB 495 DNQNLPSNRIDYSEYEDVTNDYDVAQLGNNDVNFNFGNIDSPYIIKVISKYDPNKDDY 554  
QY 481 TTIQQTVMQTTINETYGEFRTASYDNTIAFSTSSQGGQDLPPEKTYKIGDYVWEDVDK 540  
DB 555 TTIQQTVMQTTINETYGEFRTASYDNTIAFSTSSQGGQDLPPEKTYKIGDYVWEDVDK 614  
QY 541 DGIQNTNDEKPLSNVLVTLTPDGTGSKSVRTDEDEKGYQFDG 582  
DB 615 DGIQNTNDEKPLSNVLVTLTPDGTGSKSVRTDEDEKGYQFDG 656

RESULT 4

US-10-806-288-15  
; Sequence 15, Application US/10806288  
; Publication No. US20040209326A1  
; GENERAL INFORMATION:  
; APPLICANT: Guss, Bengt  
; APPLICANT: Nilsson, Martin  
; APPLICANT: Frykberg, Lars  
; APPLICANT: Flock, Jan-Ingmar  
; APPLICANT: Lindberg, Martin  
; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from  
; ; FILE REFERENCE: Coagulase-Negative Staphylococcus  
; ; CURRENT APPLICATION NUMBER: US/10/806,288  
; ; CURRENT FILING DATE: 2004-03-23  
; ; PRIOR APPLICATION NUMBER: US/09/147,405  
; ; PRIOR FILING DATE: 1999-04-11  
; ; PRIOR APPLICATION NUMBER: PCT/SE97/10191  
; ; PRIOR FILING DATE: 1997-06-18  
; ; PRIOR APPLICATION NUMBER: SE 9602496-3  
; ; PRIOR FILING DATE: 1996-06-20  
; ; NUMBER OF SEQ ID NOS: 15  
; ; SOFTWARE: Patent In Ver. 2.0  
; ; SEQ ID NO 15  
; ; TYPE: PRT  
; ; LENGTH: 1092  
; ; ORGANISM: Staphylococcus epidermidis  
US-10-806-288-15

Query Match 100.0%; Score 3013; DB 4; Length 1092;  
Best Local Similarity 100.0%; Pred. No. 5.4e-150;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSDEKNDVINNNQSIINTDDNQIIKKEBTNNYDGIKESDRTSTTNVDENEATFLQK 60  
DB 75 SSDEKNDVINNNQSIINTDDNQIIKKEBTNNYDGIKESDRTSTTNVDENEATFLQK 134  
QY 61 TPQDNTHLTEREVKSSSVSSSSSIDTAQPSHTTINREESVQTSNDVDSHVDFANS 120  
DB 135 TPQDNTHLTEREVKSSSVSSSSSIDTAQPSHTTINREESVQTSNDVDSHVDFANS 194  
QY 121 KIKESNTSGKENTIEQPNKVEDSTTSQPSGYNIDEKISQDELNLPLINEYENKAR 180  
DB 195 KIKESNTSGKENTIEQPNKVEDSTTSQPSGYNIDEKISQDELNLPLINEYENKAR 254  
QY 181 PLSTTSAQPSIKRVTVNQLAAGSGNVNHLIKVTQDSITEGYDDSEGVIKADHAENLIYD 240  
DB 255 PLSTTSAQPSIKRVTVNQLAAGSGNVNHLIKVTQDSITEGYDDSEGVIKADHAENLIYD 314  
QY 241 VTFEVDKVKSGDVTMTVDKNTVPSDLTDSFTPIKIDNSGEIATGTYNKKNQIYTT 300  
DB 315 VTFEVDKVKSGDVTMTVDKNTVPSDLTDSFTPIKIDNSGEIATGTYNKKNQIYTT 374  
QY 301 FTDYVDKYENIKAHKLTSYIDKSKVPNNNTKLDVEYKTALSSVNTKITVEYQRPENRT 360

DB 375 FTDYVDKYENIKAHKLTSYIDKSKVPNNNTKLDVEYKTALSSVNTKITVEYQRPENRT 434  
QY 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSISGDEGSGTIIDSTIIKVKYKG 420  
DB 435 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSISGDEGSGTIIDSTIIKVKYKG 494  
QY 421 DNQNLPSNRIDYSEYEDVTNDYDVAQLGNNDVNFNFGNIDSPYIIKVISKYDPNKDDY 480  
DB 495 DNQNLPSNRIDYSEYEDVTNDYDVAQLGNNDVNFNFGNIDSPYIIKVISKYDPNKDDY 554  
QY 481 TTIQQTVMQTTINETYGEFRTASYDNTIAFSTSSQGGQDLPPEKTYKIGDYVWEDVDK 540  
DB 555 TTIQQTVMQTTINETYGEFRTASYDNTIAFSTSSQGGQDLPPEKTYKIGDYVWEDVDK 614  
QY 541 DGIQNTNDEKPLSNVLVTLTPDGTGSKSVRTDEDEKGYQFDG 582  
DB 615 DGIQNTNDEKPLSNVLVTLTPDGTGSKSVRTDEDEKGYQFDG 656

RESULT 5

US-10-282-122A-70481  
; Sequence 70481, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 70481  
; LENGTH: 892  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-10-282-122A-70481

Query Match 93.3%; Score 2810.5; DB 4; Length 892;  
Best Local Similarity 93.6%; Pred. No. 1.8e-139;  
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

```
Qy 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGI EKRSDETRTESTTNVDENATFLQK 60
Db 35 SSNEEKNDVINNQSIINTDDNQ - IKKEETNSNDAIENRSKDITQSTTNVDENATFLQK 93
Qy 61 TPQDNTHLTHEBEVKSSSVSSNSSIDTAQPSHTTTINREESVQTSNDVEDSHVSDFANS 120
Db 94 TPQDNTHLTHEBEVKSSSVSSNSSMDTAQPSHTTTINSEASIQTSNDNEENSRVSDFANS 153
Qy 121 KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPLINENYENKAR 180
Db 154 KIIESNTESNKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPLINENYENKAR 213
Qy 181 PLSTTSQAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSIITEGYDDSEGVIKAHDAENLIYD 240
Db 214 PLSTTSQAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSIITEGYDDSGIKAHDAENLIYD 273
Qy 241 VTFEVDKVKSGDGMTVTDIDKNTVPSDLTDSFTPIPKIKDNGSGEIIATGYDNKNKQIITYT 300
Db 274 VTFEVDKVKSGDGMTVTDIDKNTVPSDLTDSFAIPKIKDNGSGEIIATGYDNKNKQIITYT 333
Qy 301 FTDYVDKVENIKAHKLKTSYIDKSKVPNNNTKLDVEYKTALSSVNKTITVBYQRPENRNT 360
Db 334 FTDYVDKVENIKAHKLKTSYIDKSKVPNNNTKLDVEYKTALSSVNKTITVBYQRPENRNT 393
Qy 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNWNISGNGDEGSTIIDDDSTIIKVKYKG 420
Db 394 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNWNISGNGDEGSTIIDDDSTIIKVKYKG 453
Qy 421 DNQNLPSDSNRIYDYSEYEDVTNDYDQAQLGNNDVNIINFGNIDSPYIIKVISKYPNKDDY 480
Db 454 DNQNLPSDSNRIYDYSEYEDVTNDYDQAQLGNNDVNIINFGNIDSPYIIKVISKYPNKDDY 513
Qy 481 TTIOQTVMQTTINEYTGEPRTASYDNTIAFSTSSGQGGDLPEKTYKIGDYVWEDVDK 540
Db 514 TTIOQTVMQTTINEYTGEPRTASYDNTIAFSTSSGQGGDLPEKTYKIGDYVWEDVDK 573
Qy 541 DGIQNTNDNEKPLSNVLTLTYPDGTSKSVRTDEGKYQFDG 582
Db 574 DGIQNTNDNEKPLSNVLTLTYPDGTSKSVRTDEGKYQFDG 615

RESULT 6
US-10-661-809-21
; Sequence 21, Application US/10661809
; Publication No. US20040101919A1
; GENERAL INFORMATION:
; APPLICANT: HOOK, Magnus
; TITLE OF INVENTION: BIOINFORMATIC METHOD FOR IDENTIFYING SURFACE-ANCHORED PROTEINS FR
; FILE REFERENCE: P07741US01/BAS
; CURRENT APPLICATION NUMBER: US/10/661,809
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-661-809-21
```

```
Query Match 93.3%; Score 2810.5; DB 4; Length 892;
Best Local Similarity 93.6%; Pred. No. 1.8e-139;
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

Qy 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGI EKRSDETRTESTTNVDENATFLQK 60
Db 35 SSNEEKNDVINNQSIINTDDNQ - IKKEETNSNDAIENRSKDITQSTTNVDENATFLQK 93
Qy 61 TPQDNTHLTHEBEVKSSSVSSNSSIDTAQPSHTTTINREESVQTSNDVEDSHVSDFANS 120
Db 94 TPQDNTHLTHEBEVKSSSVSSNSSMDTAQPSHTTTINSEASIQTSNDNEENSRVSDFANS 153
```

```
Qy 121 KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPLINENYENKAR 180
Db 154 KIIESNTESNKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPLINENYENKAR 213
Qy 181 PLSTTSQAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSIITEGYDDSEGVIKAHDAENLIYD 240
Db 214 PLSTTSQAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSIITEGYDDSGIKAHDAENLIYD 273
Qy 241 VTFEVDKVKSGDGMTVTDIDKNTVPSDLTDSFTPIPKIKDNGSGEIIATGYDNKNKQIITYT 300
Db 274 VTFEVDKVKSGDGMTVTDIDKNTVPSDLTDSFAIPKIKDNGSGEIIATGYDNKNKQIITYT 333
Qy 301 FTDYVDKVENIKAHKLKTSYIDKSKVPNNNTKLDVEYKTALSSVNKTITVBYQRPENRNT 360
Db 334 FTDYVDKVENIKAHKLKTSYIDKSKVPNNNTKLDVEYKTALSSVNKTITVBYQRPENRNT 393
Qy 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNWNISGNGDEGSTIIDDDSTIIKVKYKG 420
Db 394 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNWNISGNGDEGSTIIDDDSTIIKVKYKG 453
Qy 421 DNQNLPSDSNRIYDYSEYEDVTNDYDQAQLGNNDVNIINFGNIDSPYIIKVISKYPNKDDY 480
Db 454 DNQNLPSDSNRIYDYSEYEDVTNDYDQAQLGNNDVNIINFGNIDSPYIIKVISKYPNKDDY 513
Qy 481 TTIOQTVMQTTINEYTGEPRTASYDNTIAFSTSSGQGGDLPEKTYKIGDYVWEDVDK 540
Db 514 TTIOQTVMQTTINEYTGEPRTASYDNTIAFSTSSGQGGDLPEKTYKIGDYVWEDVDK 573
Qy 541 DGIQNTNDNEKPLSNVLTLTYPDGTSKSVRTDEGKYQFDG 582
Db 574 DGIQNTNDNEKPLSNVLTLTYPDGTSKSVRTDEGKYQFDG 615

RESULT 7
US-10-615-383-10
; Sequence 10, Application US/10615383
; Publication No. US20040038327A1
; GENERAL INFORMATION: Timothy
; APPLICANT: POSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLO
; FILE REFERENCE: P06335US03/BAS
; CURRENT APPLICATION NUMBER: US/10/615,383
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: 09/386,962
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-615-383-10
```

```
Query Match 93.3%; Score 2810.5; DB 4; Length 930;
Best Local Similarity 93.6%; Pred. No. 1.9e-139;
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

Qy 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGI EKRSDETRTESTTNVDENATFLQK 60
Db 73 SSNEEKNDVINNQSIINTDDNQ - IKKEETNSNDAIENRSKDITQSTTNVDENATFLQK 131
Qy 61 TPQDNTHLTHEBEVKSSSVSSNSSIDTAQPSHTTTINREESVQTSNDVEDSHVSDFANS 120
Db 132 TPQDNTHLTHEBEVKSSSVSSNSSMDTAQPSHTTTINSEASIQTSNDNEENSRVSDFANS 191
Qy 121 KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPLINENYENKAR 180
Db 192 KIIESNTESNKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNODELLNLPLINENYENKAR 251
```





Db 312 VTPEVDDKVKSGDTMTVNIIDKNTVPSDLTDSFAIPKIKDNGSEIIATGTVDNTNKQIITYT 371  
Qy 301 FTDVYDKYENIKAHKLKLTSTYDKSKVPNNNTKLDVEYKLTALSSVKNKTIITVEYQRPENRT 360  
Db 372 FTDVYDKYENIKAHKLKLTSTYDKSKVPNNNTKLDVEYKLTALSSVKNKTIITVEYQRPENRT 431  
Qy 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNISGNGDEGSDTIIDDDSTIIKVKYKVG 420  
Db 432 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNISGNGDEGSDTIIDDDSTIIKVKYKVG 491  
Qy 421 DNQNLPSNRIRYDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKVISKYDPNKDDY 480  
Db 492 DNQNLPSNRIRYDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKVISKYDPNKDDY 551  
Qy 481 TTIQQTVMQTTINEYTGEBFTASVDNTIAFSTSSGQGGDLPEPKTYKIGDYVWEDVDK 540  
Db 552 TTIQQTVMQTTINEYTGEBFTASVDNTIAFSTSSGQGGDLPEPKTYKIGDYVWEDVDK 611  
Qy 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 582  
Db 612 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 653

## RESULT 10

US-10-724-972A-5309  
; Sequence 5309, Application US/10724972A  
; Publication No. US20040147734A1  
; GENERAL INFORMATION:  
; APPLICANT: Doucette-Stamm, Lynn  
; APPLICANT: Bush, David  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: PATH03-16  
; CURRENT APPLICATION NUMBER: US/10/724,972A  
; CURRENT FILING DATE: 2003-12-01  
; PRIOR APPLICATION NUMBER: 09/450,969  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/134,001  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 7544  
; SEQ ID NO 5309  
; LENGTH: 930  
; TYPE: PRT  
; ORGANISM: S.epidermidis  
US-10-724-972A-5309

Query Match 93.3%; Score 2810.5; DB 4; Length 930;  
Best Local Similarity 93.6%; Pred. No. 1.9e-139;  
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;  
Qy 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKRSERDRTSTTNVDENEATFLQK 60  
Db 73 SSNEEKNDVINNQSIINTDDNNQ- IKKEETNSDAIENRSKDITQSTTNVDENEATFLQK 131  
Qy 61 TPQDNTHLTBEVKESSESSVSSNSIDTAQPSHTTINREESVQTSNDVDSHVSDFANS 120  
Db 132 TPQDNTHLTBEVKESSESSVSSNSMDTAQPSHTTINSEASIQTSNDNEENSRVSDFANS 191  
Qy 121 KIKESNTESGKEENTIEQPNKVKESDTSQPSGYTNIDEKISNOQELLNLPINEYENKAR 180  
Db 192 KIKESNTESGKEENTIEQPNKVKESDTSQPSGYTNIDEKISNOQELLNLPINEYENKAR 251  
Qy 181 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSIITEGYDDSEGVIKAHDAENLIYD 240  
Db 252 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSIITEGYDDSDGIIKAHDAENLIYD 311  
Qy 241 VTPEVDDKVKSGDTMTVDIDKNTVPSDLTDSFTPIPKIKDNGSEIIATGTVDNTNKQIITYT 300  
Db 312 VTPEVDDKVKSGDTMTVNIIDKNTVPSDLTDSFAIPKIKDNGSEIIATGTVDNTNKQIITYT 371

Qy 301 FTDVYDKYENIKAHKLKLTSTYDKSKVPNNNTKLDVEYKLTALSSVKNKTIITVEYQRPENRT 360  
Db 372 FTDVYDKYENIKAHKLKLTSTYDKSKVPNNNTKLDVEYKLTALSSVKNKTIITVEYQRPENRT 431  
Qy 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNISGNGDEGSDTIIDDDSTIIKVKYKVG 420  
Db 432 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNISGNGDEGSDTIIDDDSTIIKVKYKVG 491  
Qy 421 DNQNLPSNRIRYDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKVISKYDPNKDDY 480  
Db 492 DNQNLPSNRIRYDYSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIIKVISKYDPNKDDY 551  
Qy 481 TTIQQTVMQTTINEYTGEBFTASVDNTIAFSTSSGQGGDLPEPKTYKIGDYVWEDVDK 540  
Db 552 TTIQQTVMQTTINEYTGEBFTASVDNTIAFSTSSGQGGDLPEPKTYKIGDYVWEDVDK 611  
Qy 541 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 582  
Db 612 DGIQNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEGKYQFDG 653

## RESULT 11

US-10-378-674-9  
; Sequence 9, Application US/10378674  
; Publication No. US20040006209A1  
; GENERAL INFORMATION:  
; APPLICANT: PATTI, Joseph M.  
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATI  
; FILE REFERENCE: STAPHYLOCOCCAL PROTEINS  
; CURRENT APPLICATION NUMBER: US/10/378,674  
; CURRENT FILING DATE: 2003-03-05  
; PRIOR APPLICATION NUMBER: 60/361,324  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 549  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-10-378-674-9

Query Match 88.6%; Score 2670; DB 4; Length 549;  
Best Local Similarity 98.7%; Pred. No. 2.5e-132;  
Matches 519; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKRSERDRTSTTNVDENEATFLQK 60  
Db 24 SSDEENDVINNQSIINSDDNNQINKKEETNNNDGIEKSSERDRTSTTNVDENEATFLQK 83  
Qy 61 TPQDNTHLTBEVKESSESSVSSNSIDTAQPSHTTINREESVQTSNDVDSHVSDFANS 120  
Db 84 SPQDNTHLTBEVKESPESSVSSNSIDTAQPSHTTINREESVQTSNDVDSHVSDFANS 143  
Qy 121 KIKESNTESGKEENTIEQPNKVKESDTSQPSGYTNIDEKISNOQELLNLPINEYENKAR 180  
Db 144 KIKESNTESGKEENTIEQPNKVKESDTSQPSGYTNIDEKISNOQELLNLPINEYENKAR 203  
Qy 181 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSIITEGYDDSEGVIKAHDAENLIYD 240  
Db 204 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSIITEGYDDSEGVIKAHDAENLIYD 263  
Qy 241 VTPEVDDKVKSGDTMTVDIDKNTVPSDLTDSFTPIPKIKDNGSEIIATGTVDNTNKQIITYT 300  
Db 264 VTPEVDDKVKSGDTMTVDIDKNTVPSDLTDSFTPIPKIKDNGSEIIATGTVDNTNKQIITYT 323  
Qy 301 FTDVYDKYENIKAHKLKLTSTYDKSKVPNNNTKLDVEYKLTALSSVKNKTIITVEYQRPENRT 360  
Db 324 FTDVYDKYENIKAHKLKLTSTYDKSKVPNNNTKLDVEYKLTALSSVKNKTIITVEYQRPENRT 383  
Qy 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNISGNGDEGSDTIIDDDSTIIKVKYKVG 420

Db 384 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGDEGSTIIDSTIIKVKYVG 443

QY 421 DNQNLPSNRIDYSEYEDVTNDYAQLGNNDVNFNGNIDSPYIIKVISKYDPNKDDY 480

Db 444 DNQNLPSNRIDYSEYEDVTNDYAQLGNNDVNFNGNIDSPYIIKVISKYDPNKDDY 503

QY 481 TTIIQQTVMQTTINEYTGFRFRTASYDNTIAFSTSSGGQGGDLPPK 526

Db 504 TTIIQQTVMQTTINEYTGFRFRTASYDNTIAFSTSSGGQGGDLPPK 549

RESULT 12

US-10-378-674-2

; Sequence 2, Application US/10378674

; Publication No. US20040006209A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M.

; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGAT

; FILE REFERENCE: P07556US01/BAS

; CURRENT APPLICATION NUMBER: US/10/378,674

; CURRENT FILING DATE: 2003-03-05

; PRIOR APPLICATION NUMBER: 60/361,324

; PRIOR FILING DATE: 2002-03-05

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 560

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-10-378-674-2

Query Match 83.3%; Score 2510.5; DB 4; Length 560;

Best Local Similarity 93.2%; Pred. No. 6.1e-124;

Matches 490; Conservative 14; Mismatches 21; Indels 1; Gaps 1;

QY 1 SSDEEKNDVNNQSIINTDDNNQIIKKEETNNYDGEKSEBRTSTTNVDENEATFLQK 60

Db 36 SSNEEKNDVNNQSINTDDNQ-IKKEETNSDAIENRSKDIQTSTNVVDENEATFLQK 94

QY 61 TPQDNTHLTREEVKESSSVSSSLDTAQPSHTTINREESVQTSNDVEDSHVDFANS 120

Db 95 TPQDNTHLTREEVKESSSVSSSMQTSQPSHTTINSEASIQTSNEENSRRVSDFANS 154

QY 121 KIKESNTSGKEENTIEQPNKYKEDSTTSQPGYTNIDIKISQDELLMLPINEYENKAR 180

Db 155 KIIENSTSGKEENTIEQPNKYKEDSTTSQPSYKNIIDIKISQDELLMLPINEYENKVR 214

QY 181 PLSTTSAQPSIKRVTVNQLAABQGSNNVHLIKVTDQSITEGYDDSEGVIKAHDAENLIYD 240

Db 215 PLSTTSAQPSKRVTVNQLAABQGSNNVHLIKVTDQSITEGYDDSDGIIKAHDAENLIYD 274

QY 241 VTFFVDDKVKSGDTMTVIDIKNTVPSDLTDSFTPIKIDNSGEIATGYDNKNQIITYT 300

Db 275 VTFFVDDKVKSGDTMTVINIDKNTVPSDLTDSFAIPKIDNSGEIATGYDNTNKQIITYT 334

QY 301 FTDYVDKYENIKAHLKLTSDYIDKSKVPNNNTKLDVEYKTALSSVNKTITVEYQRPENRT 360

Db 335 FTDYVDKYENIKAHLKLTSDYIDKSKVPNNNTKLDVEYKTALSSVNKTITVEYQRPENRT 394

QY 361 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGDEGSTIIDSTIIKVKYVG 420

Db 395 ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGDEGSTIIDSTIIKVKYVG 454

QY 421 DNQNLPSNRIDYSEYEDVTNDYAQLGNNDVNFNGNIDSPYIIKVISKYDPNKDDY 480

Db 455 DNQNLPSNRIDYSEYEDVTNDYAQLGNNDVNFNGNIDSPYIIKVISKYDPNKDDY 514

QY 481 TTIIQQTVMQTTINEYTGFRFRTASYDNTIAFSTSSGGQGGDLPPK 526

Db 515 TTIIQQTVMQTTINEYTGFRFRTASYDNTIAFSTSSGGQGGDLPPK 560

RESULT 13

US-11-016-564-3

; Sequence 3, Application US/11016564

; Publication No. US20050287146A1

; GENERAL INFORMATION:

; APPLICANT: INHIBITEX, INC.

; TITLE OF INVENTION: METHOD OF INHIBITING CANDIDA-RELATED INFECTIONS

; FILE REFERENCE: P08140US03/BAS

; CURRENT APPLICATION NUMBER: US/11/016,564

; CURRENT FILING DATE: 2004-12-20

; PRIOR APPLICATION NUMBER: US 60/566,082

; PRIOR FILING DATE: 2004-04-29

; PRIOR APPLICATION NUMBER: US 60/561,540

; PRIOR FILING DATE: 2004-04-13

; PRIOR APPLICATION NUMBER: US 60/530,654

; PRIOR FILING DATE: 2003-12-19

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 331

; TYPE: PRT

; ORGANISM: Candida albicans

US-11-016-564-3

Query Match 56.5%; Score 1702; DB 6; Length 331;

Best Local Similarity 98.2%; Pred. No. 9.8e-82;

Matches 325; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

RESULT 14

US-10-378-674-4

; Sequence 4, Application US/10378674

; Publication No. US20040006209A1

; GENERAL INFORMATION:

; APPLICANT: PATTI, Joseph M.

; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGAT

; FILE REFERENCE: P07556US01/BAS

; CURRENT APPLICATION NUMBER: US/10/378,674

; CURRENT FILING DATE: 2003-03-05

; PRIOR APPLICATION NUMBER: 60/361,324

; PRIOR FILING DATE: 2002-03-05

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 343

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-10-378-674-4

QY 501 RTASYDNTIAFSTSSGGQGGDLPPKTYKIG 531

Db 301 RTASYDNTIAFSTSSGGQGGDLPPKTYKIG 331

```
Query Match      55.5%; Score 1672; DB 4; Length 343;
Best Local Similarity 97.9%; Pred. No. 3.8e-80;
Matches 319; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 201 AEQGSNVNHLIKVTDQSITGEGYDDSEGVKKAHAENLIYDVTFEVDDKVKSGDTMTVDID 260
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 SEQGSNVNHLIKVTDQSITGEGYDDSDGIIKAHAENLIYDVTFEVDDKVKSGDTMTVNID 77

QY 261 KNTVPSDLTDSFTPIKIKNSGEIIATGYDNKNKQIITYFTDYVDKYENIKAHKLKTSY 320
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 KNTVPSDLTDSFPAIKIKNSGEIIATGYDNTNKQIITYFTDYVDKYENIKAHKLKTSY 137

QY 321 IDKSKVPNNNTKLDVEYKTALSSVNKTIITVEYQRPENRNTANLQSMFTNIDTKNHTVEQT 380
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 138 IDKSKVPNNNTKLDVEYKTALSSVNKTIITVEYQKPNRNTANLQSMFTNIDTKNHTVEQT 197

QY 381 IYINPLRYSAKETNNVNSGDEGSTIIDDSIIKVKYKGNQNLPSNRNIYDYSEYEDV 440
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 198 IYINPLRYSAKETNNVNSGDEGSTIIDDSIIKVKYKGNQNLPSNRNIYDYSEYEDV 257

QY 441 TNDDYAOQLGNNDVNINFGNIDSPYIIKVISKYPNKDDYTTIQOQTVTMQTTINEYTGEF 500
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 258 TNDDYAOQLGNNDVNINFGNIDSPYIIKVISKYPNKDDYTTIQOQTVTMQTTINEYTGEF 317

QY 501 RTASYDNTIAFSTSSGGQGGDLPPK 526
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 318 RTASYDNTIAFSTSSGGQGGDLPPK 343

RESULT 15
US-10-378-674-6
; Sequence 6, Application US/10378674
; Publication No. US20040006209A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M.
; TITLE OF INVENTION: MONOCLONAL AND POLYCLONAL ANTIBODIES RECOGNIZING COAGULASE-NEGATI
; FILE REFERENCE: P07556US01/BAS
; CURRENT APPLICATION NUMBER: US/10/378,674
; PRIOR FILING DATE: 2003-03-05
; APPLICATION NUMBER: 60/361,324
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentcin version 3.1
; SEQ ID NO 6
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-378-674-6

Query Match      51.8%; Score 1562; DB 4; Length 316;
Best Local Similarity 97.7%; Pred. No. 2.1e-74;
Matches 298; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 201 AEQGSNVNHLIKVTDQSITGEGYDDSEGVKKAHAENLIYDVTFEVDDKVKSGDTMTVDID 260
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 12 SEQGSNVNHLIKVTDQSITGEGYDDSDGIIKAHAENLIYDVTFEVDDKVKSGDTMTVNID 71

QY 261 KNTVPSDLTDSFTPIKIKNSGEIIATGYDNKNKQIITYFTDYVDKYENIKAHKLKTSY 320
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 72 KNTVPSDLTDSFPAIKIKNSGEIIATGYDNTNKQIITYFTDYVDKYENIKAHKLKTSY 131

QY 321 IDKSKVPNNNTKLDVEYKTALSSVNKTIITVEYQRPENRNTANLQSMFTNIDTKNHTVEQT 380
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 132 IDKSKVPNNNTKLDVEYKTALSSVNKTIITVEYQKPNRNTANLQSMFTNIDTKNHTVEQT 191

QY 381 IYINPLRYSAKETNNVNSGDEGSTIIDDSIIKVKYKGNQNLPSNRNIYDYSEYEDV 440
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 192 IYINPLRYSAKETNNVNSGDEGSTIIDDSIIKVKYKGNQNLPSNRNIYDYSEYEDV 251

QY 441 TNDDYAOQLGNNDVNINFGNIDSPYIIKVISKYPNKDDYTTIQOQTVTMQTTINEYTGEF 500
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db      252 TNDDYAOQLGNNDVNINFGNIDSPYIIKVISKYPNKDDYTTIQOQTVTMQTTINEYTGEF 311
QY      501 RTASY 505
         |||||
Db      312 RTASY 316

Search completed: August 12, 2006, 09:20:36
Job time : 186 secs
```

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: August 12, 2006, 09:17:41 ; Search time 34 Seconds  
(without alignments)  
1152.223 Million cell updates/sec  
Title: US-10-806-288-13  
Perfect score: 3013  
Sequence: 1 SDEKNDVINNNQSINTDD.....PDGTSKSVRTDEGKYQFDG 582  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 239914 seqs, 67312017 residues  
Total number of hits satisfying chosen parameters: 239914  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Published Applications AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pap.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pap.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pap.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pap.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pap.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pap.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2810.5	93.3	930	7	US-11-396-565-10
2	576	19.1	1349	6	US-10-471-571A-3352
3	499	16.6	1742	7	US-11-396-565-4
4	455	15.1	995	6	US-10-471-571A-3354
5	454	15.1	927	6	US-10-471-571A-2922
6	397.5	13.2	877	6	US-10-471-571A-3884
7	377	12.5	496	6	US-11-256-173-29
8	376	12.5	948	6	US-10-471-571A-3552
9	300.5	10.0	1018	6	US-10-471-571A-3554
10	262.5	8.7	1160	7	US-11-192-046-250
11	259	8.6	1161	7	US-11-192-046-121
12	253.5	8.4	3029	6	US-10-537-642-10
13	212	7.0	2024	6	US-10-537-642-21
14	211.5	7.0	1086	6	US-11-330-403-3535
15	205	6.8	774	6	US-10-471-571A-4824
16	204	6.8	1781	6	US-10-537-642-24
17	201	6.7	1464	6	US-10-537-642-27
18	201	6.7	2478	6	US-10-471-571A-2278
19	197	6.5	2314	6	US-11-013-711-11
20	192	6.4	1234	6	US-10-537-642-14
21	190.5	6.3	1992	7	US-11-013-711-3
22	190.5	6.3	1992	7	US-11-013-711-13
23	190.5	6.3	2047	7	US-11-013-711-4
24	190.5	6.3	2047	7	US-11-013-711-7
25	187.5	6.2	450	7	US-11-165-586-64

ALIGNMENTS

RESULT 1  
US-11-396-565-10  
; Sequence 10, Application US/11396565  
; Publication No. US20060171964A1  
; GENERAL INFORMATION:  
; APPLICANT: FOSTER, Timothy  
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCI  
; FILE REFERENCE: P06335US2/BAS  
; CURRENT APPLICATION NUMBER: US/11/396,565  
; CURRENT FILING DATE: 2006-04-04  
; PRIOR APPLICATION NUMBER: US/09/386,962  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: 60/098,443  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: 60/117,119  
; PRIOR FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 930  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-11-396-565-10

Query Match	93.3%	Score	2810.5	DB 7	Length	930			
Best Local Similarity	93.6%	Pred. No.	1.1e-125						
Matches	545	Conservative	15	Mismatches	21	Indels	1	Gaps	1
1	SSDEKNDVINNNQSINTDDNNQIIKKEETNNYDGIKESDRETSSTTNVDNEATFLQK	60							
73	SSNEEKNDVINNNQSINTDDNNQ- IKKEETNSDAIENRSKOITQSTTNVDNEATFLQK	131							
61	TPQDNTHLTREEVKSESSVSSNSSIDTAQOPSHTTINREESVQTSNDVSDSHVSDFANS	120							
132	TPQDNTHLTREEVKSESSVSSNSSMDTAQOPSHTTINSEASIQTSNDSEENSRVSDFANS	191							
121	KIKESNTSGKEENTIEQPNKVKEDSTTSOPSGYNTIDBKISNQDELLNLPINEYENKAR	180							
192	KIKESNTSGKEENTIEQPNKVKEDSTTSOPSSYKNIDEKISNQDELLNLPINEYENKVR	251							
181	PLSTTSAPSKRVTVNQLAAEQGSNNVHLIKVTDQSITEGYDDSEGVKAHDAENLIYD	240							
252	PLSTTSAPSSKRVTVNQLAAEQGSNNVHLIKVTDQSITEGYDDSDGIKAHDAENLIYD	311							
241	VTFEVDKVGSGDTMTVDIDKNTVPSDLTDSFTIPKIKNSGEBIATGTVDNKNKQITVT	300							
312	VTFEVDKVGSGDTMTVNIIDKNTVPSDLTDSFAPKIKNSGEBIATGTVDNTNKKQITVT	371							

Qy	301	FTDYVDKYENIKAHKLKLSYIDKSKVPNNNTKL DVEYKLTALSSVNKTIITVEYORPNERT	360
Db	372	FTDYVDKYENIKAHKLKLSYIDKSKVPNNNTKL DVEYKLTALSSVNKTIITVEYQKPNERT	431
Qy	361	ANLQSMFTNIDTKNHTVQGTIYNPLRYSAKETNNVNSGNGDEGSTIIDDSIIIKVYKVG	420
Db	432	ANLQSMFTNIDTKNHTVQGTIYNPLRYSAKETNNVNSGNGDEGSTIIDDSIIIKVYKVG	491
Qy	421	DNQNL PDSNR IYDYSEYEDVNTDDYAQLGNNDVNINFGNIDSPYIIKVIISKYDPNKDDY	480
Db	492	DNQNL PDSNR IYDYSEYEDVNTDDYAQLGNNDVNINFGNIDSPYIIKVIISKYDPNKDDY	551
Qy	481	TTIQQTVMQTITNEYTGEFRTASVDNTIAFSTSSGQGGDLPEKTYKIGDVVWEDVDK	540
Db	552	TTIQQTVMQTITNEYTGEFRTASVDNTIAFSTSSGQGGDLPEKTYKIGDVVWEDVDK	611
Qy	541	DGIQNTNDNEKPLSNVLVTLYTPDGTSKSVRTDEGKYQFDG	582
Db	612	DGIQNTNDNEKPLSNVLVTLYTPDGTSKSVRTDEGKYQFDG	653
RESULT 2			
US-10-471-571A-3352			
; Sequence 3352, Application US/10471571A			
; Publication No. US20060115490A1			
; GENERAL INFORMATION:			
; APPLICANT: CHIRON SPA			
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS			
; FILE REFERENCE: P026927WO			
; CURRENT APPLICATION NUMBER: US/10/471,571A			
; CURRENT FILING DATE: 2003-09-12			
; PRIOR APPLICATION NUMBER: GB-0107661.1			
; PRIOR FILING DATE: 2001-03-27			
; NUMBER OF SEQ ID NOS: 5642			
; SOFTWARE: SeqWin99, version 1.03			
; SEQ ID NO 3352			
; LENGTH: 1349			
; TYPE: PRP			
; ORGANISM: Staphylococcus aureus			
; FEATURE:			
; NAME/KEY: MISC FEATURE			
; LOCATION: (1)..(1349)			
; OTHER INFORMATION: Ser-Asp rich			
US-10-471-571A-3352			

```

343 QY SVNKTIIVYQVRN--ENRTANIQSMFTNIDTKNHT-----VEQTIYNINPLRYSAKE 392
382 Db NTTTTKTANIQYDPYVYVNEKNSIGSAFT--ETVSHVGNKENPGYKQTIYVNPSENSLTN 439
393 QY TNVNI-----SGNGDEGSTIIDDSIIIKVKYKGDNDONLPDSNRRIYDYS--EYEDVTNDDYA 446
440 Db AKLKVQAYHSYSPNNICQINKOVYTDIKIYQVPGKYTL---NKGVDVNTKELTDVTN-QYL 495
447 QY Q-----LGNNDVNINFGNIDSPYIKVISKYDPNKKDYTTTQQVTVMQTINNEYTGEPRTA 503
496 Db QKITYGDNNSAVIDFGNADSAVYVVMVNTKFOYTNSESPFTLVQMATLSSTGN-----KSV 549
504 QY SYDNTIAFSTSSGOGQGDLPPEKTYKIGDYVWEDVDKDGQNTNDNEKPLSNVLVTLYP 563
550 Db STGNALGFTNNQSGGAG-----QEVYKIGNYVWEDTNKGVQEL--GEKGVGNVTVTV-FD 602
564 QY DGTSKSVR-----TDEDGKY 578
603 Db NNTNTKVGAVTKEDGSY 620

RESULT 3
US-11-396-565-4
; Sequence 4, Application US/11396565
; Publication No. US20060171964A1
; GENERAL INFORMATION:
; APPLICANT: FOSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE
; FILE REFERENCE: P06335U82/BAS
; CURRENT APPLICATION NUMBER: US/11/396,565
; CURRENT FILING DATE: 2006-04-04
; PRIOR APPLICATION NUMBER: US/09/386,962
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1742
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-11-396-565-4

```

QY 334 DVEYKALSSVNTKIITVEYQRPENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKET 393  
Db 505 PMEVTIANEVVKXDFIVDYGKKNQNTTT---AAVANVDNVDNNKHNVVILNQNNPKYA 561  
QY 394 NVNISNGDEGSIIDDSIT---IKVYKVDGNQNLPS-NRIYDYSEYEDVTNDYQAL- 448  
Db 562 KY-----FSTVKGGEFTPGVKYEVETDWTAMVDSFNPDLNNSNVKDVTSQFAPKVS 613  
QY 449 GNNVDNINFGNI---DSPYIIKISKYDPNKDDYTIIOQTVMQTTINSEYTGFEFTASY 505  
Db 614 ADGTRVDINPARGMANGKKYIVTQAVRPTGTGNVIT--EYWLTRDGTIN--TNDFYRGTK 669  
QY 506 DNTIAFSTSGGQGGDLPEKTKYKIGYVWEDVDKGIQNTNDNEXPLSNVLVTLTYPDG 565  
Db 670 STTVTVYVYSSSTAQGNP---TYSLGDYVWLDKKNQVQ--DDEKGLAGVYVTL--KDS 722  
QY 566 TSKS---VRTDEDKYQFD 581  
Db 723 NNRELQRVTTDQSGHYQFD 741

## RESULT 4

US-10-471-571A-3354  
; Sequence 3354, Application US/10471571A  
; Publication No. US20060115490A1

## GENERAL INFORMATION:

; APPLICANT: CHIRON SPA

; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE: P026927WO

; CURRENT APPLICATION NUMBER: US/10/471,571A

; PRIOR FILING DATE: 2003-09-12

; PRIOR APPLICATION NUMBER: GB-0107661.1

; NUMBER OF SEQ ID NOS: 5642

; SOFTWARE: SeqWin99, version 1.03

; SEQ ID NO 3354

; LENGTH: 995

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)-(995)

; OTHER INFORMATION: Ser-Asp rich

US-10-471-571A-3354

Query Match 15.1%; Score 455; DB 6; Length 995;

Best Local Similarity 27.2%; Pred. No. 3e-14;

Matches 158; Conservative 93; Mismatches 222; Indels 108; Gaps 25;

QY 35 GIEKSEDRTESTTNVDNEATFLQKTPQDNTHLTETEEVKSSSVES-----SNSSIDTAQ 90  
Db 45 GHEAKAAEHTNGELNQSKNETT-----APSEN-----KTKKVDLSRQLKDNQTQTATAD 92  
QY 91 QPSHTTINREESVQTSNDVEDSHVDFPANSKIKESNTSEKKEENTIEQPNKVKEDSTTSQ 150  
Db 93 QPKVT-----MDSATVVKETSSNMQS-----PQNATANQSTTK 125  
QY 151 PSGYTNIDEX---ISNDELLNLPINEYENKARPLSTTSQAQSIK-----RYTVNOLAA- 201  
Db 126 TSNVTNDKSSYTSNETDKSNL-----TQAKDVSTTPKPTTIIKPTLNRAVNTVAAP 179  
QY 202 EGGSNNVHLIKVT--DQSITEGY-DDSEGVIK--AHDANLIYDVTFEVDDKVKSGDWTMT 256  
Db 180 QQGTNVNDKVFHFNIDIAIDKGVNQTCTKTEFWATSSDVCLKANYTIDSDSVKSGDIFT 239  
QY 257 VIDKNTVPSDLTDSFTIPIKIDNKGSEIIATGYDNKQKIITYTTFDYVDKYENIKAHUK 316  
Db 240 FKYGQYFREGSVRLPFSQTQNLNAQGNIIAKGIYDSTTTTITFTNYVDQYTNVRGSPF 299  
QY 317 LTSYIDKSKVPNNTKLDVEYKLTALSSVNTKITVEYQRPENRTANLQSMFTNIDTKNHT 376  
Db 300 QVAPAKRKNATTDKTAYKMEVTLGNDTYSEEIIVDY---GNKKAQPLISSNTYINNEULS 356

QY 377 VBOQTIYIN-PLRYSAKETNV-NISGNGDEGSTIIDSTIIKVKYKVDGNQNL-----PDSN 429  
Db 357 RNMTAVNQPKNTYTKQTFVNLIT-----GYKFNPNKAFKIYEVTDAQFVDSFTPDTS 411  
QY 430 RIYDYSEYEDVTNDYQALGNNDNVDNINFGNIDS--PYLIKVI-----SKYDPNKDDYTT 482  
Db 412 KLKDVTDQDFVI---YSNDKNKTATVDLMKGQTSNKNQYIIQQVAYPDNSSTDNGKIDY-- 466  
QY 483 IOQTVMQTTINSEYTGFEFTASYDNTIAFSTSGGQGGDLPEKTKYKIGYVWEDVDKOG 542  
Db 467 -----TLDTDKTKYSW---SNSYSNVNGSGSTANGD-----QKKNLGDIYVWEDTNKOG 511  
QY 543 IQNTNDNEXPLSNVLVTLTYPDGTS-KSVRTDDEDKYQFDG 582  
Db 512 KQDA--NEKGIKGVYVILKDSNGKELDRITTTDENGKYQFTG 550

## RESULT 5

US-10-471-571A-2922

; Sequence 2922, Application US/10471571A

; Publication No. US20060115490A1

; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA

; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE: P026927WO

; CURRENT APPLICATION NUMBER: US/10/471,571A

; CURRENT FILING DATE: 2003-09-12

; PRIOR APPLICATION NUMBER: GB-0107661.1

; PRIOR FILING DATE: 2001-03-27

; NUMBER OF SEQ ID NOS: 5642

; SOFTWARE: SeqWin99, version 1.03

; SEQ ID NO 2922

; LENGTH: 927

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)-(927)

; OTHER INFORMATION: fibrinogen-binding protein

US-10-471-571A-2922

Query Match 15.1%; Score 454; DB 6; Length 927;

Best Local Similarity 26.6%; Pred. No. 3.1e-14;

Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;

QY 1 SSDEEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKESSEDRTESTTNVDNEATFLQK 60  
Db 51 SNESKNSDSSVSAAPKTDITNV-----SDTKTSNTN---NGETSVAQ 91  
QY 61 TPQDNTHLTETEEVKSSSVESNSSIDTAQPSHTTINREESVQTSNDVEDSHVDFPANS 120  
Db 92 NP-----AQQETTSSTNATTEETPVVTEGATTTTNTQANTPATQOS-SNTNAEELVN- 143  
QY 121 KIKESNTSEKKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNQDELNL-LPINEYENKA 179  
Db 144 --QTSNETTNDNTNV-----SSVNSPQNSTNAENVSTTQDTSTTEATPSN---NES 189  
QY 180 RPLSTTSQAQPSIKRVTVN-----QLAAEQGSNVNHLIKVTDQ--SITEGYDDSEGV 228  
Db 150 APQSTDAKNQDVNVQAVNTSAPRMAFSLAAVAADAPVAGTDTITNLTNVTYGI-DSGTT 248  
QY 229 IKAHDAENLIYDVTFEVDDKVKSGDWTMTVDIKNTVPSDLTDSFTIPIKIDNKGSEIIATG 288  
Db 249 VYPHQAGYVYKLVGFSVPNSAVKGDTFKITYPKELNLNGVTSSTAKVPPIMAGD-QVLANG 307  
QY 289 TYDNKQKQITTYTTFDYVDKYENIKAHKLKLTYSIDSKVPNNNTKL-DVEYKLTALSS--VN 345  
Db 308 VIDS--DGNVIYTFDYVNTKDDVKATLTMPAYID----PENVKKTGNVTLATIGISTTAN 362  
QY 346 KTIITVEYQRPENRTANLQSMFTNIDTKNHTVEQTIYINPL--RYSAKETNVNISGNGDE 403  
Db 363 KTVLDVDEYKYGKFNLSIKGTIDQDKTNTYRTQTIYVNPBGDNVIAPLVLTGNLKNPTDTS 422

Qy 404 GSTIIDSTTIKVKYKGNQNLPSNRIDYSEYEDVTNDYDQAQGNNDVNIHFG----- 459  
Db 423 NALIDQQNTSKVKYKVDNAADLSESYFV-NPENFEDVNSVNIPTPNQYKVENTPDD 481  
Qy 460 NIDSPYIIKVKISKYDPN-KDDYTTTQQVTVMQTINEYTG--FRTASYDNTIAFSTSSG 516  
Db 482 QITTFYIVVNGHIDPNSKGD-----LAURSTLYGYSNLIWRMSMDNEVAFNNGSG 534  
Qy 517 QQQG-DLP--PKTKYKIGDY--VWEDVDK-GIQNTNDN 549  
Db 535 SGDGIKVPVPEQPEGEIEBIPEDSDSDPGSDSGSDS 573  
RESULT 6  
US-10-471-571A-3884  
; Sequence 3884, Application US/10471571A  
; Publication No. US20060115490A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON Spa  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE: P026927W0  
; CURRENT APPLICATION NUMBER: US/10/471, 571A  
; CURRENT FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: GB-0107661.1  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 5642  
; SOFTWARE: SeqWinn9, version 1.03  
; SEQ ID NO 3884  
; LENGTH: 877  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(877)  
; OTHER INFORMATION: Clumping factor B  
US-10-471-571A-3884

Query Match 13.2%; Score 397.5; DB 6; Length 877;  
Best Local Similarity 24.5%; Pred. No. 1.3e-11;  
Matches 143; Conservative 81; Mismatches 207; Indels 153; Gaps 23;  
Qy 2 SDEEKNDVI---NNQSIINTDNNQIIKKEETNNYDGIKESDRTESTTNVDNEATFL 58  
Db 44 ASEQNDTTQSKKNASADSEKNWI---ETPQLTNTANDTSDISANTNSANVDSTTKP 99  
Qy 59 OKTPQDNTLTHEEVKESSESSVSIDTAQPSHTTINREESVQTSNDVEDSHVSDFA 118  
Db 100 MSTQTSNTTTE-----PASTNETPQPTAIKNQ---ATAAKMQDQTVPOEA 142  
Qy 119 NSKIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIIDEKISNQDELLNLPINEYENK 178  
Db 143 NSQVDNKT---NDANSIATNSLKNQ-----LQLP-----Q 173  
Qy 179 ARPLSTTSAQ---PSIKRVTNOLAEO-----GSNNHLIKVTDQSITGYDSDS 225  
Db 174 SSPQTSINAQTSKESVTRAVRSILAEPVVAADAKGTNN-----DKVTASNFKLE 227  
Qy 226 EGVIIKAHDAENLIYDVTFEVDKVKSGDTMTV-----DID-----DKNTVPSDLTDS 271  
Db 228 KTTFDPNQSGNTFMAANFTVTDKVKSGDYFTAFLPDSLGTGNDVDVSSNNTMP----- 281  
Qy 272 FTIPKIKNSGEIATGYDNKNGKIITFTDYVDKYENIKAKHLKLTYSIDSKVPPNNNT 331  
Db 282 --IADIKSTNGDVAKATYDILTKTYTFVFDYVNNKENINGQFSLPFLTDRAKAPKSGT 339  
Qy 332 KLDVEYKTALSSVNTIITVEYQRP-----NENRTANLQSMFTNIDTKN--HTVEQTIYINP 385  
Db 340 -YDANINIADEMNNKIITWSSPIAGIDKNGENISSQIIGVDTASQNTYKQTVFVNP 398  
Qy 386 LRYSAKETVNIISNGDSGSTIIDS-----TIIKVKYKVDNQNLPS----- 428  
Db 399 KORVLGNTWVIKGYQDK-----IESSGKVSATDTKLRIFEVNDTSKLSDSYADPNDSN 454

Qy 429 -----NRIYDYSEYEDVTNDYDQAQGNNDVNIHFGNIDSPYIIKVKISYKDPNKDD 479  
Db 455 LKEVTDQFKRIY-----YE-----HPNVASIKFGDITKTYVVLVSGHYDNTGKN 499  
Qy 480 YTT--IQOTVTMOTTINEYTGFEFRTASVDNTIAFSTSSGQGGD 521  
Db 500 LKTQVIQENVDPT-----NRDYSIFGNWNNENVVRYGGGSADGD 538  
RESULT 7  
US-11-256-173-29  
; Sequence 29, Application US/11256173  
; Publication No. US20060140979A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Sheffield  
; TITLE OF INVENTION: Antigenic Peptides  
; FILE REFERENCE: toxin  
; CURRENT APPLICATION NUMBER: US/11/256,173  
; CURRENT FILING DATE: 2005-10-24  
; PRIOR APPLICATION NUMBER: US/10/311,879  
; PRIOR FILING DATE: 2003-03-18  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-11-256-173-29

Query Match 12.5%; Score 377; DB 7; Length 496;  
Best Local Similarity 25.7%; Pred. No. 6e-11;  
Matches 127; Conservative 88; Mismatches 210; Indels 70; Gaps 19;  
Qy 1 SSDEEKNDVINNOSINTDNNQIIKKEETNNYDGIKESDRTESTTNVDNEATFLQK 60  
Db 51 SNESKSDSSSVSAAPKTDITNV-----SDTKTSNTN---NGETSVAQ 91  
Qy 61 TPQDNTLTHEEVKESSESSVSIDTAQPSHTTINREESVQTSNDVEDSHVSDFANS 120  
Db 92 NP-----AQETQSSSTNATTBETPVGTGATTTTNTQANTPATOS-SNTNABELVN- 143  
Qy 121 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIIDEKISNQDELLN-LPINEYENKA 179  
Db 144 --QTSNETTNDTV-----SSVNSPQNSTNAENVSTTQDTSPEATPSN---NES 189  
Qy 180 RPLSTTSAQPSIKRVTN-----OLAAEQSGSNVHLIKVTDQ---SITEGYDDSGV 228  
Db 190 APQSTDASNKQVNVQAVNTSAPRMRAPSLAAVAADAPAAAGTDITNQLTNTVTG-I-DSGTT 248  
Qy 229 IKAHDAENLIYDVTFEVDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKNSGEBIATG 288  
Db 249 VYPHQAQGVKUNYGFSPNSAVKGDFTKIVPKELNLNGVTSATAKVPPIMAGD-QVLANG 307  
Qy 289 TYDNKNKIITFTDYVDKYENIKAKHLKLTYSIDSKVPPNNNTKL-DVEYKTALSS--VN 345  
Db 308 VIDS-DGNVIYTFDYVNTKDDVKATLTMPAID----PENVKKTGNVTLATGIGSTTAN 362  
Qy 346 KTIITVEYQRPENENTANLQSMFTNIDTKNHTVEQTIYINPL--RYSAKETVNIISNGNDE 403  
Db 363 KTVLVDYKEYGKFNLSIKGTIDQIDKTNNTYRTIYVNPSPGDNVIAFVLTLGNLKPNTDS 422  
Qy 404 GSTIIDSTTIKVKYKGNQNLPSNRIDYSEYEDVTNDYDQAQGNNDVNIHFG----- 459  
Db 423 NALIDQQNTSKVKYKVDNAADLSESYFV-NPENFEDVNSVNIPTPNQYKVENTPDD 481  
Qy 460 NIDSPYIIKVKISKYD 474  
Db 482 QITTFYIVVNGHID 496  
RESULT 8  
US-10-471-571A-3552  
; Sequence 3552, Application US/10471571A



```
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927MO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3552
; LENGTH: 948
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(948)
; OTHER INFORMATION: fibronectin-binding protein
US-10-471-571A-3552

Query Match      12.5%; Score 376; DB 6; Length 948;
Best Local Similarity 23.4%; Pred. No. 1.5e-10;
Matches 138; Conservative 110; Mismatches 217; Indels 124; Gaps 22;

QY 35 GIEKSEDRTESTTNDENEATFLQKTPDNTHTLTHTEEVKSSSVSSSSIDTAQ---- 90
Db 38 GQKEAAAEQNNTTVEES-----GSSATESKASETQTNTNNVTIDETQSYSA 86

QY 91 -----OPSHTT-INREESVOT--SDNVSDSHVDFPANSKIKESNTESGKEENTIEQPNKYK 143
Db 87 TDEQPSQSTQTTEEAPKTVQAPKVESRV-DLPSEKVDKETTGTQVD--IAQSNYS 143

QY 144 EDSITTSQPSGYTNIDEKISQDELNLPLINEYENKARPLSTTSAQPSIKRVTVNQLAERQ 203
Db 144 E-----IPRMKRSITDVTAVAEK 161

QY 204 -----GSNNHLIKVTDQSITEGYDSDSEGVKAKHAENLIYDVTFEVDKVKSGDT 254
Db 162 EVVEETKATGTDVTKNKEVEEGSEIVGHKQDNTNVNPHNAERVTLKYKWFGEKIGAGDY 221

QY 255 MTVDIDKNTVPSDLTDSFTPIKIDKSGEIIATGYDKNKQITFTFTDYDVKYENIKAH 314
Db 222 FDTLSNDNVETHGISLTKRVPEIKSTDGQVMATGEIIGERK-VRYTFKEIYVQEKDILTAE 280

QY 315 LKLTSDYDKSKVPNNNTKLDVYKTAALSNVNTITVEY---QKPNENRTANLQSMFTNID 371
Db 281 LSLNLFIDFTTQKGNQ-NVEVKLGETTVSKIFNLQYLGVRDNGWVTAN-----GRID 334

QY 372 TQKHT---VEQTIYINPLRYSAKETNVNISGNGDEGSTIIDSTIIKVKYKVGDNQNLPS 428
Db 335 TLNKVDGKFSHFAYMKPNQSL--SSVTVTGQVTKGNKPGVNNPTVKYKHYGSDDLAES 392

QY 429 ---NRIYDYSEYEDVTDNDYDAQLGNNDVNINFGNIDSP--YIIKVISKYDPNKDDYTIQ 484
Db 393 VYAKLDDVSKFEDVDNMSLDFDTNGGYSLSNLFNLDQSKNYVIKGYEYDYSNAN----- 447

QY 485 QVTVMQTTINEYTGFRTA--SYDNTIAPSTSSGQOG-----DLPPEKTYKIG 531
Db 448 --LEFQTHLFGYNYNYYSNLTKWGVAFYSNNAQGDGDKKKEPIIEHSTFIELEFKSE 505

QY 532 DYVVEDVDKQGTQNTNDNEKPLSNLVTLT-----YPDGTSKSVRTDED 575
Db 506 PPVEKHELTGTIEESNDS-KPIDFEVHTAVEGAEGHAGT---IETED 550
```

## RESULT 9

```
US-10-471-571A-3554
; Sequence 3554, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
```

```
; FILE REFERENCE: P026927MO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3554
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1018)
; OTHER INFORMATION: fibronectin-binding protein
US-10-471-571A-3554

Query Match      10.0%; Score 300.5; DB 6; Length 1018;
Best Local Similarity 21.2%; Pred. No. 6.3e-07;
Matches 123; Conservative 118; Mismatches 243; Indels 97; Gaps 25;

QY 35 GIEKSEDRTESTTNDENEATFLQKTPDNTHTLTHTEEVKSSSVSSSSIDTAQ 90
Db 30 GQKEAAAEQKTTTVEEN-----GNSATDNKTSETQTATNVNHIETQSYNATV--TE 82

QY 91 QPSHTT-INREB---SVQTSNDVSDSHVDFPANSKIKESNTESGKEENTIEQPNKYKEDS 146
Db 83 QPSNATQVTEEAPRAVQAPQAPQAPANIETVKEVVKE-----EAKPQVKETT 130

QY 147 TTSQPSG---YNNIDKISQDELNLPLINEYENKARPLSTTSAQPSIKRVT-----V 196
Db 131 QSDNSGSDQORQVDLTPEKATQNQVAETQV---EVAQPRTASESKPRVTRSDVAEAKEA 186

QY 197 NQLAAEQSGNVNHLIKVTDQSITEGVDSSEGVKAKHAENLIYDVTFEVDKVKSGDTMT 256
Db 187 SNAKVETGTDVTSKVTVEIGSI-EGHNNTNKV-EPHAGQRAVLKYKLFENGHLQGDYFD 244

QY 257 VDIDKNTVPSDLTDSFTPIKIDKNS-----GBIIATGYDKNKQITFTFTDYDVKYENI 311
Db 245 FTLSNNVNTGHVSTARKVPEIKNGSVWMAETGEVLEGG-----KIRYFTNDIEDKVDV 297

QY 312 KAHLKLTSDYDKSKVPNNNTKLDVYKTAALSNV-----KITVEYQRPENRTANLQSM 366
Db 298 TAELEINLFDIPKTVQTNNGN-----QTTTSLNEEQTSKELDVKYKDGIGNYYANLNGS 351

QY 367 PTNIDTKHNTVEQTIYINPLRYSAKETNVNISGNGDEGSTIIDSTIIKVKYK-VGDNQNL 425
Db 352 IETFKANNRRSHVAFIRP--NNGKTTTSVTVTGTLMKSGSNQNGQPKVRIEYLGNNEDI 409

QY 426 PDSNRIY---DYSEYEDVTDNDYDAQLG--NNNDVNINFGNIDSPYIIKVISKYDPNKD- 478
Db 410 AKS--VYANTTDTSKFEKVTSNMGNLNLQNNGSYSLSNLENLDKTVVHYDGEYLGNTDE 467

QY 479 -DYTTIQOVTVMQTTINEYTGFRTAQSYDNTIAPSTSSGQOGDLPP-----EKTYYKIG 532
Db 468 VDFERT-QMVGHPEQLKYIYDRGYTLTWNGLGLYSNKANGNEKNGPIIQNNKFEYK---- 523

QY 533 YVVEDVDKQGTQNTNDNEKPLSNLVTLTYPDGTSKSVRTD 573
Db 524 ---EDTIKETTLGQYDKN-----LVTTVEBEYDSSTLDDID 555
```

## RESULT 10

```
US-11-192-046-250
; Sequence 250, Application US/11192046
; Publication No. US20060165716A1
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; APPLICANT: Barocchi, Michelle
; APPLICANT: Rappuoli, Rino
; APPLICANT: Grandi, Guido
; APPLICANT: Lauer, Peter
; APPLICANT: Mora, Marirosa
```



Db 180 HAAFKMSPELKQKSEINPGDFTVLQDRRLNPKGISQD--IPKIIYDSANSPLAIG 237  
QY 289 TYDNKNKQIYTYFTDYVDKYENIKAHKLKTSYIDSKSVNNNTKLDVEYKLTALSSVYKTI 348  
Db 238 KYHAENHQLIYTYFTDYIAGLDKVLQSAELSLFLENKEVLEN-----TSISNFKSTI 268  
QY 349 -----TVEYQRPNE-----NRTANLQSMFTNIDTKNHTVEQTIYINPLURISA 390  
Db 289 GGOEITYKGFVNLYGNESTKESNYITNGLSNVGGSIESYNTGTBGFVWYVYVNPRTNI 348  
QY 391 KETNVNISGNG-----DEGSTIIDSTIIKVKYKVDNQLNPSNRIDYSEYEDV 440  
Db 349 PYATMLWGEGRARSNTSLENDANTSSAELGIEQVTEVPEGEKLPSSYGV-----DV 401  
QY 441 T-----NDVYALQGNNDV-----NINFGN--IDSPYIIKVISYDPNKDDYTTIQOTVTM 489  
Db 402 TKLTLRTDITAGLNGFQMTKQRIDFGNNIQNKAFIIVTGTQDS-----GRPLVV 454  
QY 490 OTTINEYTGFEFTAS-----YNTTAFSTSSGQGG-----DLPEKTYKIGDY 533  
Db 455 QSNLASFRGASEYAAFTPVGGNYVFNQETALSFGSGSGKSEFTKPSITVANLKRVAQL 514  
QY 534 VNEDVDKGIQNTNDNEKPLSNVLVLTYPDGTSKSVR--TDEDGKYQF 580  
Db 515 RFKXKSTDNV-----FLPEAAFEIIRSGNSGSKLEASSNTQGEVHF 555

RESULT 12  
US-10-537-642-10  
; Sequence 10, Application US/10537642  
; Publication No. US20060165719A1  
; GENERAL INFORMATION:  
; APPLICANT: Epimmune, Inc.  
; APPLICANT: The United States of America as Represented by the  
; APPLICANT: Secretary of the Navy  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Doolan, Denise L.  
; APPLICANT: Carucci, Daniel J.  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE  
; FILE REFERENCE: EPI-103X  
; CURRENT APPLICATION NUMBER: US/10/537,642  
; CURRENT FILING DATE: 2005-06-06  
; PRIOR APPLICATION NUMBER: US 60/431,494  
; PRIOR FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1161  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 3029  
; TYPE: PRT  
; ORGANISM: Plasmodium falciparum  
US-10-537-642-10

Query Match 8.4%; Score 253.5; DB 6; Length 3029;  
Best Local Similarity 21.3%; Pred. No. 0.00042;  
Matches 150; Conservative 95; Mismatches 265; Indels 195; Gaps 31;  
QY 6 KNDVNNQISINTDDNNQIIKKEETNNYDIEKRSDETRSTNVDENEATFLOKT----- 61  
Db 926 KNENDNIPSSYSQIHHQICKVEEYTYNSIQ-----NTNNFNNNVMMMLMNTSNNI 977  
QY 62 PQDNT-----HLTEBEVKESS-----VESSNSSIDTAQ----- 90  
Db 978 PLDNNYNSKNKIYKHINDHINQKONNVEYENLNSCDNTQNKETFCNODLINSNI 1037  
QY 91 -----QPSHTTINREESVQ-----TSDNVYEDSHVSDFANSKIESNTESG 130  
Db 1038 NNNISSYTFQNNDFYTKKSKQYNHDNIYKINTTSENVGSPH-----TNKTSIYNHKG 1093  
QY 131 KEENTIEQPNKVEDSTTSQPSGYTNDKIS-----NDELLMLPINEYENKARPLSTTSA 187  
Db 1094 GYEQTIEQNEQNEQNSQ-----NIEQIEQNEQNAQNAQNAQNAQNAQNAQNAQNAQ 1148

QY 188 QPSIKRVTYN-QLAAEQGSGNVNHLIKV-----TDQSITEGYDDESEGI--KAHDAENLIYD 240  
Db 1149 QNVEQNVQEQKAFQNSN-NESEIKTNTVEIFKRNKQITNSNVIKQOHDNTNILNN 1207  
QY 241 VTFEVDDKV-----KSGDWTMTVIDKNTVPSDLTDSFTIPKIKDNGSEIATGT 289  
Db 1208 ININIKENINRHKINEFOWEKS----KIDIEKNCC---LTTKY--DKDNDNENDNDNT 1259  
QY 290 YDNKNKQIYTYFTDYVDKYENIKAHKLKTSYIDSKSVNNNTKLDVEYKLTALSS-----V 344  
Db 1260 Y-KNNDIV-----ICNNHNSSHVQKNYNNMESMINENIITTEGENLMNSTBEYFT 1312  
QY 345 NKTITVEYQRPNEENTANLQSMFTNIDTKNHTVEQ--TIYNPLURYSAKETN----- 394  
Db 1313 NELIKKSLKESKSDTKFLJLKLNEIKKEEKKONINIFINNIIYELKEINGKNRSDYF 1372  
QY 395 -----VNISGN-----GDEGSTIIDSTIIKVKYKVDNQLNPSNRIDY 434  
Db 1373 HNTKDDKENITNVSSNNHLSVPLNKYNDE-----DKQLIKOMNHASNMNF-----IYDY 1421  
QY 435 SEYEDVTNDVYALQGNNDVNI-NFGNIDSPYIIKVISYDPN-----KDDY--- 480  
Db 1422 NYHNNYSSTNSOOLIKNNTENLHSPKNETHTSYVYKIKSEINNMNNSIGVPTKKNNDYMT 1481  
QY 481 -----TTIQOTVTMTTINEYTGFEFTASVDNTIAFSTSSGQGGDLPPKTYKI 530  
Db 1482 NYLNMHEHIKMMNMEKIEIKKGNNDNEIKGRIQVEHDDRVHNTYQENNIINNQNPT--- 1538  
QY 531 GQYVVEDVDKGIQNTNDNEKPLSNVLVLT-LYVPDGTSKSVRDE 574  
Db 1539 -----NHDGDMNIN-----SNKFMPTTLKKEKYQNNINTNE 1571

RESULT 13  
US-10-537-642-21  
; Sequence 21, Application US/10537642  
; Publication No. US20060165719A1  
; GENERAL INFORMATION:  
; APPLICANT: Epimmune, Inc.  
; APPLICANT: The United States of America as Represented by the  
; APPLICANT: Secretary of the Navy  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Doolan, Denise L.  
; APPLICANT: Carucci, Daniel J.  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ANTIGENS AND METHODS OF USE  
; FILE REFERENCE: EPI-103X  
; CURRENT APPLICATION NUMBER: US/10/537,642  
; CURRENT FILING DATE: 2005-06-06  
; PRIOR APPLICATION NUMBER: US 60/431,494  
; PRIOR FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1161  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 21  
; LENGTH: 2024  
; TYPE: PRT  
; ORGANISM: Plasmodium falciparum  
US-10-537-642-21

Query Match 7.0%; Score 212; DB 6; Length 2024;  
Best Local Similarity 20.7%; Pred. No. 0.023;  
Matches 132; Conservative 121; Mismatches 249; Indels 136; Gaps 33;  
QY 15 SINTDDNNQIIKKEETN-----NYDIEKRSDETRSTNVDENEATFLOKTPODNTL 68  
Db 31 SLNYSKNYGLNDQELRAMLFGNLDPSKRNKNKV--NRDVIKNESSLLRLNINEETL 88  
QY 69 TEEVEKSESSVESSNS-----IDTAQPSHTTINREESVQTSNDVSDSHVDFANSK--I 122  
Db 89 SEKNDKVNDIKMMNTEKINSKGNNNIHNENQNAVNLKTONILNTSEQDDI 148

```
QY 123 KESNTESGK-----EENTIEQPNKVKEDSTTSQPSGYNTNDEKISNOQDELLNLPINE-Y 175
Db 149 NEKNNDNGDMVHKNTYNNILSDPYDINSNAYINKSDITNLN--YSSNDVINNDKVKNSY 206
QY 176 ENKARPLSTSAQPSIKRVTVNQL-AAEQGSNVNHLIKVTDQ-----SITEGYDDSEGI 229
Db 207 BEK-----NIVNNTLNKLTESDDHSNQNIDINKTEKNTKFTNSSSTSEKKQTDI 256
QY 230 KAHDAENLIYVTF---EVDKVKSGDWT--VDIDKNTVPDLTDSFTPIKONSG--- 282
Db 257 KQGNKNDLNNHEIFNNNDINNYYKKNVNIISVDKNNTDRDNNLY-----ETNNGDLK 311
QY 283 ---ELIATGYDNKKQIYTFDVTVDVKYENIKAKHLKLTYSIDKSKVP-----NN--- 330
Db 312 YNNDLIGENKRNKNKJANNKFN--MNKVNDMKNFNKYTEIYNKESEPEKQNNNNILGI 369
QY 331 ---TKLDVEYK--TALSSVNKTI-----TVYORPENRNTANLQSMFTNIDTNNH-T 376
Db 370 PTLIKKEVHIKHNHTFSSNGKILENKDIDKMSDTSKKNDRFRSNDIKFNKNDTKNAT 429
QY 377 VEQTIYINPLRYSAKETNNISNGDEGSTIIDSTIIKVKYKVGDNQNLPSNRIFYDSE 436
Db 430 LSED---NKNRY-----NITTKNNEK-----KEY-----NMKKSNEVEAFNTE 466
QY 437 YEDVTND-----DYAOLGNNDVNIINFGNIDSPYIIKVIKSKYDPNKDDYTTIOQVTM 489
Db 467 KTNVNDALKBERNNKYVNNQTDVNIIN--NLQE-----RDINLYKNKESD-KKLEQSPRE 519
QY 490 OTTINEYTGEPRTASYDNTIAPTSSGOGQGLPPEKTYKIGDYVWEDVDKQIGNQ--- 545
Db 520 EDIKNAYLPE--NKNFQKTL---TNNEKNEDNKIPIH-----DPSNELDKKGNKYEI 569
QY 546 ---TNDNEKPLSNVLVTIYPDGTSKSVRTDBDGKYQF 580
Db 570 GKIKKNEENKQNTVE---ENINPEKIRKDEQNIQY 604

RESULT 14
US-11-330-403-3535
; Sequence 3535, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 3535
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Candida albicans SC5314
US-11-330-403-3535
```

```
Query Match 7.0%; Score 211.5; DB 7; Length 1086;
Best Local Similarity 21.0%; Pred. No. 0.011;
Matches 125; Conservative 80; Mismatches 253; Indels 137; Gaps 20;

QY 4 BEKNDVINNNOSINTDDNNQIIKKEETNNYDGIKRESDRTSTTNVDENEATFLQKTPQ 63
Db 344 DESSSLSSSTSEQSSSATSVSASETSDTSTQESSSSSVSSTQEPSS-----STPE 397
QY 64 DNTHLTEBEVKSSSVESNSGIDTAQO-----PSHTTINREESVQTSNDVEDSHV 114
Db 398 PSSSSTSTQBSSTSTQSSSTDSSTSEASSESSTAPSSST--EASSSTESSTEPS 454
QY 115 SDFANSKIKESN-----TESGKEENTIEQPNKVKEDSTTSQPSGYNTNIDEKI--- 161
Db 455 STEGPSSQSSSSSESSTQEPSSSTKSSSSTEGPSSSTESSTEGPSSSTDSSTDTISA 514
QY 162 SNQDELLNLPINEYENKARPLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQISITEG 221
Db 515 SSTDSQSSSGTQSSSTEDPIDSTEDTS-----SATDSS----- 549
```

```
QY 222 YDSEGVIKAHDAENLIYDVTFFVEDDKVKSGDWTMTVDIDKNTVPS-----DLTDSFTIPK 276
Db 550 -----TATDSSATNTDNTSESTDSSTATDTSST--DSNTASSTETNTDVTDSST--- 596
QY 277 IKDNGSEIIATGYDNKKQIYTFDVTVDVKYENIKAKHLKLTYSIDKSKVPNNNTKLDVE 336
Db 597 -DSNTGA-----TESSTATDNTDATD-----SSTVSETGATDSSSTATDTN 636
QY 337 YKTALSSVNKTIITVEYORPENRNTA--NLQSMFTNIDTNNHTEQTIYINPLRYSAKET 393
Db 637 TGATESSTDSNTGA-----TESSTATDNTSATNTDNTGNTATNTDNTDNTATDTSSTET 691
QY 394 NVNISNGDEGST-IIDSTIIKVKYKVGDNQNLPSNRIFYSEYEDVTNDDYAOLGNNN 452
Db 692 NTATNTDGTETNTGATETNTDTSASNTDDNTG---SNTATNTGGTD--TNTDNTGGTDT 746
QY 453 DVNINFGNIDSPYIIKVIKSKYDPNKDDYTTIOQVTVMQTTINEYTGEPRTASYDNTIAPS 512
Db 747 NTGNTGGTDT-----KTGTNTATGNN-TGATETNTATNTNGNG 784
QY 513 TSSGQGGQGLPPEKTYKIGDYVWEDVDKQIGNTNDNEKPLSNVLVTIYPDGT 567
Db 785 TINTGTATDTATNTATGTTN-----TNTGATDNTNTGATVNTATNTDNTDVS 832

RESULT 15
US-10-471-571A-4824
; Sequence 4824, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqMin99, version 1.03
; SEQ ID NO 4824
; LENGTH: 774
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(774)
; OTHER INFORMATION: serine protease Htra
US-10-471-571A-4824
```

```
Query Match 6.8%; Score 205; DB 6; Length 774;
Best Local Similarity 18.7%; Pred. No. 0.014;
Matches 119; Conservative 121; Mismatches 209; Indels 186; Gaps 26;

QY 3 DEEKNDVINNNOSINTDDNNQIIKKEETNNYDGIKRE-----SEDRTESTTNVDENEA 55
Db 29 NEDREENLNQHQDKQNDINTTSKKADQIHKSDIKKHERFNKNSLSHLEQRNDRVNEKNA 88
QY 56 TFLQKTPQDNT-----HLTEEBEVKSSSVESNSSSIDTA---QQPSHTTINREESVQT 105
Db 89 E-EKSNODSKSAYNRDHYLTDDVYSKQNSLSDVDQDTEKSKYEQNSEATL---STKS 143
QY 106 SDNVEDSHVSDFANSKIKESNTE-----SGKEENTIEQPNKVKED 145
Db 144 TDKVESTEMRKLSDDKKNKVGHEEQHVLSPKSEHDKETRIDSESSRTDSDSMQTEKIKD 203
QY 146 STTSQPSG-----YTNIDKISNODELLNLPINEYENKARPLSTTSAQPSIKRVTV 196
Db 204 SSDGNKSNLKSSEVISDKSNVTPKLSESDDEV-----NNQKPLTLPEEQ----- 247
QY 197 NQLAAEQGSNVNHLIKVTDQISITEGYDDSEGIYKAHDAENLIYDVTFFVEDDK----- 248
Db 248 -KLAKRQSQSN-----EQTKTYTGDSEQDNKSNHNDLSHHIPSISSDDKDNVRENH 298
```



***This Page Blank (uspto)***

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2006, 08:59:56 ; Search time 42 Seconds  
(without alignments)  
1333.289 Million cell updates/sec

Title: US-10-806-288-13  
Perfect score: 3013  
Sequence: 1 SSDEKNDVINNNQSIINTDD.....PDGTSKSVRTDDBGKYQPDG 582  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3013	100.0	1092	2 T30214	fibrinogen-binding
2	1144.5	38.0	1166	2 T28680	fibrinogen-binding
3	1137.5	37.8	1141	2 E89824	hypothetical prote
4	576	19.1	1315	2 T28679	fibrinogen-binding
5	559	18.6	1385	2 D89824	hypothetical prote
6	489	16.2	953	2 C89824	hypothetical prote
7	452	15.0	933	2 S41539	fibrinogen-binding
8	452	15.0	989	2 D89852	fibrinogen-binding
9	397.5	13.2	877	2 F90070	Clumping factor B
10	376	12.5	940	2 S19702	fibronectin-bindin
11	344.5	11.4	961	2 G90053	hypothetical prote
12	326	10.8	1038	2 H90053	hypothetical prote
13	300.5	10.0	1018	2 A32192	fibronectin-bindin
14	239	7.9	1039	2 T30256	protein F2 - Strep
15	225	7.5	1463	2 T30290	AAS surface protei
16	216.5	7.2	1959	2 AG1085	hypothetical prote
17	216.5	7.2	3394	2 T18501	hypothetical prote
18	212.5	7.1	1125	2 E90598	membrane nucleas
19	211.5	7.0	2206	2 G71611	hypothetical prote
20	208.5	6.9	1072	2 A86827	hypothetical prote
21	208	6.9	1127	2 T28317	ORF MSV156 hypothe
22	208	6.9	3724	2 T18427	hypothetical prote
23	207.5	6.9	1711	2 T18429	hypothetical prote
24	207.5	6.9	2401	2 T28676	hypothetical prote
25	207	6.9	769	2 F89870	rhoctry protein -
26	207	6.9	1939	2 T18372	serine proteinase
27	207	6.9	4550	2 T18440	repeat organellar
28	206.5	6.9	821	2 S67087	hypothetical prote
29	206	6.8	1302	1 JC6009	surface-located me

ALIGNMENTS

RESULT 1

T30214  
fibrinogen-binding protein - Staphylococcus epidermidis  
C:Species: Staphylococcus epidermidis  
C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T30214  
R:Nilsson, M.; Frykberg, L.; Flock, J.I.; Pei, L.; Lindberg, M.; Guss, B.  
Infect. Immun. 66, 2666-2673, 1998  
A:Title: A Fibrinogen-binding protein of Staphylococcus epidermidis.  
A:Reference number: Z20781; MUID:98261511; PMID:9596732  
A:Accession: T30214  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1092 <NIL>  
A:Cross-references: UNIPROT:O70022; UNIPARC:UPI00000AFCA6; EMBL:Y17116; NID:61296734; P

Query Match	100.0%;	Score 3013;	DB 2;	Length 1092;
Best Local Similarity	100.0%;	Pred. No. 5.4e-122;		
Matches	582;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

QY	1	SSDEKNDVINNNQSIINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDNEATFLQK	60
DB	75	SSDEKNDVINNNQSIINTDDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDNEATFLQK	134
QY	61	TPQDNTHLTEREVKSSSVSSNSSIDTAQPSHTTINREESVQTSNVEDSHVSDPANS	120
DB	135	TPQDNTHLTEREVKSSSVSSNSSIDTAQPSHTTINREESVQTSNVEDSHVSDPANS	194
QY	121	KIKESNTSGKBEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNQDELNLPLINVEYENKAR	180
DB	195	KIKESNTSGKBEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNQDELNLPLINVEYENKAR	254
QY	181	PLSTTSQAQSIKRVTVNQLAAEQGSNNVHLIKVTQDSITEGYDDSEGVKAHAENLIYD	240
DB	255	PLSTTSQAQSIKRVTVNQLAAEQGSNNVHLIKVTQDSITEGYDDSEGVKAHAENLIYD	314
QY	241	VTFEVDKVKSGDVTVDIDKNTVPSDLTDSFTTPKIKDNGSEIITATGYDNKNQIYTT	300
DB	315	VTFEVDKVKSGDVTVDIDKNTVPSDLTDSFTTPKIKDNGSEIITATGYDNKNQIYTT	374
QY	301	FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKTALSSVNKTIITVEYQRPENRT	360
DB	375	FTDYVDKYENIKAHKLKLTYSIDKSKVPNNNTKLDVEYKTALSSVNKTIITVEYQRPENRT	434
QY	361	ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSIIDDSIIKVKYKG	420
DB	435	ANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVNSGNGDEGSIIDDSIIKVKYKG	494
QY	421	DNQNLPSNRIDYSEYEDVTNDYDQAQGNNDVNINFGNIDSPYIIKVIISKYDPNKDYY	480
DB	495	DNQNLPSNRIDYSEYEDVTNDYDQAQGNNDVNINFGNIDSPYIIKVIISKYDPNKDYY	554

impl protein - Myc  
hypothetical prote  
FmTB protein limpo  
asparagine/asparta  
asparagine-rich pr  
DNA helicase II BR  
rhoctry protein -  
1-phosphatidylinos  
hypothetical prote  
hypothetical prote  
similar to late em  
hypothetical prote  
probable membrane  
internalin protein  
hypothetical prote





## RESULT 4

T28679  
T28679  
fibrinogen-binding protein homolog - *Staphylococcus aureus*  
C:Species: *Staphylococcus aureus*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T28679  
R:Johansson, E.; McCrea, K.; Ni Eidhin, D.; O'Connell, D.; Cox, J.; Hook, M.; Foster, T.  
Microbiology 144, 3387-3395, 1998  
A:Title: Three new members of the serine-aspartate repeat protein multigene family of *S.*  
A:Reference number: Z20510; MUID:99098700; PMID:9884231  
A:Accession: T28679  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1315 <JOS>  
A:Cross-references: UNIPROT:O86488; UNIPARC:UPI00000052285; EMBL:AJ005646; NID:e1318791;  
C:Genetics:  
A:Gene: sdrD

Query Match 19.1%; Score 576; DB 2; Length 1315;  
Best Local Similarity 30.1%; Pred. No. 2.1e-17;  
Matches 186; Conservative 112; Mismatches 238; Indels 92; Gaps 29;

Qy	1	SSDEBKNDV---INNQSINTDDNNQIIKKGETNNYDGIKRSBDRTESTTNVDE-NEAT	56
Db	55	SYNKLNEATTSASQNSDDKVDNQQLNQEDNTKDNQKEMVSSQGNTESTNGKNKLIKE	114
Qy	57	FLQKTPQDNTHLTEBEVKESSSVSSNSSIDTAQOPSHHTTINREESVQTSNDVDSHVSD	116
Db	115	SVQSTGKNKVEVSTAKSDEQASPKSTWEDLNKQ-----TJSNQEAHQ-PDLOENKSVVN	168
Qy	117	FANSKIKESNTESGKEENTIBQPNKVKEDSTTSOPSGYTN-DEKISNQDELL--NLPLN	173
Db	169	-----VQPTNEENKKVD-----AKTESIT--LNVKSDAIKSNDETLVDNNNS	209
Qy	174	EYENKARPLSTTSAP-----SIKRVYNQLAAEQGSNVNHLIKVTPQSITEGYDDESGVI	229
Db	210	NNENNADLIILPKSTAPKRLNTRMRIAAVQPSSEAKVNVNDLITSNTTLTVVDADKNNKIV	269
Qy	230	KAHDAENLIYDVTFEVDKVKSGDTMTVDIDKNTV-----PSDLTDSFTPIPKID-NSG	282
Db	270	PAQDYLSLSQIT--VDDKVKSGDYFIKY-SDTVQVYGLNPEDIKN---IGDIKDPNG	323
Qy	283	ELIATGTVDNKQKQITFTFYDVKYENIKAHKLKTSYIDKSKVPNNNTKLDVVEYKTALS	342
Db	324	ETIATAKHDTANNLIYTFYDVRFSVQMGINSIYMDADTIP--VSKNDVEFNVNITG	381
Qy	343	SVNKTITVEYQRPN-ENRNTANLOSMTFTNIDTKHT-----VQOTYINPLRSYAKE	392
Db	382	NTYTKTIANIQPYDVVNEKNSIGSAT--ETVSHGVGNKENPGYYQTYIVNPSNSLTN	439
Qy	393	TNVNI-----SGNGDEGSTIIDDSITIKVYKVGDNQNLPSNRRIYDS--EYEDVTNDYYA	446
Db	440	AKLKVQAVHSSYPNNIGQINKRDVTDIKIYQVPKGYL---NKGYDVNTKELTDVTN-QYL	495
Qy	447	Q-----LGNNDVNIINFGNIDSYIIKVIKSYDPNKDDYTIQOVTVMQTTINEYTGEPRTA	503
Db	496	QKITVGDNNASAVIDFGNADSAVYVNVMTKQYTNSESPTLVQMATLSSTGN-----KSV	549
Qy	504	SYDNTIAFSTSGOQGLDPPEKTYKIGDYVWEDVDKDGQONTNDNEKPLSNVLVLTLYP	563
Db	550	STGNALGFTNNQSGAG---QEVYKLGYNVWEDTNGKVQEL--GEKGVGNVTTV-PD	602
Qy	564	DGTSKSVR---TDEBGKY	578
Db	603	NNNTNKVGAEAVTKEDGSY	620

**DEPT. 5**

hypothetical protein sdrD [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: D89824

R;Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: D89824  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1385 <KUR>  
A:Cross-references: UNIPROT:Q99W47; UNIPARC:UPI000000CAALF; PID:gl37000454;  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: *sdhD*

Query Match 18.6%; Score 559; DB 2; Length 1385;  
Best Local Similarity 28.8%; Pred. No. 1.2e-16;  
Matches 177; Conservative 117; Mismatches 235; Indels 86; Gaps 27;

Qy	1	SSDEEKNDV----	INNQSITDDNNQIIKKEETNNYDGI	EKRSEBDRSTSTTVNDBN	-EAT	56	
		: : : : :	: : : : :	: : : : :	: : : : :		
Db	55	STNKELNEATT	SADNQSOKVDMMQOLNQEN	TKNDNQEMVSSQCNETSTNGKNSIEKE		114	
		: : : : :	: : : : :	: : : : :	: : : : :		
Qy	57	FLOKTPDNDHL	TEEBEVKESSVESSNS	IDTAQOPSHTTINRRESVQTS	DNVEDSHSYSD	116	
		: : : : :	: : : : :	: : : : :	: : : : :		
Db	115	SVSGTTGNKEV	STAKSDEQSPKSTNEDLTKQ	-----TISNQBGLO	-PDLEKNKSVVN	168	
		: : : : :	: : : : :	: : : : :	: : : : :		
Qy	117	FANSKIKESNT	ESGKEENTIEQPN	-VKVEDSTTSQPGYTNIDEKIS	NOQDELLNLPINEY	175	
		: : : : :	: : : : :	: : : : :	: : : : :		
Db	169	-----VQPT	NEENKVKDAKTEST	TLNVKSDAIKS	-----NAETLVDNNSNN	-----211	
		: : : : :	: : : : :	: : : : :	: : : : :		
Qy	176	ENKARPLUST	TSQAQPSIKRVTYNQALAEQGS	-----NVNHLIKVTDQSIT	EGYDDSGVIVKA	231	
		: : : : :	: : : : :	: : : : :	: : : : :		
Db	212	ENNAIIILPK	STAPKSLNTRMRMAAIQPN	STSDSKRVNDLITSNT	TLTVVDADNSKTI	271	
		: : : : :	: : : : :	: : : : :	: : : : :		
Qy	232	HDAENLIYDV	TFEVDKVKSGDWTVIDDKNTV	-----PSGLTDSFTPIKID	-NSGSI	284	
		: : : : :	: : : : :	: : : : :	: : : : :		
Db	272	QDYLSLKSOIT	-----VDDKVKSGDYFTIKY	-SDTVQVYGLNPEDIKN	-----IGDIKDPNGST	325	
		: : : : :	: : : : :	: : : : :	: : : : :		
Qy	285	IATGTYDNKKQ	ITYTTFDVKYKENTKAHLKUTSID	KSKVPNNNTKLDVEYKTALSSV		344	
		: : : : :	: : : : :	: : : : :	: : : : :		
Db	326	IATAKHDTAN	LITYTFTDYVDRFNSVKMGINYSI	YMDADTIPVD	--KKDVPFSVTYIGNQ	383	
		: : : : :	: : : : :	: : : : :	: : : : :		
Qy	345	NKTIITVEYQRP	-----NENRTANLQSMFTNID	TKNHT-----VEQTIYINPLRY	LSAKETN	394	
		: : : : :	: : : : :	: : : : :	: : : : :		
Db	384	ITTTADITPAY	KEADNNSIGSAFT	--ETVSHVGNVEDPGYVQVYVNP	MDKDLKGAK	441	
		: : : : :	: : : : :	: : : : :	: : : : :		
Qy	395	VNISNGDEGST	-----IIDDSITIIKVKYKGNQNL	PDPSNRRIYD	-----SEYEDVTND	-----DYA	446
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	
Db	442	LKKEAVHPKYPT	NIGQINQVNTNIIKIRVP	PEGYTL--NKGYDVNTNDL	VDTDFEKNKM	498	
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	
Qy	447	QLGNNDVNI	NFGNIDSPYIIKVLISKYDP	PNKDYTTIIQOVTMQTTINEY	TEGFTASVD	506	
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	
Db	499	TYGNSQSNV	LDFGDITTSAYVVMVNTKFPQY	TNSESPTLVQMATLS	TSGN-----KSVSTG	552	
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	
Qy	507	NTTAFSTSGO	QGDLPPEKTYIKGVYVEDVDKDG	QNTNDNKEPLSNVLTY	LPDGT	566	
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	
Db	553	NALGFTNNQSG	AG-----QEVYKIGNYV	WEDTNKGVQEL--GEKGVGNTVTV	-FDNNT	605	
		: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	
Qy	567	SKSVR----	TDDEGKY	578			
		: : : : :	: : : : :	: : : : :	: : : : :		
Db	606	NKTVGEAVTK	EDGSGY	620			
		: : : : :	: : : : :	: : : : :	: : : : :		

9. T. J. S. P. 6

RES001 6  
C89824  
hypotheoretical protein adrc [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: C89824  
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Havanishi, H.; Hirataetsu, K.



```
Db 51 SNESKNDSSVSAAPKTDITV-----SDTKTSNTN---NGETSVAQ 91
Qy 61 TPONTHLTVEEVKSSVSSSSSIDTAQPSHTTINREESVQTSNDVEDSHVDFANS 120
Db 92 NP-----AQOETQSSSNATTEETPVTEGATTTTINQANTPATQOS- SNTNAEELVN- 143
Qy 121 KIKESNTESGKEENTIEQPNKVEDSTTQPSGYTWIDKISNQDELLN- LPINEYENKA 179
Db 144 ---QTSNETTSDNTNTV-----SVNSPQNSTNAENVSTTQDTSTEAATPSN---NES 189
Qy 180 RPLSTTSA-----QPSIKAVTVNQAAA-----EGSNVNHLIKVTQDSITEGYDD 224
Db 190 AFQNTDASHKDVQSVQAVNESTPMRAFSLAAVAADAPAAAGTDITN---QUTDVKVT---ID 244
Qy 225 SEGVIAKAHAENLIYDVTFEVDKVKSGDGTMTVDIDKNTVPDLTDSFTPIPKIKNSGGEI 284
Db 245 SGTTVVPHQAGYVKLVNGFSVPSNAVKGDFKTIPTVKELNLNGVTSTAKVPPIMAGD-QV 303
Qy 285 IATGYDKNKQIITYFTDYVDKYENIKAHKLKUTSIDSKVPPNNTKL-DVEYKTAAL-- 341
Db 304 LANGVIDS-DGNVIYFTDYVDKNENVTANITMPAYID----PENVTKTGNVTLTIGT 358
Qy 342 SSVNTKITIYVEORPNERNRANLQSMFTNIDTKNHTVQETIYINPLYSAKETNV----- 395
Db 359 NTASKVLIDYKYGOFHLSIKGTIDQIDKNTNTYRQTIYVNP-----SGDNVVLPAIT 413
Qy 396 -NISGNGDRGSTIIDSTIIKVKYKVDNQNLPSNRIDYSEYEDVTNDYQAQLGNNDV 454
Db 414 GNLIPTKSNALIDAKNTDIIKVRV-DNANDLSSEYVNPSEFEDVTNQVRISFPNANQY 472
Qy 455 NINF-----GNISPIIKVISKYDPNKODYTTIQVTVMTQTTINEYTGFEF--RTASYDNT 508
Db 473 KVEFPTDDQIITPYIVVNGHIDPASTG-----DLALRSTFYGYDSNFWRKSNWDNE 526
Qy 509 IAFSTSSGGOG-DLP-PEKYTKIGDY--VVEDVDKD-GIQNTWDN 549
Db 527 VAFNNGSGGDGIDKPVVPEQDEPGEIBIPEDSDSPGSDGSDS 573

RESULT 9
F90070
Clumping factor B [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F90070
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguda, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89750; PMID:21311952; PMID:11418146
A:Accession: F90070
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-877 <KUR>
A:Cross-references: UNIPROT:Q99R07; UNIPARC:UPI000000CADCA; GB:BA0000018; PID:g13702588; H
A:Experimental source: strain N315
C:Genetics:
A:Gene: clfB

Query Match 13.2%; Score 397.5; DB 2; Length 877;
Best Local Similarity 24.5%; Pred. No. 5.6e-10;
Matches 143; Conservative 81; Mismatches 207; Indels 153; Gaps 23;

Qy 2 SDEKNDVI---NNQSIINTDNNQIIKKEETNNYDGIKESREDTESTTNVDENEATFL 58
Db 44 ASEQNDTFTQSKKNASADSEKKNMI---ETPQLNTTANDTSDISANTNSANVDSSTTKP 99
Qy 59 QKTPODTHLTBEVKSSVSSSSSIDTAQPSHTTINREESVQTSNDVEDSHVSDFA 118
Db 100 MSTQTSNTTTE-----PASTNETPQTAIKNO---ATAAKMQDQTVPOBA 142
Qy 119 NSKIKESNTESGKEENTIEQPNKVEDSTTSPSGYTTNIDKISNQDELLNLPINEYENK 178
```

```
Db 143 NSQVDNKT---NDANSIATNSLKNSTQ-----LDLP-----Q 173
Qy 179 ARPLSTTSAQ---PSIKVTVNQAAEQ-----GSNVNHLIKVTQDSITEGYDSS 225
Db 174 SSPQTISNAQGTSKPSVTRAVRSCLAVAPVVAADAKGTNVN-----DKVTASNFKLE 227
Qy 226 EGVIAKAHAENLIYDVTFEVDKVKSGDGTMTV-----DID-----KNTVPSDLTDS 271
Db 228 KTFPDPNQSGNTFMAANFTVTDKVASGDYFTAKLPDLSTGNGDGDVDSNSNTWP----- 281
Qy 272 FTIPKIKNSGGEIATGYDKNKQIITYFTDYVDKYENIKAHKLKUTSIDSKVPPNNNT 331
Db 282 --IADIKSTNGDVAKATYDILTKTFTVFTDVNNKENINGQFSLPLFTDRAKAPKSGT 339
Qy 332 KLDVEYKTAALSSVNTKITIYVEYQRP---NENRTANLQSMFTNIDTKN--HTVEQTIYINP 385
Db 340 -YDANINIADEPNFNKTIYNSPSPIAGIDKPNGANISSQIIIGVDTASGQNTYKQTVFVNP 398
Qy 386 LYSAKETNVNISGNGDEGSTIIDDS-----TIKVKYKVDNQNLPS----- 428
Db 399 KQVRLGNTWVYIKGYQDK---IBESSGKVSATDTKLRIFEVNDTSKLSDSYYADPNDSN 454
Qy 429 -----NRIYDYSEYEDVTNDYQAQLGNNDVNINFGNIDSPYIIKVISKYDPNKOD 479
Db 455 LKEVTDQFKRIY---YE-----HPNVASIKFGDITKTVVLVEGHYDNTGKN 499
Qy 480 YTT--IQQVTVMTQTTINEYTGFEFTASVDNTIAFTSSSGGGQGD 521
Db 500 LKTQVIOENVDVPT-----NRDYSIFGMNENNVRYGGGSADGD 538

RESULT 10
S19702
fibronectin-binding protein B - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S19702
R:Joensson, K.; Signaee, C.; Mueller, H. P.; Lindberg, M.
Eur. J. Biochem. 202, 1041-1048, 1991
A:Title: Two different genes encode fibronectin binding proteins in Staphylococcus aureus
A:Reference number: S19702; PMID:92111475; PMID:1837266
A:Accession: S19702
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-940 <JOB>
A:Cross-references: UNIPROT:Q53682; UNIPARC:UPI000000B7719; EMBL:X62992; NID:g49040; PID:
C:Keywords: fibronectin binding

Query Match 12.5%; Score 376; DB 2; Length 940;
Best Local Similarity 23.4%; Pred. No. 5.1e-09;
Matches 138; Conservative 110; Mismatches 217; Indels 124; Gaps 22;

Qy 35 GIEKESDRTESTTNVDENEATFLQKTPQDNTHLTEEVKSSVSSSSSIDTAQ----- 90
Db 30 GQEKAAASAEQNNTTVEES-----GSSATESKASETQTTNNVNTIDETQSYSA 78
Qy 91 ----QPSHTT-INREESVQT--SDNVEDSHVSDFANSKIKESNTESGKEENTIEQPNKYK 143
Db 79 TSTEQPSQSTQVTTTEEAPKTVQAPKVSERV-DLPSEKVDKETTGTQVD--IAQPSNVS 135
Qy 144 EDSTTSQPSGVNTIDEKISNQDELLNLPINEYENKARPLSTTSAQPSIKRVTVNQAAEQ 203
Db 136 E-----IPKMRKSTDTVTAABK 153
Qy 204 -----GSNVNHLIKVTQDSITEGYDDSEGVIAKAHAENLIYDVTFEVDKVKSGPT 254
Db 154 EVVETKATGDTVTKVVEEGSEIVGHKQDNTVNVNPNABRVTLKYKWKFGEGIKAGDY 213
Qy 255 MTVIDKKTVPDLTDSFTIPKIKNSGEIATGYDKNKQIITYFTDYVDKYENIKAH 314
Db 214 FDFTLSDNVETHGISLTKRVPKPEIKSTQGVMAATGEIIGERK-VRYTFPEYVQEKDLTAE 272
```





Qy	49	-NVDENEATFLQKTPQDNTH-----LTE--EVBKSSSSSVESN-----SSIDTTAQQPSH 94
Db	240	NAVSSNEDVASSDVQKQDGTGTHSDNASSDLDTDQNESVAQNKAETSNEDVASSDVQKQDTH 299
Qy	95	TTIN-----REESVQTSNDVEDSHVSFANSKIKESNTESG-----KENTTLEQPN- 140
Db	300	SDANASDVADQNESQETQNDNAESSNEDDVASSDVNQDDTHSDANASDDVKQKQNESQND 359
Qy	141	-----KVKEDSTTS--OPSGYTNIDEKISNQDELLNLPINEYENKARPLSTP 185
Db	360	KAETSNEDDVASSDVQKQDTHSDANASDIADQNESVAQNKA-----ETSNEDVASS 411
Qy	186	SAQPSIKRVTYNOLAAEQGSNNVHLIKVT--DQSITEGYDSS-----EGVIK-AHDAENLI 238
Db	412	DKQDTHSDANASDIADQNESATQDKATSKEDDDVVSNDKQDNAKVSNIIKEASTAENKV 471
Qy	239	YDVTF--EVDKVKSGDTM--TVDIKNTVPSDLTDSFTPIPKIKDNGSBEIATGYVDNKN 294
Db	472	QPAIFSAKVTPKLRVAITTSANTAVATRAVNTKEATTAAALPKY-----S 515
Qy	295	KQITVTFDYVDKYENIKA---HLKLTSYDKSKVPNNNTKLDVRYKLTALSSVNTKITVTE 351
Db	516	PKVASSINNYIRK--NNFKAPNYEQDIANYLPQYNYRYGKPEGIVMHDTA--NDNSTITGE 572
Qy	352	YQRPNEHTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISGNDGSGSTIIDS 411
Db	573	INYMKNVT---SAFVHAYVDGDRIIEFANTDYLAWGA-----GPOANDRP 615
Qy	412	TIIKYKVGDNQNLPSNRIYDSEYEDVTNDDYAQLGNNDVNINFGNIDSPYIKVIS 471
Db	616	IHVELVHTHDYDSFARS--INNYADYA-ATNLQYYGLVPD---SABYDGVGTWVTHQAVS 669
Qy	472	KY-----DPN-----KDDYTIQQTVMQTTINEYTGFRFASDNTIAFSI- 513
Db	670	NYLGSDHSDPHGYLAAHNYSYDELYDLIYEKYLKIGT-----QAAAWGTSSGSGTG 721
Qy	514	----SSGOGQ--GDLPPER--TVKIGDYVWEDVDKQGIQNTNDNEKPLSNVLVTLTYPDGT 566
Db	722	GTGSGTSGSNGTTPPSKSGTVK-----TENNGVGRINSK-----NDGLTYTVYDQKG 770
Qy	567	SKSVRTDED-----GKYQF 580
Db	771	KKTRVNTQTLKVTKSATLGKEQY 793

Search completed: August 12, 2006, 09:05:38  
Job time : 44 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2006, 08:57:16 ; Search time 304 Seconds  
(without alignments)  
1770.918 Million cell updates/sec

Title: US-10-806-288-13  
Perfect score: 3013  
Sequence: 1 SSDEEKNDVINNNQSIINTDD.....PDGTSKSVRTDEGKYQPDG 582

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trnbl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3013	100.0	1056	2	Q8CQ72 STAES
2	3013	100.0	1092	2	O70022 STAEF
3	2810.5	93.3	892	2	O5HR16 STAEQ
4	2810.5	93.3	931	2	O9KI13 STAEF
5	1209.5	40.1	1137	2	O6GJA6 STAEF
6	1165.5	39.3	1113	2	O2YSAL STAEF
7	1160.5	38.5	1171	2	O9KWX6 STAEF
8	1144.5	38.0	1166	2	O86489 STAEF
9	1143.5	38.0	1141	2	O6GHS4 STAEF
10	1143.5	38.0	1141	2	O8NXX5 STAEF
11	1142.5	37.9	1166	2	O5HIB2 STAEF
12	1137.5	37.8	1141	2	O932F7 STAEF
13	1137.5	37.8	1141	2	O99W46 STAEF
14	1018	33.8	444	2	O2UW70 STAEF
15	1018	33.8	444	2	O2UW91 STAEF
16	973	32.3	444	2	O2UW60 STAEF
17	969	32.2	444	2	O2UW93 STAEF
18	968	32.1	444	2	O2UW63 STAEF
19	966	32.1	444	2	O2UW63 STAEF
20	966	32.1	444	2	O2UW63 STAEF
21	965	32.0	444	2	O2UW74 STAEF
22	965	32.0	444	2	O2UW96 STAEF
23	962	31.9	444	2	O2UW77 STAEF
24	652	21.6	1563	2	O4LAH6 STAEF
25	576	19.1	1315	2	O86488 STAEF
26	576	19.1	1381	2	O5HIB3 STAEF
27	567	18.8	1347	2	O8NXX6 STAEF
28	567	18.8	1365	2	O6GHS5 STAEF
29	559	18.6	1385	2	O7A780 STAEF
30	559	18.6	1385	2	O99W47 STAEF
31	499	16.6	1733	2	O9KI14 STAEF

32	497	16.5	1633	2	Q8CMP4 STAES	Q8CMP4 staphylococ
33	489	16.2	953	2	O7A781 STAAH	O7A781 staphylococ
34	489	16.2	953	2	O99W48 STAAH	O99W48 staphylococ
35	485.5	16.1	1893	2	Q8KWM1 STASA	Q8KWM1 staphylococ
36	478.5	15.9	906	2	O6GJA7 STAAH	O6GJA7 staphylococ
37	470.5	15.6	928	1	CLFA STAAH	O6GJA7 staphylococ
38	470.5	15.6	946	1	CLFA STAAH	O6GJA7 staphylococ
39	465	15.4	955	2	O8NXX7 STAAH	O8NXX7 staphylococ
40	465	15.4	957	2	O6GHS6 STAAH	O6GHS6 staphylococ
41	460.5	15.3	881	2	O93MH7 STAAH	O93MH7 staphylococ
42	458.5	15.2	566	2	O8KR22 STAAH	O8KR22 staphylococ
43	456	15.1	1029	1	CLFA STAAH	O6GJA7 staphylococ
44	455	15.1	933	1	CLFA STAAH	O6GJA7 staphylococ
45	455	15.1	947	2	O86487 STAAH	O86487 staphylococ

ALIGNMENTS

RESULT 1  
Q8CQ72 STAES PRELIMINARY; PRT; 1056 AA.  
AC Q8CQ72;  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 22.  
DE Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein.  
GN OrderedLocusNames=SE0331; ORFNames=SE\_0331;  
OS Staphylococcus epidermidis (strain ATCC 12228).  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
RX NCBI\_TaxID=176280;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=12950922; DOI=10.1046/j.1365-2958.2003.03671.x;  
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,  
RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,  
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;  
RT "Genome-based analysis of virulence genes in a non-biofilm-forming  
RT Staphylococcus epidermidis strain (ATCC 12228).";  
RL Mol. Microbiol. 49:1577-1593(2003).  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License

-----  
EMBL; AE015929; RAO03928.1; -; Genomic\_DNA.  
DR HSP; G53653; IN67.  
DR SMR; Q8CQ72; 278-598.  
DR BioCyc; SEPI176280:SE0331-MONOMER; -.  
DR GO; GO:0009986; C:cell surface; IEA.  
DR GO; GO:0005618; C:cell wall; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR InterPro; IPR008454; Cna B.  
DR InterPro; IPR001899; Gpos\_Ysirk.  
DR Pfam; PF05738; Cna B; 2.  
DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
DR Pfam; PF02412; TSP\_3; 1.  
DR Pfam; PF04650; Ysirk\_signal; 1.  
DR TIGRFAMs; TIGR01167; LPXTG\_anchor; 1.  
DR TIGRFAMs; TIGR01168; Ysirk\_signal; 1.  
DR PROSITE; PS50847; GRAM\_POS\_ANCHORING; 1.  
KW Cell wall; Complete proteome; Peptidoglycan-anchor.  
SQ SEQUENCE 1056 AA; 115728 MW; 015869A9B5CA2723 CRC64;

Query Match 100.0%; Score 3013; DB 2; Length 1056;  
Best Local Similarity 100.0%; Pred. No. 2.9e-115;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSDEEKNDVINNNQSIINTDDNNQIIKKEETNNYDGIKRSBDRSTTNNVDNEATFLQK 60  
|||||  
DB 75 SSDEEKNDVINNNQSIINTDDNNQIIKKEETNNYDGIKRSBDRSTTNNVDNEATFLQK 134

QY 61 TPQDNTHLTTEBEVKESSESSNSSIDTAQPSHTTINREESVQTSNDVESHVSDPANS 120  
Db 135 TPQDNTHLTTEBEVKESSESSNSSIDTAQPSHTTINREESVQTSNDVESHVSDPANS 194  
QY 121 KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNOQDELLNLPINEYENKAR 180  
Db 195 KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNOQDELLNLPINEYENKAR 254  
QY 181 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSEGVKAHDAENLIYD 240  
Db 255 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSEGVKAHDAENLIYD 314  
QY 241 VTFFVDDKVKSGDWTVDIDKNTVPSDLTDSFTPIPKIDNSGEIITATGYDNKNKQIITYT 300  
Db 315 VTFFVDDKVKSGDWTVDIDKNTVPSDLTDSFTPIPKIDNSGEIITATGYDNKNKQIITYT 374  
QY 301 FTDYVDKYENIKAHKLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTTITVEYQRPENRT 360  
Db 375 FTDYVDKYENIKAHKLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTTITVEYQRPENRT 434  
QY 361 ANLOSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVINSNGDEGSIIDDSTIIKVKYKG 420  
Db 435 ANLOSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVINSNGDEGSIIDDSTIIKVKYKG 494  
QY 421 DNQNLPSNRNIYDYSEYEDVTDNDYAOLGNNNDVNNFNGNIDSPYIIKVISKYDPNKDDY 480  
Db 495 DNQNLPSNRNIYDYSEYEDVTDNDYAOLGNNNDVNNFNGNIDSPYIIKVISKYDPNKDDY 554  
QY 481 TTIQQTVMQTTINEYTGFEPTASVDNTIAFSTSSGQGGDLPPPKTKYKIGDYVWEDVDK 540  
Db 555 TTIQQTVMQTTINEYTGFEPTASVDNTIAFSTSSGQGGDLPPPKTKYKIGDYVWEDVDK 614  
QY 541 DGIQNTNDNEKPLSNVLVTLTPDGTSKSVRTDEGKYQFDG 582  
Db 615 DGIQNTNDNEKPLSNVLVTLTPDGTSKSVRTDEGKYQFDG 656

RESULT 2  
O70022 STAEQ PRELIMINARY; PRT; 1092 AA.  
AC O70022;  
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.  
DT 01-AUG-1998, sequence version 1.  
DT 07-FEB-2006, entry version 28.  
DE Fibrinogen-binding protein precursor.  
OS Staphylococcus epidermidis.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1282;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HB;  
RX MEDLINE=98261511; PubMed=9596732;  
RA Nilsson M., Frykberg L., Flock J.I., Pei L., Lindberg M., Guss B.;  
RT "A fibrinogen-binding protein of Staphylococcus epidermidis";  
RL Infect. Immun. 66:2666-2673 (1998).  
CC  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
CC  
CC EMBL; Y17116; CAA76638.1; -; Genomic\_DNA.  
DR PIR; T30214; T30214.  
DR HSSP; Q53653; IN67.  
DR SMR; O70022; 278-598.  
DR GO; GO:0009986; C:cell surface; IEA.  
DR GO; GO:0005618; C:cell wall; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005509; P:calcium ion binding; IEA.  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR InterPro; IPR008454; Cna B.  
DR InterPro; IPR005877; Gpos YSIRK.  
DR InterPro; IPR001899; Gram\_pos\_anchor.  
DR Pfam; PF05738; Cna\_B; 2.

DR Pfam; PF00746; Gram\_pos\_anchor; 1.  
DR Pfam; PF02412; TSP\_3; 1\_  
DR Pfam; PF04650; YSIRK\_signal; 1.  
DR TIGRFAMs; TIGR01167; LPTXG\_anchor; 1.  
DR TIGRFAMs; TIGR01168; YSIRK\_signal; 1.  
DR PROSITE; PS0847; GRAM\_POS\_ANCHORING; 1.  
KW Cell wall, Peptidoglycan-anchor; Signal.  
FT SIGNAL 1 51 Potential.  
FT CHAIN 52 1092 fibrinogen-binding protein.  
SQ SEQUENCE 1092 AA; 119293 MW; 6542BC39AAD8B984 CRC64;  
Query Match 100.0%; Score 3013; DB 2; Length 1092;  
Best Local Similarity 100.0%; Pred. No. 3e-115;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSSEKNDVINNNQSIINTDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENATFLQK 60  
Db 75 SSSEKNDVINNNQSIINTDNNQIIKKEETNNYDGIKRSSEDRTESTTNVDENATFLQK 134  
QY 61 TPQDNTHLTTEBEVKESSESSNSSIDTAQPSHTTINREESVQTSNDVESHVSDPANS 120  
Db 135 TPQDNTHLTTEBEVKESSESSNSSIDTAQPSHTTINREESVQTSNDVESHVSDPANS 194  
QY 121 KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNOQDELLNLPINEYENKAR 180  
Db 195 KIKESNTESGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNOQDELLNLPINEYENKAR 254  
QY 181 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSEGVKAHDAENLIYD 240  
Db 255 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTDQSITEGYDDSEGVKAHDAENLIYD 314  
QY 241 VTFFVDDKVKSGDWTVDIDKNTVPSDLTDSFTPIPKIDNSGEIITATGYDNKNKQIITYT 300  
Db 315 VTFFVDDKVKSGDWTVDIDKNTVPSDLTDSFTPIPKIDNSGEIITATGYDNKNKQIITYT 374  
QY 301 FTDYVDKYENIKAHKLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTTITVEYQRPENRT 360  
Db 375 FTDYVDKYENIKAHKLKLTSYIDKSKVPNNNTKLDVEYKTALSSVNKTTITVEYQRPENRT 434  
QY 361 ANLOSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVINSNGDEGSIIDDSTIIKVKYKG 420  
Db 435 ANLOSMFTNIDTKNHTVEQTIYINPLRYSAKETNNVINSNGDEGSIIDDSTIIKVKYKG 494  
QY 421 DNQNLPSNRNIYDYSEYEDVTDNDYAOLGNNNDVNNFNGNIDSPYIIKVISKYDPNKDDY 480  
Db 495 DNQNLPSNRNIYDYSEYEDVTDNDYAOLGNNNDVNNFNGNIDSPYIIKVISKYDPNKDDY 554  
QY 481 TTIQQTVMQTTINEYTGFEPTASVDNTIAFSTSSGQGGDLPPPKTKYKIGDYVWEDVDK 540  
Db 555 TTIQQTVMQTTINEYTGFEPTASVDNTIAFSTSSGQGGDLPPPKTKYKIGDYVWEDVDK 614  
QY 541 DGIQNTNDNEKPLSNVLVTLTPDGTSKSVRTDEGKYQFDG 582  
Db 615 DGIQNTNDNEKPLSNVLVTLTPDGTSKSVRTDEGKYQFDG 656

RESULT 3  
Q5HR16 STAEQ PRELIMINARY; PRT; 892 AA.  
ID Q5HR16 STAEQ PRELIMINARY; PRT; 892 AA.  
AC Q5HR16;  
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.  
DT 15-FEB-2005, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE SdrG protein.  
OS OrderedLococcusNames=SERP0207;  
GN Staphylococcus epidermidis (strain ATCC 35984 / RP62A).  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=176279;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;  
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,  
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,



```
RA Dadeon R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathavan J.J., Khouri H., Uterback T.R., Lee C.,
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RL J. Bacteriol. 187:2426-2438(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000029; AAW53571.1; -; Genomic_DNA.
DR TIGR; SERP0207; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008454; Cna_B.
DR Pfam; PF05738; Cna_B_2.
DR Pfam; PF02412; TSP_3; 1_
DR TIGRfam; TIGR01167; LPXG anchor; 1.
DR PROSITE; PS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 892 AA; 98747 MW; EC35C932B58EF497 CRC64;

Query Match 93.3%; Score 2810.5; DB 2; Length 892;
Best Local Similarity 93.6%; Pred. No. 4.5e-107;
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

QY 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKRSDETRSTTNVDENEATFLQK 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 35 SSNEKNDVINNQSIINTDDNNQ-IKKEETNSDAIENRSKDIQTSTTNVDENEATFLQK 93
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 TPQDNTLTHEEVKSSSVSSNSSIDTAQPSHTTINREESVQTSNDVDSHVSDFPANS 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 94 TPQDNTQLKEEVKVPSSVESNSSMDTAQPSHTTINSEASIQTSDEENSRVDFPANS 153
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNQDELLMLPINEYENKAR 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 154 KIIESNTSKEENTIEQPNKVRSDITSQPSSYKNIDEKISNQDELLMLPINEYENKVR 213
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTQDSITEGYDDSEGVIKAHDAENLIYD 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 214 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTQDSITEGYDDSEGVIKAHDAENLIYD 273
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 VTFEVDKVKSGDWTVDIDKNTVPSDLTDSFTIPKIKDNGSEIITATGYDNKNQIYTT 300
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 274 VTFEVDKVKSGDWTVDIDKNTVPSDLTDSFTIPKIKDNGSEIITATGYDNKNQIYTT 333
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 FTDYVDKVENIKAHKLTSYIDKSKVPNNNTKLDVEYKTALSSVKNKTIITVEYQRPENRT 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 334 FTDYVDKVENIKAHKLTSYIDKSKVPNNNTKLDVEYKTALSSVKNKTIITVEYQRPENRT 393
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 ANLQSMFTNIDPKNTVEGTIYINPLRYSAKETNNVNSGNDEGSTIIDDSITIIKVKYKG 420
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 394 ANLQSMFTNIDPKNTVEGTIYINPLRYSAKETNNVNSGNDEGSTIIDDSITIIKVKYKG 453
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 DNQNLPSNRIYDYSEYEDVTNDYDQAQLGNNDNVNINFGNIDSPYIIKVISYDPNKDXY 480
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 454 DNQNLPSNRIYDYSEYEDVTNDYDQAQLGNNDNVNINFGNIDSPYIIKVISYDPNKDXY 513
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 TTIQQTVMQTTINETYGEFRFASVDNTIAFTSSGQGGDLPPBKTYKIGYVWEDVDK 540
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 514 TTIQQTVMQTTINETYGEFRFASVDNTIAFTSSGQGGDLPPBKTYKIGYVWEDVDK 573
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 541 DGIQNTNDEKPLSNVLTLYTPDGTSKSVRTDEGKYQFDG 582
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 574 DGIQNTNDEKPLSNVLTLYTPDGTSKSVRTDEGKYQFDG 615
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 4
Q9KIL13 STAEF PRELIMINARY; PRT; 931 AA.
AC Q9KIL13_
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Fibrinogen-binding protein SdrG.
GN Name=sdrG;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K28;
RX MEDLINE=20340957; PubMed=10878118;
RA McCrea K.W., Hartford O., Davis S., Ni Eidhin D., Lina G.,
RA Speziale P., Foster T.J., Hook M.;
RT "The serine-aspartate repeat (sdr) protein family in Staphylococcus
RT epidermidis.";
RL Microbiology 146:1535-1546(2000).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF245042; AAF72510.1; -; Genomic_DNA.
DR PDB; 1R17; X-ray; A/B=C/D=274-598.
DR PDB; 1R19; X-ray; A/B=C/D=274-598.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpos_Ysirk.
DR Pfam; PF05738; Cna_B_2.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02412; TSP_3; 1_
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRfam; TIGR01167; LPXG anchor; 1.
DR TIGRfam; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 931 AA; 102956 MW; 591E657D97027116 CRC64;

Query Match 93.3%; Score 2810.5; DB 2; Length 931;
Best Local Similarity 93.6%; Pred. No. 4.8e-107;
Matches 545; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

QY 1 SSDEKNDVINNQSIINTDDNNQIIKKEETNNYDGIKRSDETRSTTNVDENEATFLQK 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 74 SSNEKNDVINNQSIINTDDNNQ-IKKEETNSDAIENRSKDIQTSTTNVDENEATFLQK 132
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 TPQDNTLTHEEVKSSSVSSNSSIDTAQPSHTTINREESVQTSNDVDSHVSDFPANS 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 133 TPQDNTQLKEEVKVPSSVESNSSMDTAQPSHTTINSEASIQTSDEENSRVDFPANS 192
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 KIKESNTSGKEENTIEQPNKVKEDSTTSQPSGYTNIDEKISNQDELLMLPINEYENKAR 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 193 KIIESNTSKEENTIEQPNKVRSDITSQPSSYKNIDEKISNQDELLMLPINEYENKVR 252
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTQDSITEGYDDSEGVIKAHDAENLIYD 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 253 PLSTTSAQPSIKRVTVNQLAAEQGSNVNHLIKVTQDSITEGYDDSEGVIKAHDAENLIYD 312
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 VTFEVDKVKSGDWTVDIDKNTVPSDLTDSFTIPKIKDNGSEIITATGYDNKNQIYTT 300
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 313 VTFEVDKVKSGDWTVDIDKNTVPSDLTDSFTIPKIKDNGSEIITATGYDNKNQIYTT 372
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 FTDYVDKVENIKAHKLTSYIDKSKVPNNNTKLDVEYKTALSSVKNKTIITVEYQRPENRT 360
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```

Db 373 FTDYVDKYENIKAKHLKLTSTYIDSKSVNNNTKLDVEYKLTALSSVNKTITVEYQKPNERT 432
Qy 361 ANLOSMFTNIDTKNHTVQGTIYINPLRYSAKETNWNISGNDGEGSTIIDSTIIKVKYVG 420
Db 433 ANLOSMFTNIDTKNHTVQGTIYINPLRYSAKETNWNISGNDGEGSTIIDSTIIKVKYVG 492
Qy 421 DNQNLPSNRIYDYSEYEDVNDNDYAQLGNNDNINFGNIDSPYIIKVKISYKDNKDDY 480
Db 493 DNQNLPSNRIYDYSEYEDVNDNDYAQLGNNDNINFGNIDSPYIIKVKISYKDNKDDY 552
Qy 481 TTIQQTVMQTTINBYTGEFTASVDNTIAFSTSSGQGGDLPPBKTKYKIGDYVWEDYK 540
Db 553 TTIQQTVMQTTINBYTGEFTASVDNTIAFSTSSGQGGDLPPBKTKYKIGDYVWEDYK 612
Qy 541 DGIQNTNDNEKPLSNVLVTLTPDGTSKSVRTDEGKYQFDG 582
Db 613 DGIQNTNDNEKPLSNVLVTLTPDGTSKSVRTDEGKYQFDG 654

```

## RESULT 5

```

Q6GJ46 STAA8 PRELIMINARY; PRT; 1137 AA.
AC Q6GJ46;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 14.
DE Bone sialoprotein-binding protein.
GN Name=bbp; OrderedLocusNames=SAK0567;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitz E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----

```

```

DR EMBL; BX571856; CAG39588.1; -; Genomic_DNA.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; P:calcium ion binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpos_YSRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003367; tsp_3.
DR Pfam; PF05738; Cna_B; 3.
DR Pfam; PF02412; TSP_3; 3.
DR Pfam; PF04650; YSRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YSRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1137 AA; 123326 MW; 2C7DB7BABDC8FB81 CRC64;

```

```

Query Match 40.1%; Score 1209.5; DB 2; Length 1137;
Best Local Similarity 44.6%; Pred. No. 1.9e-41;
Matches 279; Conservative 98; Mismatches 180; Indels 69; Gaps 20;

```

```

Qy 1 SSDEKVD---VINNQSIINTDNNQIIKKETN-----NYDGIKESDEORTTESTTVD 51
Db 57 STENAKQDEASGNKEVSVETENNSTQKNLDLTPIKKETNTDSHQEAKAPTTSSTQQ 116
Qy 52 ENAEATFLQKTPQDNTHLTETEEVKES---SSVESNSSIDTAQAPSHHTTINREESVQTSN 108
Db 117 QNNATTSTETKPN--LEKENVKPSTDKTATEDSVILEEKKAPNT--NNDVTTKPS-- 170
Qy 109 VEDSHVSDFANSKIKESNT---ESGKEHTIEQPNKVKEDSTTSQPSGYTHIDEKIS-NQ 164
Db 171 -----TSEIQTTPPTPQESTNIENSQPTPSKVD---NQVTDATNPKPEPVNSK 217
Qy 165 DELNLNP-----INEYENKARPLSTTSAQPSIKRV-----TVNQLAAEQGSNNVH 209
Db 218 BELKNNPEKLKELVRNDSNTDRSKPATAPTSVAPKRVNAKIRFAVAQPAVASNNVND 277
Qy 210 LIKVTQSIETGYDDSEGVKAHDAENLIYDVTPEVDDKVKSGDTMTVDIDKNTVPSDLT 269
Db 278 LITVTKQMITEGIKD-DGVIQAHGDEHIITSDPKIDNAVKAAGDTMTVKYDKHTIPSDIT 336
Qy 270 DSFTPIKIDKNSGEIATGTYDNKNKQIYTYFTDYVDKYENIKAKHLKLTSTYIDSKSVNN 329
Db 337 DDFTPVDITDPSGEVIAKGTFLNTKTITTKYKFTDYVDKYENIKAKHLKLTSTYIDSKSVNN 395
Qy 330 NTKLDVEYKLTALSSVNKTITVEYQKPNERTANLQSMFTNIDTKNHTVQGTIYINPLRY 389
Db 396 ETNLNLTFATADKETSNNKVKVEYQKPIVKDSNQSIPSHLDTTKHEVEQGTIYVNPGLKN 455
Qy 390 AKETNVAI-----SCNGD-----EGSTIIDSTIIKVKYKVGDNQNLPSNRIYDYSEYEDV 440
Db 456 AKNTNVIKSGGVADNGDYTGDCSTIIDSTNTEIKVKYKVASGQQLPQSNKIYDYSQYEDV 515
Qy 441 TNDYIAQLGNN---NDVNINFGNIDSPYIIKVKISYKDNKDDYTTIQTVMQTTINBYT 497
Db 516 TNS--VTINKNYGTNMANINFGIDISAYIVKVSQKTPGAEDDLAVQCGVRM--TTNKNY 572
Qy 498 GEFTASVDNTIAFSTSSGQGGDL-PPEKTKYKIGDYVWEDVDKDGIGTNTNDNEKPLSNV 556
Db 573 YS-SYAGVTNLTSTTSSGGDGGTVKPEEKYKIGDYVWEDVDKDGIGTNTNDNEKPLSNV 631
Qy 557 LVLTITPDGTSKSVRTDEGKYQFDG 582
Db 632 LVLTITPDGTSKSVRTDANGHYEFGG 657

```

## RESULT 6

```

Q2YSAL STAA8 PRELIMINARY; PRT; 1113 AA.
ID Q2YSAL STAA8 PRELIMINARY; PRT; 1113 AA.
AC Q2YSAL;
DT 20-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 20-DEC-2005, sequence version 1.
DE 07-MAR-2006, entry version 4.
DE Ser-Asp rich fibrinogen-binding/bone sialoprotein-binding protein.
GN OrderedLocusNames=SAB0513;
OS Staphylococcus aureus (strain bovine RP122).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=273036;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Herron-Olson L., Musser J.M., Kapur V.;
RT "Whole-genome sequencing and comparative analysis of bovine mastitis-
RT associated Staphylococcus aureus";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ938182; CAI80201.1; -; Genomic DNA.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1113 AA; 120914 MW; 10D4C7B2ABA54C1C CRC64;

```

```

Query Match 39.3%; Score 1185; DB 2; Length 1113;

```

	Best Local Similarity	44.1%;	Pred. NO. 1.8e-40;	
	Matches	273;	Conservative	98; Mismatches 184; Indels 64; Gaps 20
Qy	1	SSDBEKNDVINNGOSITDDNNQI---	IKKEETNNYDGI	EKESDRTEGTNTVNDENAEFTL 58
Db	66	ATTSDNKEVSETENNSTTENNTPIKE--	TWTDSPQEAKESGTT	SSTQQQNVTAT 123
Qy	59	KQTPODNTHLTREEVKES----	SVSESSNSIDTAQPSH	TTINREESVQTSNVDSDSHVS 115
Db	124	TETRPON--IBKNVPKSTDKATEDT	SVILLEEKAPNNT--	NNDVTTTKPS----- 170
Qy	116	DFANSKIKESNT---ESGKEENTIE	QPNKVVEDSTTSQPSGYTNIDEXIS-	NODELLNLP 171
Db	171	--TSEIQTKPTTQESTNIENSOPPT	PSKD---NQVDTATPKPVPNVSKELKNP	224
Qy	172	-----INEYENKARPLSTSAQPS	KIRV-----TVNQLAAEQGSNNNHIL	KVTDQ 216
Db	225	EKLKELVRNDSNTDRSTKPAATA	PTSVAPEKRVNAKMFAPAQAASNNVNDLI	TVTQK 284
Qy	217	SITGEYDDSEGVIKAHDANLIYDV	FVDDKVKSGDGMTVDIDKNTVPSDL	TSTFIPK 276
Db	285	TIITEGID-DGVIQAHDGEHIYYT	SDFKIDNSVMKGDMTMTVKYDKHTL	PSDLTDFSPVD 343
Qy	277	IKDMSGEIIATGTYDNKNQIITY	TFD VVDKYENIKAHCLKITSYDKSKVPNN	TKLDVE 336
Db	344	ITDSPGEVIAKTGFVNNTIITY	KFTDYDREYNVNAKLELNSTYDKCTVP-	NEANINLT 402
Qy	337	YKTALSSVNKTIITVEYORPENR	NANTLQSMFTNIDTKNHTVEQITIYNPL	RYSAKETNVN 396
Db	403	FGTADKETSKNVNVEYQPIVKDES	NIQSIFSLHDTTWKHEVEQIYYVSP	LKNAKNTVT 462
Qy	397	I-----SNGBD-----EGSTI	IDDSTIIKVVYKGNQNLPSNRIRYDY	SEYEDVNDNYAQ 447
Db	463	IKSGGVADNGDYTTGGDSTIIDS	NTEIKVYVASQQLPQSNKIYDYSQY	EDVTNS--VT 520
Qy	448	LGNN--NDVNIINGNIDSPVII	KVISKYDPNKDDYTIIQOTVTMOTTIN	EYTGEPRTAS 504
Db	521	INKNYGTMMANINFGDISA	YIVKVSXYTPGABDLEVOQGVRM-T	TNTNKYNYS-SYAG 578
Qy	505	YDNTIAFSTSQQOQGLD-PPEK	TYKIGDYVWEVDKDGIGNTNDNKP	LSNLVLTLTP 563
Db	579	YTNILTSTDGGGDTAKPEEL	YKIGDYVWEVDKGVQGTDSKEKPM	ANVLTLTLTP 638
Qy	564	DGTSKSVRTDEDGKIQFDG	582	
Db	639	DGTTKSVRTDDKGHYEFGG	657	

```

RESULT 7
Q9KWX6_STAAU
ID Q9KWX6 STAAU PRELIMINARY; PRT; 1171 AA.
AC Q9KWX6;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Bone sialoprotein-binding protein.
GN Name=bbp;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_taxid=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=024;
RX MEDLINE=20115096; PubMed=10642520; DOI=10.1042/0264-6021.3450611;
RT Tung H.S., Guss B., Hellman U., Persson L., Rubin K., Ryden C.;
RA "A bone sialoprotein-binding protein from Staphylococcus aureus: a
RL member of the staphylococcal Sdr family ].";
RN Biochem. J. 345:611-619(2000).
[2]
RN RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=024;
RX Tung H.;
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL

```

```

CC CC CC CC CC CC CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; Y18653; CAB75732.1; -; Genomic_DNA.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpos_YSRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF05738; Cna_B_3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02412; TSP_3; 2.
DR Pfam; PF04650; YSIRK_signal; 1.
DR TIGRPFAMS; TIGR01167; LPXTG_anchor; 1.
DR TIGRPFAMS; TIGR01168; YSIRK_signal; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor.
DR KW SEQUENCE 1171 AA; 127124 MW; C5BC812F9DA5A884 CRC64:

```

Query Match 38.5%; Score 1160.5; DB 2; Length 1171;  
Best Local Similarity 42.9%; Pred. No. 2e-39;  
Matches 271; Conservative 99; Mismatches 182; Indels 79; Gaps 20;

[illegible]

## RESULT 8

```

O86489 STAAU
ID O86489 STAAU PRELIMINARY; PRT; 1166 AA.
AC O86489;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Sdr E protein.
GN Name=sdr E;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Newman;
RX MEDLINE=99098700; PubMed=9884231;
RA JOSEPHSON E., McCrea K., Ni Eidhin D., O'Connell D., Cox J., Hook M.,
RA Foster T.J.;
RT "Three new members of the serine-aspartate repeat protein multigene
RT family of Staphylococcus aureus.";
RL Microbiology 144:3387-3395 (1998).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AJ005647; CA06652.1; -; Genomic_DNA.
DR PIR; T28680; T28680.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003367; tsp_3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02412; TSP_3; 3.
DR Pfam; PF04650; YsIRK_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 1166 AA; 126549 MW; 750A7B0135287D4A CRC64;

Query Match 38.0%; Score 1144.5; DB 2; Length 1166;
Best Local Similarity 42.6%; Pred. NO. 8.8e-39;
Matches 263; Conservative 108; Mismatches 191; Indels 55; Gaps 18;

QY 1 SSDEKNDVNNQSIINTDDNNQI--IKKEETNNYDGIKESDEBTSTTNVDENEATFL 58
DB 66 ATTSNKEVSETENNSTENNSTNPICKK--TNTDSQPEAKKESTSSSTOKQNNVTAT 123

QY 59 OKTPQDNTLHTEEEVKES---SSVBSNSSIDTAQPSHTTINREESVQTSNDVEDSHVS 115
DB 124 TETKQD--IKENVKPTDKTATEDTSVILEEKAPNNT--NNDVTYKPS-----TS 172

QY 116 DFANSKIKESNT---ESGKEENTIEQPNKVRKEDSTTSQPSGYNTIDEKIS-NQDELLNLP 171
DB 173 EPSTSEIQTKPTTPQESTNIENSQOPPTPSKVD---NQVTDATNPKEPVNYSKEELKNP 229

QY 172 -----INYEYENKARPLSTTSQAQSIKRV-----TVNQLAAEQSNVNHLIKVDQ 216
DB 230 EKLKELVRNDSNTDSTHSTFVAPTSTSVAPKNAKRFAPAFAVAASNNVNDLIKVTQ 289

QY 217 SITEGYDDSEGVKKAHDENLIYDVTFEVDKVKSGDGTMTVDIDKNTVPSDLTSTFTIPK 276
DB 290 TIKVG-DGKDNVAAHDGDKDEYDEFTIDNKVKGGDGTWTINYNKVPISLDTKNDPID 348

QY 277 IKDNGSEIATGYDNKKNQITTYTFTDYVDKYENIKAKHLKLTYSIDKSKVPNNNTKLDV 336
DB 349 ITDPSGEVIANGTDPKATQITTYTFTDYVDKYEDIKSLRLTLYSIDKKTVP-NETSLNLT 407

```

## RESULT 9

## Q6GBS4 STAAU

ID Q6GBS4 STAAU PRELIMINARY; PRT; 1141 AA.

AC Q6GBS4;

DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 07-FEB-2006, entry version 13.

DE Bone sialoprotein-binding protein.

GN OrderedLocusNames=SAS0521;

OS Staphylococcus aureus (strain MSSA476).

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI\_TaxID=282459;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed=15213324; DOI=10.1073/pnas.0402521101;

RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,

RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,

RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Dowd L.,

RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,

RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,

RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,

RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,

RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,

RA Spratt B.G., Parkhill J.;

RT "Complete genomes of two clinical Staphylococcus aureus strains:

RT evidence for the rapid evolution of virulence and drug resistance.";

RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; BX571857; CAG42296.1; -; Genomic\_DNA.

DR GO; GO:0009986; C:cell surface; IEA.

DR GO; GO:0005618; C:cell wall; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR005877; Gpos\_YsIRK.

DR InterPro; IPR001899; Gram\_pos\_anchor.

DR InterPro; IPR003367; tsp\_3.

DR Pfam; PF05738; Cna\_B; 3.

DR Pfam; PF00746; Gram\_pos\_anchor; 1.

DR Pfam; PF02412; TSP\_3; 3.

DR Pfam; PF04650; YsIRK\_signal; 1.

DR TIGRFAMs; TIGR01167; LPXTG\_anchor; 1.

DR TIGRFAMs; TIGR01168; YsIRK\_signal; 1.

DR PROSITE; PS00847; GRAM\_POS\_ANCHORING; 1.

KW Cell wall; Complete proteome; Peptidoglycan-anchor.

SQ SEQUENCE 1141 AA; 123998 MW; 372E5860850A332C CRC64;

Query Match 38.0%; Score 1143.5; DB 2; Length 1141;

[illegible]

Db	346	DPSGEVIAKGTDFKATKQITTYFTDVKYEDIKSRLTLYSYDKKTPV-NETSLNLTPA	404
Qy	339	TALLSSNKKITTVBYQBPENRNTANLQSMFTNIDTKNHTVEOTIYNPLRYSAKETNNIS	398
Db	405	TAGKETSONVTVDYQDPVHVGDSNIQSIFTKLDEDKQIEQQIYVNPKKSATNKKVDIA	464
Qy	399	GNNG-----DEGSTIIDSTIIKVKYGVGNQNLPLDSNRIYDYSEYEDVTND-DYAQL	448
Db	465	GSQVDDYGNIKLGNGSTIIDQNTIEIKVKYKNSDQQLPQSNRIYDFSQYEDVTSQFDNKK	524
Qy	449	GNNDVNVNFGNIDSPYIIKVKISYDPNKKDDYTTIOQTVMQTITNEYTGEPFTASVDNT	508
Db	525	FSNNVATLDFGDINSAYIIKWSKYTPTSDGELDIAQGTSMRTT-DKY-GYVNYAGSYNF	582
Qy	509	IAPSTSSGGCGDL-PPEKTYKIGDVWVEDVDKGGTQNTNDNEKPLSNVLVTLITYPDGTS	567
Db	583	IVTNSDGGGDDGVKPEEKLYKIGDVWVEDVDKGGVQGGTDSKEKPMANVLVTLITYPDGTT	642
Qy	568	KSVRTDEDGKYQFDG	582
Db	643	KSVRTDAKGHYFEGG	657

RESULT 11  
Q5HIB2\_STAAC  
ID\_CSHIB2\_STAAC DBP1\_IMINABV. DBP1\_1166\_AA

```
AC Q5H1B2;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE SdrE protein.
GN Name=sdrE; OrderedLocusNames=SACOL0610;
OS Staphylococcus aureus (strain COL).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=93062;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RL J. Bacteriol. 187:2426-2438(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000046; AAW37719.1; -, Genomic_DNA.
DR TIGR; SACOL0610; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0036020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR005877; Gpob_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003367; tsp_3.
DR Pfam; PF05738; Cna_B; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF02412; Tsp_3; 3.
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_signal; 1.
DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1166 AA; 126563 MW; 92DFC023B75AB88F CRC64;

Query Match 37.9%; Score 1142.5; DB 2; Length 1166;
Best Local Similarity 42.7%; Pred. No. 1.le-38;
Matches 262; Conservative 107; Mismatches 196; Indels 49; Gaps 18;

QY 1 SSDEKNDVINNQSIQNDNNQI--IKKEETNNYDGIKRSDETRSTTNVDNEATFL 58
DB 66 ATTSNDKEVSVSTENNSTENNTPIKKE--TNIDSQPEAKKESTSSSTQKQNNVTAT 123
QY 59 OKTPDNDTHLTREEEVKES---SSVSSNSSIDTAQPSHTTINREESVQTSNDVSDSHV 115
DB 124 TETKPN--IEKENVKPSDKTATDTSVILEEKKAPNNT--NNDVTTKPS-----TS 172
QY 116 DPANSKIKESNT--ESGKEENTIEQPKVKED---STTSQPSGYTNI--DEKISNQDEL 167
DB 173 EPTSEIQTKPTTPESTNIENSQPTFSKVDNQVDTATNPKVPVNSKELKKNPKRL 232
QY 168 LMLPINE--YENKARPLSTTSQAQSIKRV-----TVNQLAAEQGSNNVHLIKVTDQSIT 219
DB 233 KELVNDSTNDHTSKPVTAPTSPVAKRVNAKMFAPAQPAVASNNVNDLIKVTQTIK 292
QY 220 EGYDSEGVYKAHDAENLIYDVTPEVDKVKSGDWTVDIDKNTVPSDLTDSFTPKIKD 279
DB 293 VG-DGKDNVAAAHGDKIEYDTEFTIDNKKVGGDTMTINIDKNVTPSLDIDKNDPIDTD 351
QY 280 NSGEIATGTYNKKNQITTYTFTDYYDKYENIKAHKLKLTSDYDKSKVPNNNTKLDVEYKT 339
```

```
Db 352 PSGEVIAKGTEDKATKQITTYTFTDYYDKYEDIKRLTYLSYIDKKTVP-NETSLNLTFA 410
QY 340 ALSSVNKTIITVEYQRPNEENRTANLQSMFTNIDTKNHTVEQTIYINPLYSAKETNNVNSG 399
Db 411 AGKTSQNVTVDYQDPWVHGDSNIQSIPTKLDEDKQTIEQQIYVNPFLKKSATNTRKVDIAG 470
QY 400 NG-----DEGSTIIDDSITIKVKYKVGONQLPDSNRIYDYSEYEDVND-DYAQIG 449
Db 471 SQVDDYGNIKLNGSTIIDQNTETIKVKVKNVSDQQLPQSNRIYDFSQYEDVTSQPFNKKS 530
QY 450 NNNDVNFNGNIDSPYIKVSKYDPNKDDVTYITQOVTMTTINEXYTGEPRTASYDNTI 509
Db 531 SNNVATLDFGINSAYIKVSKVTPPTSDGELDTAQTSMRTT-DKY-GYNYAGYSNFI 588
QY 510 AFTSSSGQGQGLD-PPEKTYKIGDYMVEDVDKGIQNTNDNEKPLSNVLVLTYPDGTGSK 568
Db 589 VTSNDTGGGDTGVKPEEKLYKIGDYMVEDVDKGVQGTDSKEKPMANVLVLTYPDGTGTTK 648
QY 569 SVRTDEGKYQFDG 582
Db 649 SVRTDANGHYEFG 662

RESULT 12
Q932F7_STRAAM
ID Q932F7_STRAAM PRELIMINARY; PRT; 1141 AA.
AC Q932F7;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein.
GN Name=sdrE; OrderedLocusNames=SAV0563;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K., Nagai Y., Lian J.-Q., Ito T., Kanamori M.,
RA Matsunaru H., Maruyama A., Murakami H., Hasegawa A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BA000017; BAB56725.1; -, Genomic_DNA.
DR BiOCYC; SAURI58878:SAV0563-MONOMER; -.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR008454; Cna_B.
DR InterPro; IPR005877; Gpob_Ysirk.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR003367; tsp_3.
DR Pfam; PF05738; Cna_B; 3.
DR Pfam; PF02412; Tsp_3; 3.
DR Pfam; PF04650; Ysirk_signal; 1.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR TIGRFAMs; TIGR01168; Ysirk_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Complete proteome; Peptidoglycan-anchor.
SQ SEQUENCE 1141 AA; 124039 MW; E679F7C2991846D9 CRC64;
```



```
||||| :|:|:|
643 KSVRTDANGHYEFG 657

Db
RESULT 14
Q2UW65 STAAU
AC Q2UW65 STAAU PRELIMINARY; PRT; 444 AA.
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein
DE (Fragment).
GN Name=adrE;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=GE149;
RX PubMed=16352833; DOI=10.1128/JB.188.1.169-178.2006;
RA Kuhn G., Francioli P., Blanc D.S.;
RT "Evidence for clonal evolution among highly polymorphic genes in
RT methicillin resistant Staphylococcus aureus.";
RL J. Bacteriol. 188:169-178(2006).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AM076274; CAJ27911.1; -; Genomic_DNA.
FT NON TER 1 444
FT NON TER 444 444
SQ SEQUENCE 444 AA; 49117 MW; 8086D6B66F994224 CRC64;

Query Match 33.8%; Score 1018; DB 2; Length 444;
Best Local Similarity 56.3%; Pred. No. 4.4e-34;
Matches 205; Conservative 51; Mismatches 90; Indels 18; Gaps 8;

Qy 232 HDAENLIYDVTFFVDDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIIATGYD 291
Db 1 HDGEHIIYTSDFKIDNAVKAGDTMTVKYDKHTIPSDITDDFTPVDITDPSGEVIAGTFFD 60

Qy 292 NKNKQITFTFYDYDKYENIKAHKLTSYIDKSKVPNNNTKLDVYEKLTALSSVNKTITVE 351
Db 61 LNTKTIYKFTDYDRYENVNNAKLELSYIDKKEVP-NETNLNLTPTADKETSKNVKE 119

Qy 352 YQRPENRNTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVI-----SGNGD--- 402
Db 120 YQKPIVKDESNIQSFHLDTTKHEVEQTIYVNPFLKLNKNTNVTIKSGGVADNGDYTG 179

Qy 403 EGSTIIDSTIIKYKVGDNQNLPSNRIDYSEYEDVTDNDYVLAQLGN---NDVNINFG 459
Db 180 DGSIIIDSNTTEIKYKVASGQQLPQSNKIYDYSQYEDVTNS--VTINKYGTNNANINFG 237

Qy 460 NIDSPYIIKVISKYPNKKDYTTIQQVTVMQTTINEYTGERTASVDNTIAFSSGQGG 519
Db 238 DIDSAYIVKVVSKYTPGAEDDLAVQQGVRM-TTNKNYNS-SVAGYNTILSTTDSGGD 295

Qy 520 GDL-PPEKTYKIGDYVWEDVDKGIQNTNDNEKPLSNVLTLYPDGTSKSVRTDEGKY 578
Db 296 GTVKPEKLYKIGDYVWEDVDKGVQGTDSKEKPMANVLTLYPDGTTKSVRTDANGHY 355

Qy 579 QFDG 582
Db 356 EFGG 359

Search completed: August 12, 2006, 09:04:49
Job time : 305 secs

643 KSVRTDANGHYEFG 657

Db
RESULT 15
Q2UW70 STAAU
AC Q2UW70 STAAU PRELIMINARY; PRT; 444 AA.
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DE Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein
DE (Fragment).
GN Name=adrE;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=GE149;
RX PubMed=16352833; DOI=10.1128/JB.188.1.169-178.2006;
RA Kuhn G., Francioli P., Blanc D.S.;
RT "Evidence for clonal evolution among highly polymorphic genes in
RT methicillin resistant Staphylococcus aureus.";
RL J. Bacteriol. 188:169-178(2006).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AM076279; CAJ27916.1; -; Genomic_DNA.
FT NON TER 1 444
FT NON TER 444 444
SQ SEQUENCE 444 AA; 49117 MW; 8086D6B66F994224 CRC64;

Query Match 33.8%; Score 1018; DB 2; Length 444;
Best Local Similarity 56.3%; Pred. No. 4.4e-34;
Matches 205; Conservative 51; Mismatches 90; Indels 18; Gaps 8;

Qy 232 HDAENLIYDVTFFVDDKVKSGDTMTVDIDKNTVPSDLTDSFTIPKIKDNGSEIIATGYD 291
Db 1 HDGEHIIYTSDFKIDNAVKAGDTMTVKYDKHTIPSDITDDFTPVDITDPSGEVIAGTFFD 60

Qy 292 NKNKQITFTFYDYDKYENIKAHKLTSYIDKSKVPNNNTKLDVYEKLTALSSVNKTITVE 351
Db 61 LNTKTIYKFTDYDRYENVNNAKLELSYIDKKEVP-NETNLNLTPTADKETSKNVKE 119

Qy 352 YQRPENRNTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVI-----SGNGD--- 402
Db 120 YQKPIVKDESNIQSFHLDTTKHEVEQTIYVNPFLKLNKNTNVTIKSGGVADNGDYTG 179

Qy 403 EGSTIIDSTIIKYKVGDNQNLPSNRIDYSEYEDVTDNDYVLAQLGN---NDVNINFG 459
Db 180 DGSIIIDSNTTEIKYKVASGQQLPQSNKIYDYSQYEDVTNS--VTINKYGTNNANINFG 237

Qy 460 NIDSPYIIKVISKYPNKKDYTTIQQVTVMQTTINEYTGERTASVDNTIAFSSGQGG 519
Db 238 DIDSAYIVKVVSKYTPGAEDDLAVQQGVRM-TTNKNYNS-SVAGYNTILSTTDSGGD 295

Qy 520 GDL-PPEKTYKIGDYVWEDVDKGIQNTNDNEKPLSNVLTLYPDGTSKSVRTDEGKY 578
Db 296 GTVKPEKLYKIGDYVWEDVDKGVQGTDSKEKPMANVLTLYPDGTTKSVRTDANGHY 355

Qy 579 QFDG 582
Db 356 EFGG 359

RESULT 15
Q2UW70 STAAU
AC Q2UW70 STAAU PRELIMINARY; PRT; 444 AA.
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
```



Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	1746	100.0	1746	2	AR533703		AR533703 Sequence
2	1746	100.0	3600	2	BD009814		BD009814 Novel fib
3	1746	100.0	3600	2	AR533704		AR533704 Sequence
4	1746	100.0	3600	15	SEY17116		Y17116 Staphylococ
5	1745	98.9	1781	2	BD009812		BD009812 Novel fib
6	1745	98.9	1781	2	BD009812		BD009812 Novel fib
7	1744	99.9	1744	2	BD009813		BD009813 Sequence
8	1742.8	98.8	110000	15	AE015929_03		Continuation (4 of
9	1613.8	92.4	2676	2	CQ891594		CQ891594 Sequence
10	1613.8	92.4	2796	15	AF245042		AF245042 Staphyloc
11	1613.8	92.4	2976	2	BD245130		BD245130 Polypteri
12	1613.8	92.4	2976	2	AR410983		AR410983 Sequence
13	1613.8	92.4	2976	2	AR482276		AR482276 Sequence
14	1613.8	92.4	110000	15	CP000029_02		Continuation (3 of
15	507.2	29.0	837	2	AR484931		AR484931 Sequence
16	507.2	29.0	837	2	AX143977		AX143977 Sequence
17	507.2	29.0	3236	2	AR485406		AR485406 Sequence
18	507.2	29.0	3236	2	AX144770		AX144770 Sequence

**Db**

Db 181 ACCCCTCAAGATAATACTCATG

D**b** 181 ACCCTCAAGATAATACTCATCTTACAGAAGAGGTAAGAATCCTCATCAGTCGAA 240

QY 241 TCCTCAAAATTCATCAATGATGACTGCCCAACCAACCATCTCACACAACTAAATAGAGAA 300  
Db |||||  
241 TCCTCAAAATTCATCAATGATGACTGCCCAACCAACCATCTCACACAACTAAATAGAGAA 300  
QY 301 GAATCTGTTCAAACAAGTGATAATGTAGAAGATTCACACGATATCAGATTTTGGCTAACTCT 360  
Db |||||  
301 GAATCTGTTCAAACAAGTGATAATGTAGAAGATTCACACGATATCAGATTTTGGCTAACTCT 360  
QY 361 AAAATAAAGAGAGTAACAACCTGATCTCTGTTAAAGAGAGAAATATATAGAGCAACCTAAT 420  
Db |||||  
361 AAAATAAAGAGAGTAACAACCTGATCTCTGTTAAAGAGAGAAATATATAGAGCAACCTAAT 420  
QY 421 AAAGTAAAGAGAGATTCACACCAAGTCAGCCGCTCTGCTATACAAATATAGATGAAAAA 480  
Db |||||  
421 AAAGTAAAGAGAGATTCACACCAAGTCAGCCGCTCTGCTATACAAATATAGATGAAAAA 480  
QY 481 ATTTCAAATCAAGATGAGTTATTAATTTTACCAATTAATGAATATGAAAAATAAGGCTAGA 540  
Db |||||  
481 ATTTCAAATCAAGATGAGTTATTAATTTTACCAATTAATGAATATGAAAAATAAGGCTAGA 540  
QY 541 CAATATCTACAACATCTGCCCAACCATCGATTAACCGTAAACCGTAAATCAATTAGCG 600  
Db |||||  
541 CCATATCTACAACATCTGCCCAACCATCGATTAACCGTAAACCGTAAATCAATTAGCG 600  
QY 601 GCGGAACAAGGTTCCGAATGTTAAACCAATTTAAAGTTTACTGATCAAAAGTATTACTGAA 660  
Db |||||  
601 GCGGAACAAGGTTCCGAATGTTAAACCAATTTAAAGTTTACTGATCAAAAGTATTACTGAA 660  
QY 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Db |||||  
661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
QY 721 GTAACCTTTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
Db |||||  
721 GTAACCTTTGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
QY 781 AAGATACAGTTCCATCAGATTTTAAACCGATGATTTTAAACCGATGATTTTAAACCGAT 840  
Db |||||  
781 AAGATACAGTTCCATCAGATTTTAAACCGATGATTTTAAACCGATGATTTTAAACCGAT 840  
QY 841 TCTGAGAAATCATCGCTACAGTACTTATGATGATGATGATGATGATGATGATGATGATGAT 900  
Db |||||  
841 TCTGAGAAATCATCGCTACAGTACTTATGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 901 TTTACAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
Db |||||  
901 TTTACAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
QY 961 ATTGATAAATCAAGGTTCCAAATTAATTAACCAAGTTAGATGATGATGATGATGATGATGAT 1020  
Db |||||  
961 ATTGATAAATCAAGGTTCCAAATTAATTAACCAAGTTAGATGATGATGATGATGATGATGAT 1020  
QY 1021 CTTTCATCAGTAAATAAACAATTAACGTTGATATCAAGACCTTAACGAAATCGGACT 1080  
Db |||||  
1021 CTTTCATCAGTAAATAAACAATTAACGTTGATATCAAGACCTTAACGAAATCGGACT 1080  
QY 1081 GCTAACCTTCAAAGTATGTTTCAAAATATAGATGATGATGATGATGATGATGATGATGATGAT 1140  
Db |||||  
1081 GCTAACCTTCAAAGTATGTTTCAAAATATAGATGATGATGATGATGATGATGATGATGATGAT 1140  
QY 1141 ATTTATATTAACCTCTCTGTTTATTCAGCCAGGAAACAAATGTTAAATATTTTCAGGGAAT 1200  
Db |||||  
1141 ATTTATATTAACCTCTCTGTTTATTCAGCCAGGAAACAAATGTTAAATATTTTCAGGGAAT 1200  
QY 1201 GGTGATGAGGTTTCAACATTTATAGACGATAGCACAAATTTAAAGTTTATAAGGTTGGA 1260  
Db |||||  
1201 GGTGATGAGGTTTCAACATTTATAGACGATAGCACAAATTTAAAGTTTATAAGGTTGGA 1260  
QY 1261 GATAATCAAAATTTACGATAGTAAACAGAAATTTATGATTAACGATGATTAAGATGTC 1320  
Db |||||  
1261 GATAATCAAAATTTACGATAGTAAACAGAAATTTATGATTAACGATGATTAAGATGTC 1320  
QY 1321 ACAAATGATGATTTATGCCCAATTTAGGAAATATAATGATGTTGAATTTTATTTTGGTAAT 1380

Db |||||  
1321 ACAAATGATGATTTATGCCCAATTTAGGAAATATAATGATGTTGAATTTTATTTTGGTAAT 1380  
QY 1381 ATAGATTCACCATATATTTAAAGTTTATTAGTAAATATGACCCCTAAATTAAGGATGATTAC 1440  
Db |||||  
1381 ATAGATTCACCATATATTTAAAGTTTATTAGTAAATATGACCCCTAAATTAAGGATGATTAC 1440  
QY 1441 ACGACTATACAGCAAACTGTGACAAATCGACAGCACTATAAATGATGATTAACCTGGTGAGTTT 1500  
Db |||||  
1441 ACGACTATACAGCAAACTGTGACAAATCGTACAGCACTATAAATGATGATTAACCTGGTGAGTTT 1500  
QY 1501 AGAAGACATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
Db |||||  
1501 AGAAGACATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
QY 1561 GACTTGCTCTCGTAAACCTTTATAAATCGGAGATTAACCTGATGATGATGATGATGATGATGAT 1620  
Db |||||  
1561 GACTTGCTCTCGTAAACCTTTATAAATCGGAGATTAACCTGATGATGATGATGATGATGATGAT 1620  
QY 1621 GATGTTTCAAATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
Db |||||  
1621 GATGTTTCAAATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
QY 1681 ACATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
Db |||||  
1681 ACATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
QY 1741 GATGGA 1746  
Db |||||  
1741 GATGGA 1746

RESULT 2  
BD009814  
LOCUS  
DEFINITION Novel fibrinogen binding protein originating from  
3600 bp DNA linear PAT 31-JAN-2002  
coagulase-negative staphylococcus.  
ACCESSION BD009814  
VERSION BD009814.1 GI:18638187  
KEYWORDS JP 2001503609-A/12.  
SOURCE Staphylococcus epidermidis  
ORGANISM Staphylococcus epidermidis  
REFERENCE 1 (bases 1 to 3600)  
AUTHORS Guss, B., Nilsson, M., Frykberg, L., Flock, J.I. and Lindberg, M.  
TITLE Novel fibrinogen binding protein originating from  
coagulase-negative staphylococcus  
JOURNAL Patent: JP 2001503609-A 12 21-MAR-2001;  
BENGT GUSS, MARTIN NILSSON, LARS FRYKBERG, JAN INGVAR FLOCK, ARTIN  
LINDBERG  
COMMENT OS Staphylococcus epidermidis  
PN JP 2001503609-A/12  
PD 21-MAR-2001  
PF 18-JUN-1997 JP 1998502819  
PR 20-JUN-1996 SE 9602496-3  
PI BENGT GUSS, MARTIN NILSSON, LARS FRYKBERG, JAN INGVAR FLOCK, PI  
MARTIN LINDBERG  
PC C07K14/31  
FH Key Location/Qualifiers  
FT CDS Location/Qualifiers  
source 1..3600  
/organism="Staphylococcus epidermidis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:1282"

FEATURES  
ORIGIN  
Query Match 100.0%; Score 1746; DB 2; Length 3600;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCTAGTGATGAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60

Db 255 TCTAGTGATGAAGAAAGAAATGATGTGATCAATAATAACAGTCAATAAACAACCGACGAT 314  
QY 61 AATAACCAATATATATAAAGAAAGAAACGAATAACTACGATGGCATAGAAAAACCTCTCA 120  
Db 315 AATAACCAATATATATAAAGAAAGAAACGAATAACTACGATGGCATAGAAAAACCTCTCA 374  
QY 121 GAAGATAGAACAGAGTCAACAACAAATGTAGATGAAAAAGAAAGCAACATTTTTACAAAG 180  
Db 375 GAAGATAGAACAGAGTCAACAACAAATGTAGATGAAAAAGAAAGCAACATTTTTACAAAG 434  
QY 181 ACCCTCAAGATAATACTCATCTTACAGAGAGAGGTAAAGAAATCCTCATCAGTCGAA 240  
Db 435 ACCCTCAAGATAATACTCATCTTACAGAGAGAGGTAAAGAAATCCTCATCAGTCGAA 494  
QY 241 TCCCTCAAAATTCATCAATGTGATCTGCCCAACCAACCATCTCACAAACAATAATAGAGAA 300  
Db 495 TCCCTCAAAATTCATCAATGTGATCTGCCCAACCAACCATCTCACAAACAATAATAGAGAA 554  
QY 301 GAATCTGTTCAACAAGTGAATGTAGAAAGATTCAACGATACAGATTTTGGTAACTCT 360  
Db 555 GAATCTGTTCAACAAGTGAATGTAGAAAGATTCAACGATACAGATTTTGGTAACTCT 614  
QY 361 AAAATAAAGAGAGTAACACTGAATCTGCTTAAGAGAGAACTACTATAGAGCAACTAAT 420  
Db 615 AAAATAAAGAGAGTAACACTGAATCTGCTTAAGAGAGAACTACTATAGAGCAACTAAT 674  
QY 421 AAAATAAAGAGAGTAACACTGAATCTGCTTAAGAGAGAACTACTATAGAGCAACTAAT 480  
Db 675 AAAATAAAGAGAGTAACACTGAATCTGCTTAAGAGAGAACTACTATAGAGCAACTAAT 734  
QY 481 ATTTCAAATCAAGATGAGTTATTAATTTTCAATTAATGAAATGAAATGAAAGCTAGA 540  
Db 735 ATTTCAAATCAAGATGAGTTATTAATTTTCAATTAATGAAATGAAAGCTAGA 794  
QY 541 CCATATCTACACATCTGCCCAACCATCGATTAACCGTGAACCGTAAATCAATTAGCG 600  
Db 795 CCATATCTACACATCTGCCCAACCATCGATTAACCGTGAACCGTAAATCAATTAGCG 854  
QY 601 GCGGAACAAGGTTTCAAGTGTAAACCAATTTTAAAGTTTACTGATCAAAAGTATTAAGTAA 660  
Db 855 GCGGAACAAGGTTTCAAGTGTAAACCAATTTTAAAGTTTACTGATCAAAAGTATTAAGTAA 914  
QY 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Db 915 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 974  
QY 721 GTAACCTTTGAAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
Db 975 GTAACCTTTGAAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1034  
QY 781 AAGAATACAGTTTCCATCAGATTTAACCGATAGCTTTTACAAATACCAAAATAAAGATAAT 840  
Db 1035 AAGAATACAGTTTCCATCAGATTTAACCGATAGCTTTTACAAATACCAAAATAAAGATAAT 1094  
QY 841 TCTGGAGAAATCATCGCTACAGTACTTATGATAACAAAAATAAACAATCACTATACT 900  
Db 1095 TCTGGAGAAATCATCGCTACAGTACTTATGATAACAAAAATAAACAATCACTATACT 1154  
QY 901 TTTACAGATTATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
Db 1155 TTTACAGATTATGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1214  
QY 961 ATTGATAAATCAAGGTTTCAAAATATAATACCAAGTTAGATGATGATGATGATGATGATGAT 1020  
Db 1215 ATTGATAAATCAAGGTTTCAAAATATAATACCAAGTTAGATGATGATGATGATGATGATGAT 1274  
QY 1021 CTTTCATCAGTAAATAAACAATTTACGGTTGAATATCAAGACCTAAACGAAATCGGACT 1080  
Db 1275 CTTTCATCAGTAAATAAACAATTTACGGTTGAATATCAAGACCTAAACGAAATCGGACT 1334  
QY 1081 GCTAACCTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140

Db 1335 GCTAACCTTTCAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAACG 1394  
QY 1141 ATTTATATTAACCCCTCTTCGTTATTTCAGCCAAAGGAAACAAATGTAAATATTTTCAGGGAAT 1200  
Db 1395 ATTTATATTAACCCCTCTTCGTTATTTCAGCCAAAGGAAACAAATGTAAATATTTTCAGGGAAT 1454  
QY 1201 GGTGATGAAGGTTTCAACAATTTATAGACGATAGACAAATTAATAAGTTTATATAAGTTGGA 1260  
Db 1455 GGTGATGAAGGTTTCAACAATTTATAGACGATAGACAAATTAATAAGTTTATATAAGTTGGA 1514  
QY 1261 GATAATCAAAATTTACCAGATAGTACAGAAATTTATGATTACAGTCAATATAGAGATGTC 1320  
Db 1515 GATAATCAAAATTTACCAGATAGTACAGAAATTTATGATTACAGTCAATATAGAGATGTC 1574  
QY 1321 ACAATATGATGATTTATGCCCCAATTTAGGAAATAATAATGATGTGAATTAATTTTGGTAAT 1380  
Db 1575 ACAATATGATGATTTATGCCCCAATTTAGGAAATAATAATGATGTGAATTAATTTTGGTAAT 1634  
QY 1381 ATAGATTTCAACCATATATTTATTAAGGTTTATAGTAAATATGACCCCTAAATAGGATGATTAC 1440  
Db 1635 ATAGATTTCAACCATATATTTATTAAGGTTTATAGTAAATATGACCCCTAAATAGGATGATTAC 1694  
QY 1441 ACAGCTATACAGCAAACTGTGACATGACAGCACTATAAATGAGTATATCTGGTGAATTT 1500  
Db 1695 ACAGCTATACAGCAAACTGTGACATGACAGCACTATAAATGAGTATATCTGGTGAATTT 1754  
QY 1501 AGAACAGCATCTTATGATAATAACAATTTGCTTTCTCTACAGTTTCAGGTCAGGACAAGGT 1560  
Db 1755 AGAACAGCATCTTATGATAATAACAATTTGCTTTCTCTACAGTTTCAGGTCAGGACAAGGT 1814  
QY 1561 GACTTGCCTCTTGAAAAAATTTATTAATTCGGAGATTACGTTATGGAAGATGTAGATAAA 1620  
Db 1815 GACTTGCCTCTTGAAAAAATTTATTAATTCGGAGATTACGTTATGGAAGATGTAGATAAA 1874  
QY 1621 GATGTTATTCAAATACAAATGATTAATGAAACACCGCTTAGTAATGTATTGGTAACTTTG 1680  
Db 1875 GATGTTATTCAAATACAAATGATTAATGAAACACCGCTTAGTAATGTATTGGTAACTTTG 1934  
QY 1681 ACCTATCTGATGGAACCTTCAAAATCAGTCAGAACAGATGGAAGTGGGAAATATCAATTT 1740  
Db 1935 ACCTATCTGATGGAACCTTCAAAATCAGTCAGAACAGATGGAAGTGGGAAATATCAATTT 1994  
QY 1741 GATGGA 1746  
Db 1995 GATGGA 2000

RESULT 3  
AR533704  
LOCUS AR533704  
DEFINITION Sequence 14 from patent US 6733758.  
ACCESSION AR533704  
VERSION AR533704.1 GI:53923722  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3600)  
AUTHORS Guss,B., Nilsson,M., Frykberg,L., Flock,J.-I. and Lindberg,M.  
TITLE Fibrinogen binding protein originating from coagulase-negative staphylococcus  
JOURNAL Patent: US 6733758-A 14 11-MAY-2004;  
FEATURES  
source Location/Qualifiers  
1..3600  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 100.0%; Score 1746; DB 2; Length 3600;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCTAGTGATGAAGAAAGAAAGATGATGTGATCAATTAATAACAGTCAATAAACAACCGACGAT 60





```
Db      1760 AGAACAGCATCCTATGATAATACAAATGCTTTCTCTCAAGTTTCAGGTCAAGGACAAGGT 1819
Qy      1561 GACTTGCCTCTCGAAGAACTTATATAATCGGAGATTACGTATGGGAAGATGTAGATAAA 1620
Db      1820 GACTTGCCTCTCGAAGAACTTATATAATCGGAGATTACGTATGGGAAGATGTAGATAAA 1879
Qy      1621 GATGCTATTCAAATACAAATGATATGAAATACCGCTTAGTAAATGTTTGGTAACTTTG 1680
Db      1880 GATGCTATTCAAATACAAATGATATGAAATACCGCTTAGTAAATGTTTGGTAACTTTG 1939
Qy      1681 ACGTATCCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT 1740
Db      1940 ACGTATCCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT 1999
Qy      1741 GATGGA 1746
Db      2000 GATGGA 2005

RESULT 5
BD009812
LOCUS      1781 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Novel fibrinogen binding protein originating from
ACCESSION BD009812
VERSION   BD009812.1 GI:18638185
KEYWORDS JP 2001503609-A/10.
SOURCE    Staphylococcus epidermidis
ORGANISM  Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 1781)
AUTHORS   Guss,B., Nilsson,M., Frykberg,L., Flock,J.I. and Lindberg,M.
TITLE     Novel fibrinogen binding protein originating from
           coagulase-negative staphylococcus
JOURNAL   Patent: JP 2001503609-A 10 21-MAR-2001;
           BENGT GUSS,MARTIN NILSSON,LARS FRYKBERG,JAN INGVAR FLOCK, ARTIN
           LINDBERG
COMMENT   OS Staphylococcus epidermidis
           PN JP 2001503609-A/10
           PD 21-MAR-2001
           PF 18-JUN-1997 JP 1998502819
           PR 20-JUN-1996 SE 9602496-3
           PI BENGT GUSS,MARTIN NILSSON,LARS FRYKBERG,JAN INGVAR FLOCK, PI
           MARTIN LINDBERG
           PC C07K14/31
           CC
           FH Key Location/Qualifiers
           FT CDS (3)..(1781).

FEATURES             source
             1..1781
             Location/Qualifiers
             /organism="Staphylococcus epidermidis"
             /mol_type="genomic DNA"
             /db_xref="taxon:1282"

ORIGIN
Query Match 99.9%; Score 1745; DB 2; Length 1781;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1745; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TCTAGTGATGAAGAAAGAAATGATGTGATCAATAATATATCACTCAATAAACAACCGACGAT 60
Db      24 TCTAGTGATGAAGAAAGAAATGATGTGATCAATATATATCACTCAATAAACAACCGACGAT 83
Qy      61 AATAACCAAAATTAATAAAGAAAGAAACGAATAACTACGATGGCATAGAAAAACGCTCA 120
Db      84 AATAACCAAAATTAATAAAGAAAGAAACGAATAACTACGATGGCATAGAAAAACGCTCA 143
Qy      121 GAAGATAGACAGCTCAACAAATGTAGATGAAGAAAGCAACATTTTTCACAAAG 180
Db      144 GAAGATAGACAGCTCAACAAATGTAGATGAAGAAAGCAACATTTTTCACAAAG 203
Qy      181 ACCCCTCAAGATAAATCTCATCTTACAGAAAGAGGTAAAAAGAAATCCTCATCAGTCGAA 240
```

```
Db      204 ACCCCTCAAGATAAATCTCATCTTTACAGAAAGAGGTAAAAAGAAATCCTCATCAGTCGAA 263
Qy      241 TCCTCAAATTCATCAATTTGATACCTGCCCAACAACATCTCTCACAAACAATTAATAGAGAA 300
Db      264 TCCTCAAATTCATCAATTTGATACCTGCCCAACAACATCTCTCACAAACAATTAATAGAGAA 323
Qy      301 GAATCTGTTTCAAAACAAGTGATAATGTAGAAGATTACACAGTATCAGATTTTGTCTAACTCT 360
Db      324 GAATCTGTTTCAAAACAAGTGATAATGTAGAAGATTACACAGTATCAGATTTTGTCTAACTCT 383
Qy      361 AAAATAAAGAGAGCTAACACATCTGGTAAAGAGAGAAATACTATAGACCAACCTAAT 420
Db      384 AAAATAAAGAGAGCTAACACATCTGGTAAAGAGAGAAATACTATAGACCAACCTAAT 443
Qy      421 AAAGTAAAGAGAGATTCAACAAGTCAGCCGCTCGGCTATACAAATATATAGATGAAAAA 480
Db      444 AAAGTAAAGAGAGATTCAACAAGTCAGCCGCTCGGCTATACAAATATATAGATGAAAAA 503
Qy      481 ATTTCAAATCAAGATGAGTTATTAAATTTTCAACAATAATGAATATGAAAAATAAGGCTAGA 540
Db      504 ATTTCAAATCAAGATGAGTTATTAAATTTTCAACAATAATGAATATGAAAAATAAGGCTAGA 563
Qy      541 CCATTATCTCAACATCTGCCCAACCATCGATTAAACGCTGTAACCGTAAATCAATTAGCG 600
Db      564 CCATTATCTCAACATCTGCCCAACCATCGATTAAACGCTGTAACCGTAAATCAATTAGCG 623
Qy      601 GCGGAACAGGTTTCAAGTTCGAATTTAAACCATTAATTAAGTTACTGATCAAGTATTACTGAA 660
Db      624 GCGGAACAGGTTTCAAGTTCGAATTTAAACCATTAATTAAGTTACTGATCAAGTATTACTGAA 683
Qy      661 GGATATGATGATAGTGAAGGTGTTTATTAAAGCACATGATGCTGAAAACTTAATCTATGAT 720
Db      684 GGATATGATGATAGTGAAGGTGTTTATTAAAGCACATGATGCTGAAAACTTAATCTATGAT 743
Qy      721 GTAACTTTTGAAGTAGATGATAAGGTGAAATCTCGTGTATACGATACAGTGGATATAGAT 780
Db      744 GTAACTTTTGAAGTAGATGATAAGGTGAAATCTCGTGTATACGATACAGTGGATATAGAT 803
Qy      781 AAGAAATACAGTTCCATCGATTTAACCGATAGCTTTTACAAATACCAAAAATAAAGATATAT 840
Db      804 AAGAAATACAGTTCCATCGATTTAACCGATAGCTTTTACAAATACCAAAAATAAAGATATAT 863
Qy      841 TCTGAGAGAAATCATCGCTACAGGTACTTTATGATAACAAAAATAAACAATCACCTATACT 900
Db      864 TCTGAGAGAAATCATCGCTACAGGTACTTTATGATAACAAAAATAAACAATCACCTATACT 923
Qy      901 TTTACAGATTATGTAGATAGTATGAAATAATTTAAAGCACACCTTTAAATTTAAGCTCATAC 960
Db      924 TTTACAGATTATGTAGATAGTATGAAATAATTTAAAGCACACCTTTAAATTTAAGCTCATAC 983
Qy      961 ATTGATAAATCAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATATAAACAACGGCC 1020
Db      984 ATTGATAAATCAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATATAAACAACGGCC 1043
Qy      1021 CTTTCATCAGTAAATAAAACAATTAACGGTTCGAATATCAAGAACCTTAACGAAAAATCGGACT 1080
Db      1044 CTTTCATCAGTAAATAAAACAATTAACGGTTCGAATATCAAGAACCTTAACGAAAAATCGGACT 1103
Qy      1081 GCTAACCTTCAAGATGTGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAAAACG 1140
Db      1104 GCTAACCTTCAAGATGTGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAAAACG 1163
Qy      1141 ATTTATATTAACCTCTTCGTTTATTCAGCCCAAGGAAACAAATGTAAATTTTTCAGGGAT 1200
Db      1164 ATTTATATTAACCTCTTCGTTTATTCAGCCCAAGGAAACAAATGTAAATTTTTCAGGGAT 1223
Qy      1201 GGTGATGAAGGTTCAACAATTTATAGACGATAGCACAATAATTAAGTTTATAAGGTTGGA 1260
Db      1224 GGTGATGAAGGTTCAACAATTTATAGACGATAGCACAATAATTAAGTTTATAAGGTTGGA 1283
Qy      1261 GATAATCAAAATTTTACAGATAGTAAACAGAAATTTATGATTCAGTGAATATGAAGATGTC 1320
Db      1284 GATAATCAAAATTTTACAGATAGTAAACAGAAATTTATGATTCAGTGAATATGAAGATGTC 1343
```





```

Qy 1321 ACAATGATGATTATGCCCAATTAGCAATAATAATGATGCGAATATTAATTTTGGTAAT 1380
Db 1344 ACAATGATGATTATGCCCAATTAGCAATAATAATGATGCGAATATTAATTTTGGTAAT 1403
Qy 1381 ATAGATTCCACCATATATTATTAAAGTTATTAGTAAATATGACCCCTAAATAAGGATGATTAC 1440
Db 1404 ATAGATTCCACCATATATTATTAAAGTTATTAGTAAATATGACCCCTAAATAAGGATGATTAC 1463
Qy 1441 ACGACTATACAGCAAACTGTGCAATGCAGACGACTATAAATGAGTATCTGGTGAGTTT 1500
Db 1464 ACGACTATACAGCAAACTGTGCAATGCAGACGACTATAAATGAGTATCTGGTGAGTTT 1523
Qy 1501 AGAAGAGCATCTATGATATAACAATTTGCTTCTCTACAGTTTCAGGTCAGGACAAGGT 1560
Db 1524 AGAAGAGCATCTATGATATAACAATTTGCTTCTCTACAGTTTCAGGTCAGGACAAGGT 1583
Qy 1561 GACTTGGCTCCCTGAAAAAACCTTATAAAATCGGAGATTACGATGCGAAGATGTAGATAAA 1620
Db 1584 GACTTGGCTCCCTGAAAAAACCTTATAAAATCGGAGATTACGATGCGAAGATGTAGATAAA 1643
Qy 1621 GATGGTATTCAAATACAAATGATTAATGAAAACCGCTTAGTAAATGTTTGGTAACTTTG 1680
Db 1644 GATGGTATTCAAATACAAATGATTAATGAAAACCGCTTAGTAAATGTTTGGTAACTTTG 1703
Qy 1681 ACGTATCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGGAATATCAATTT 1740
Db 1704 ACGTATCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGGAATATCAATTT 1763
Qy 1741 GATGG 1745
Db 1764 GATGG 1768

```

```

RESULT 7
LOCUS BD009813 1744 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel fibrinogen binding protein originating from
coagulase-negative staphylococcus.
ACCESSION BD009813
VERSION BD009813.1 GI:18638186
KEYWORDS JP 2001503609-A/11.
SOURCE Staphylococcus epidermidis
ORGANISM Staphylococcus epidermidis
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 1744)
AUTHORS Guss,B., Nilsson,M., Frykberg,L., Flock,J.I. and Lindberg,M.
TITLE Novel fibrinogen binding protein originating from
coagulase-negative staphylococcus
JOURNAL Patent: JP 2001503609-A 11 21-MAR-2001;
BENGT GUSS,MARTIN NILSSON,LARS FRYKBERG,JAN INGMAR FLOCK, ARTIN
LINDBERG
COMMENT OS Staphylococcus epidermidis
PN JP 2001503609-A/11
PD 21-MAR-2001
PF 18-JUN-1997 JP 199802819
PR 20-JUN-1996 SE 9602496-3
PI BENGT GUSS,MARTIN NILSSON,LARS FRYKBERG,JAN INGMAR FLOCK, PI
MARTIN LINDBERG
PC C07K14/31
CC
FH Key Location/Qualifiers
FT source 1..1744
FT /organism='Staphylococcus epidermidis'.
FEATURES
source 1..1744
/organism='Staphylococcus epidermidis'
/mol_type='genomic DNA'
/db_xref='taxon:1282'
ORIGIN
Query Match 99.9%; Score 1744; DB 2; Length 1744;
Best Local Similarity 100.0%; Pred. No. 0;

```

```

Matches 1744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCTAGTGATGAAGAAAAGAATGATGTGATCAATTAATTAATCAATCAATTAATAAACAACCGACGAT 60
Db 1 TCTAGTGATGAAGAAAAGAATGATGTGATCAATTAATTAATCAATCAATTAATAAACAACCGACGAT 60
Qy 61 AATAACCAAAATAATTTAAAAAAGAAAGAACGAATTAACATGATGGCATAGAAAACGGCTCA 120
Db 61 AATAACCAAAATAATTTAAAAAAGAAAGAACGAATTAACATGATGGCATAGAAAACGGCTCA 120
Qy 121 GAAGATAGAAACAGAGTCAACAAACAAATGTAGATGAAAAAGAAAGCAACATTTTTTACAAAAG 180
Db 121 GAAGATAGAAACAGAGTCAACAAACAAATGTAGATGAAAAAGAAAGCAACATTTTTTACAAAAG 180
Qy 181 ACCCTCTCAAGATAATATCTCATCTTTACAGAAAGAGGTAAAAAGAAATCTCTCATCAGTCGAA 240
Db 181 ACCCTCTCAAGATAATATCTCATCTTTACAGAAAGAGGTAAAAAGAAATCTCTCATCAGTCGAA 240
Qy 241 TCCTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCACACAACAAATAAATAGAGAA 300
Db 241 TCCTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCACACAACAAATAAATAGAGAA 300
Qy 301 GAATCTGTGTTCAAAACAAGTGATAATGTAGAAAGATTACACCGTATCAGATTTTTGCTAACTCT 360
Db 301 GAATCTGTGTTCAAAACAAGTGATAATGTAGAAAGATTACACCGTATCAGATTTTTGCTAACTCT 360
Qy 361 AAAATAAAGAGAGTAACACTGAATCTGGTAAAGAGAGAAATCTATATAGAGCAACCTTAAT 420
Db 361 AAAATAAAGAGAGTAACACTGAATCTGGTAAAGAGAGAAATCTATATAGAGCAACCTTAAT 420
Qy 421 AAAGTAAAGAGAGATTCAACAAACAAGTCAGCCGCTGCTGTATACAAATATATAGATGAAAAA 480
Db 421 AAAGTAAAGAGAGATTCAACAAACAAGTCAGCCGCTGCTGTATACAAATATATAGATGAAAAA 480
Qy 481 ATTTCAAATCAAGATGAGTTTAAATTTTAAATTAACAATAATTAATGAATTAAGGCTAGA 540
Db 481 ATTTCAAATCAAGATGAGTTTAAATTTTAAATTAACAATAATTAAGGCTAGA 540
Qy 541 CCATTTATCAACAATCTGCCCAACCATCGATTAACCGTGTAAACGGTAAATCAATTAGCG 600
Db 541 CCATTTATCAACAATCTGCCCAACCATCGATTAACCGTGTAAACGGTAAATCAATTAGCG 600
Qy 601 GCGGAACAAGGTTTCGAATGTTAAACATTTAAAGTTTACTGTCAAGTATTACTGAA 660
Db 601 GCGGAACAAGGTTTCGAATGTTAAACATTTAAAGTTTACTGTCAAGTATTACTGAA 660
Qy 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Qy 721 GTAACTTTTGAAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 721 GTAACTTTTGAAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy 781 AAGAATACAGTTTCCATCAGATTTTAAACCGATAGCTTTTAAATCAACAAAAATAAAGATAAT 840
Db 781 AAGAATACAGTTTCCATCAGATTTTAAACCGATAGCTTTTAAATCAACAAAAATAAAGATAAT 840
Qy 841 TCTGAGAAAAATCATCGCTACAGGTACTTTATGATAACAAAAATAAACAATCACTTACT 900
Db 841 TCTGAGAAAAATCATCGCTACAGGTACTTTATGATAACAAAAATAAACAATCACTTACT 900
Qy 901 TTTACAGATTATGTAGATAAGTATGAAATAATTAAGACACACCTTTAAATTAACGTCATAC 960
Db 901 TTTACAGATTATGTAGATAAGTATGAAATAATTAAGACACACCTTTAAATTAACGTCATAC 960
Qy 961 ATTGATAAATCAAAAGTTTCCAAATAATTAATACCAAGTTAGTATGATATATAAAGCGCC 1020
Db 961 ATTGATAAATCAAAAGTTTCCAAATAATTAATACCAAGTTAGTATGATATATAAAGCGCC 1020
Qy 1021 CTTTCATCAGTAAATAAACAATTAACGGTTGAATATCAAGACCTTAACGAAATCGGACT 1080
Db 1021 CTTTCATCAGTAAATAAACAATTAACGGTTGAATATCAAGACCTTAACGAAATCGGACT 1080

```



QY	1081	GCTAACCTTCAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAAAACG	1140
Db	1081	GCTAACCTTCAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAAAACG	1140
QY	1141	ATTATATTAAACCTCTTCGTTATTCAGCCAGGAAACAAATGTAATATTTTCAGGGAAT	1200
Db	1141	ATTATATTAAACCTCTTCGTTATTCAGCCAGGAAACAAATGTAATATTTTCAGGGAAT	1200
QY	1201	GGTGATGAAGGTTCAACAAATATAGACGATAGACAAATATTAAGTTTATAGGTTTGA	1260
Db	1201	GGTGATGAAGGTTCAACAAATATAGACGATAGACAAATATTAAGTTTATAGGTTTGA	1260
QY	1261	GATAATCAAATTTACAGATAGTAACAGAAATTTATGATTCACAGTGAATGAAGATGTC	1320
Db	1261	GATAATCAAATTTACAGATAGTAACAGAAATTTATGATTCACAGTGAATGAAGATGTC	1320
QY	1321	ACAAATGATGATTTATGCCCAATTTAGGAATTAATGATGTTGAATATTAATTTTGGTAAT	1380
Db	1321	ACAAATGATGATTTATGCCCAATTTAGGAATTAATGATGTTGAATATTAATTTTGGTAAT	1380
QY	1381	ATAGATTCACCATATATTTAAAGTTTATAGTAAATATGACCTTAATAGGATGATTAC	1440
Db	1381	ATAGATTCACCATATATTTAAAGTTTATAGTAAATATGACCTTAATAGGATGATTAC	1440
QY	1441	ACGACTATACAGCAAACTGTGCAATGCGACGACTATATAATGAGTATATCTGGTGAGTTT	1500
Db	1441	ACGACTATACAGCAAACTGTGCAATGCGACGACTATATAATGAGTATATCTGGTGAGTTT	1500
QY	1501	AGAACAGATCCTATGATTAATACAAATGCTTCTCTACAGTTTCAGGTCAAGCAAGGT	1560
Db	1501	AGAACAGATCCTATGATTAATACAAATGCTTCTCTACAGTTTCAGGTCAAGCAAGGT	1560
QY	1561	GACTTGCCTCCTGAAAAAATTTATAAAATCGGAGATTACGTATGGGAAGATGTAGATAAA	1620
Db	1561	GACTTGCCTCCTGAAAAAATTTATAAAATCGGAGATTACGTATGGGAAGATGTAGATAAA	1620
QY	1621	GATGGTATTTCAAATAACAAATGATAATGAAAAACCGCTTTAGTAATGATTTGGTAACTTTG	1680
Db	1621	GATGGTATTTCAAATAACAAATGATAATGAAAAACCGCTTTAGTAATGATTTGGTAACTTTG	1680
QY	1681	ACGTATCCTGATGGAACTTTCAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT	1740
Db	1681	ACGTATCCTGATGGAACTTTCAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT	1740
QY	1741	GATG 1744	
Db	1741	GATG 1744	

RESULT 8  
AE015929\_03  
WPCOMMENT

Sequence split into 25 fragments LOCUS AE015929 Accession AE015929

Fragment Name	Begin	End
AE015929_00	1	110000
AE015929_01	100001	210000
AE015929_02	200001	310000
AE015929_03	300001	410000
AE015929_04	400001	510000
AE015929_05	500001	610000
AE015929_06	600001	710000
AE015929_07	700001	810000
AE015929_08	800001	910000
AE015929_09	900001	1010000
AE015929_10	1000001	1110000
AE015929_11	1100001	1210000
AE015929_12	1200001	1310000
AE015929_13	1300001	1410000
AE015929_14	1400001	1510000
AE015929_15	1500001	1610000
AE015929_16	1600001	1710000
AE015929_17	1700001	1810000

AE015929_18	1800001	1910000
AE015929_19	1900001	2010000
AE015929_20	2000001	2110000
AE015929_21	2100001	2210000
AE015929_22	2200001	2310000
AE015929_23	2300001	2410000
AE015929_24	2400001	249279
Continuation (4 of 25) of AE015929 from base 300001 (AE015929 Staphylococcus epidermidis)		
Query Match 99.8%; Score 1742.8; DB 15; Length 110000;		
Best Local Similarity 99.9%; Pred. No. 0;		
Matches 1744; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	1	TCTAGTGATGAAGAAAGAAATGATGTGATCAATAATAATCAGTCAATAAACCCGACGAT 60
Db	32323	TCTAGTGATGAAGAAAGAAATGATGTGATCAATAATAATCAGTCAATAAACCCGACGAT 32382
QY	61	AATACCAATTAATTAATAAAGAAAGAAATGATGTGATCAATAATAATCAGTCAATAAACCCGACGAT 120
Db	32383	AATAACCAATTAATTAATAAAGAAAGAAATGATGTGATCAATAATAATCAGTCAATAAACCCGACGAT 32442
QY	121	GAAGATAGAACAGAGTCAACAAATGTAGATGAAGAAAGAAAGAAATGATGTGATCAATAATAATCAGTCAATAAACCCGACGAT 180
Db	32443	GAAGATAGAACAGAGTCAACAAATGTAGATGAAGAAAGAAAGAAATGATGTGATCAATAATAATCAGTCAATAAACCCGACGAT 32502
QY	181	ACCCCTCAAGATAATACTCATCTTACAGAAAGAGAGTAAAGAAATCCTCATCAGTCGAA 240
Db	32503	ACCCCTCAAGATAATACTCATCTTACAGAAAGAGAGTAAAGAAATCCTCATCAGTCGAA 32562
QY	241	TCTCAAATTCATCAATGATGATCTGCCCAACCAACCATCTCACACAAATAATAGAGAA 300
Db	32563	TCTCAAATTCATCAATGATGATCTGCCCAACCAACCATCTCACACAAATAATAGAGAA 32622
QY	301	GAATCTGTTTCAACCAAGTGAATGATGAGAAATTCACAGTATCAGATTTTGTCTACTCT 360
Db	32623	GAATCTGTTTCAACCAAGTGAATGATGAGAAATTCACAGTATCAGATTTTGTCTACTCT 32682
QY	361	AAAAATAAGAGAGTAACAACATCTGTTAAAGAGAGAAATATCTATAGAGCAACCTAAT 420
Db	32683	AAAAATAAGAGAGTAACAACATCTGTTAAAGAGAGAAATATCTATAGAGCAACCTAAT 32742
QY	421	AAAGTAAAGAGAGTCAACAAAGTCAGCGCTCTGGCTATACAAATATAGATGAAAAA 480
Db	32743	AAAGTAAAGAGAGTCAACAAAGTCAGCGCTCTGGCTATACAAATATAGATGAAAAA 32802
QY	481	ATTTCAATCAAGATGAGTTTAAATTTACCAATAAATGAATATCAAAATAAGGCTAGA 540
Db	32803	ATTTCAATCAAGATGAGTTTAAATTTACCAATAAATGAATATCAAAATAAGGCTAGA 32862
QY	541	CCATTATCTACAAATCTGCCCAACCATCGATTTAAACGTTGAACCGTAAATCAATTTAGCG 600
Db	32863	CCATTATCTACAAATCTGCCCAACCATCGATTTAAACGTTGAACCGTAAATCAATTTAGCG 32922
QY	601	CGGAAACAGGTTTCAAGATTTAAACCAATTTAAAGTTTACTGATCAAAAGTATTTACTGAA 660
Db	32923	CGGAAACAGGTTTCAAGATTTAAATCATTTTAAAGTTTACTGATCAAAAGTATTTACTGAA 32982
QY	661	GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db	32983	GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 33042
QY	721	GTAACTTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db	33043	GTAACTTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 33102
QY	781	AAGAAATACAGTTTCCATCAGATTTTAAACCGATCTTTTACAAATACCAAAAAATAAAGATAAT 840
Db	33103	AAGAAATACAGTTTCCATCAGATTTTAAACCGATCTTTTACAAATACCAAAAAATAAAGATAAT 33162
QY	841	TCTGGAGAAATCATCGCTACAGGTTTATGATTAACAAATAAATAAATAAATAAATAAATAAATA 900
Db	33163	TCTGGAGAAATCATCGCTACAGGTTTATGATTAACAAATAAATAAATAAATAAATAAATAAATA 33222

Qy	901	TTTACAGATTATGTGATGAATGATGAAAAATATTTAAAGCACACCTTAAATTAACGTCATAC	960
Db	33223	TTTACAGATTATGTGATGAATGATGAAAAATATTTAAAGCACACCTTAAATTAACGTCATAC	33282
Qy	961	ATTGATAAATCAAAGGTTCCAAATATATATACCAAGTTAGATGTAGATATATAAAGCGCC	1020
Db	33283	ATTGATAAATCAAAGGTTCCAAATATATATACCAAGTTAGATGTAGATATATAAAGCGCC	33342
Qy	1021	CTTTTCATCAGTAAATAAAACAAATTACGGTTGAAATATCAAAAGACCTTAAACGAAATCCGACT	1080
Db	33343	CTTTTCATCAGTAAATAAAACAAATTACGGTTGAAATATCAAAAGACCTTAAACGAAATCCGACT	33402
Qy	1081	GCTAACCTTCAAAGTATGTTTACAAATATAGATACAGAAAAATCATACAGTTGAGCAACG	1140
Db	33403	GCTAACCTTCAAAGTATGTTTACAAACATAGATACAGAAAAATCATACAGTTGAGCAACG	33462
Qy	1141	ATTATATATTAACCGTCTTCGTTATTCAGCGAAGGAAAAATGTTAAATATTTTCAGGGAAT	1200
Db	33463	ATTATATATTAACCGTCTTCGTTATTCAGCGAAGGAAAAATGTTAAATATTTTCAGGGAAT	33522
Qy	1201	GGTGATGAAGGTTCAACAATTTATAGACGATAGCACAAATAATTTAAAGTTTATAAGGTTGGA	1260
Db	33523	GGTGATGAAGGTTCAACAATTTATAGACGATAGCACAAATAATTTAAAGTTTATAAGGTTGGA	33582
Qy	1261	GATAATCAAAATTTTACCAGATAGTAAACAGAAATTTATGATTACAGTGAATATGAAGATGTC	1320
Db	33583	GATAATCAAAATTTTACCAGATAGTAAACAGAAATTTATGATTACAGTGAATATGAAGATGTC	33642
Qy	1321	ACAAATGATGATTATGCCCCAATTAGGAAATATAATATGATGTGAAATATTAATTTTGGTAAAT	1380
Db	33643	ACAAATGATGATTATGCCCCAATTAGGAAATATAATATGATGTGAAATATTAATTTTGGTAAAT	33702
Qy	1381	ATAGATTCACCATATATTATTAAGTTATTAGTAAATATGACCCCTAATAAGGATCATTTAC	1440
Db	33703	ATAGATTCACCATATATTATTAAGTTATTAGTAAATATGACCCCTAATAAGGATCATTTAC	33762
Qy	1441	ACGACTATACAGCAAACTGTGACAAATCGACAGACCTATAAAATGAGTATACTGGTGAGTTT	1500
Db	33763	ACGACTATACAGCAAACTGTGACAAATCGACAGACCTATAAAATGAGTATACTGGTGAGTTT	33822
Qy	1501	AGAACAGCATCCTATGATATAACAATTTGCTTTCTCTCAAGTTTCAGGTCAGGCAACAGGT	1560
Db	33823	AGAACAGCATCCTATGATATAACAATTTGCTTTCTCTCAAGTTTCAGGTCAGGCAACAGGT	33882
Qy	1561	GACTTGCTCCTGAAAAAACTTATAAAATCGGAGATTACGTATGGAGAGTGTAGATAAA	1620
Db	33883	GACTTGCTCCTGAAAAAACTTATAAAATCGGAGATTACGTATGGAGAGTGTAGATAAA	33942
Qy	1621	GATGGTATTCAAATACAAATGATATGAAAAACCGCTTAGTAAATGTTATGTTAACTTTG	1680
Db	33943	GATGGTATTCAAATACAAATGATATGAAAAACCGCTTAGTAAATGTTATGTTAACTTTG	34002
Qy	1681	ACGTATCCTGATGGAACTTCAAATCAGTCAGAAACAGATGAAAGTGGGAAATATCAATTT	1740
Db	34003	ACGTATCCTGATGGAACTTCAAATCAGTCAGAAACAGATGAAAGTGGGAAATATCAATTT	34062
Qy	1741	GATGGA 1746	
Db	34063	GATGGA 34068	

[illegible]



Db 517 GCATCTATTCAACCAAGTGATAATGAAGAAATTTCCCGCGTATCAGATTTTGTGCTAACTCT 576

Qy 361 AAAATAAAGAGAGTAACACTGAATCTGTGTTAAAGAGAGAAATACCTATAGAGCAACCTTAAT 420

Db 577 AAAATAATAGAGAGTAACACTGAATCCCAATAAAGAGAGAAATACCTATAGAGCAACCTTAAC 636

Qy 421 AAAGTAAAGAGAGATTCAACCAACAGTCAGCGCTCTGGCTATACAAATATATAGATGAAGAAA 480

Db 637 AAAGTAAAGAGAGATTCAATTAACCAAGTCACCGTCTAGCTATAAAATATATAGATGAAGAAA 696

Qy 481 ATTTCAAATCAAGATGAGTATTAATTTTAAATTTTCAATATAATGAATATGAAGTAAAGCTAGA 540

Db 697 ATTTCAAATCAAGATGAGTATTAATTTTAAATTTTCAATATAATGAATATGAAGTAAAGCTAGA 756

Qy 541 CCATTATCTACAACATCTGCCCAACCAATCGATTTAAACCGTGTAAACCGTAAATCAATTAGCG 600

Db 757 CCGTTATCTACAACATCTGCCCAACCAATCGAGTAAAGCGTGTAAACCGTAAATCAATTAGCG 816

Qy 601 CGGGAACAAGGTTCCGAATGTTAAACCAATTTAATTAAGTTTACTGATCAAGTATTACTGAA 660

Db 817 GCAGAACCAAGGTTCCGAATGTTAATCAATTTAATTAAGTTTACTGATCAAGTATTACTGAA 876

Qy 661 GGATATGATGATGAGGAGGTTTATTAAAGCACATGATGCTGAAACCTTAACTTATCTATGAT 720

Db 877 GGATATGATGATGAGGAGGTTTATTAAAGCACATGATGCTGAAACCTTAACTTATCTATGAT 936

Qy 721 GTAACTTTTGAAGTATGATAAGGTGAAATCTCGTGATACGATGACAGTGGATATAGAT 780

Db 937 GTAACTTTTGAAGTATGATAAGGTGAAATCTCGTGATACGATGACAGTGGATATAGAT 996

Qy 781 AAGATACAGTTCACATCAGATTTAACCGATAGCTTTCAATACCAAAATTAAGATAT 840

Db 997 AAGATACAGTTCACATCAGATTTAACCAGTATGTTTGCATACCAAAATTAAGATAT 1056

Qy 841 TCTGAGAAATCATCGCTACAGGTACTTATGATAACAAATAAACAATCACCTTACT 900

Db 1057 TCTGAGAAATCATCGCTACAGGTACTTATGATAACAAATAAACAATCACCTTACT 1116

Qy 901 TTTACAGATTTATGATAGATGATAAGTATGAAATATTAAGCACACACTTAAATTAACGTATAC 960

Db 1117 TTTACAGATTTATGATAGATGATAAGTATGAAATATTAAGCGCACCTTAAATTAACATCATAC 1176

Qy 961 ATTGATTAATCAAGGTTCCAAATTAATTAACCAAGTTAGATGATAGATATAAAGCGCC 1020

Db 1177 ATTGATTAATCAAGGTTCCAAATTAATTAACCAAGTTAGATGATAGATATAAAGCGCC 1236

Qy 1021 CTTTCATCAGTAAATTAACCAATTAACGTTGAAATCAAGACCTTAACGAAATCGGACT 1080

Db 1237 CTTTCATCAGTAAATTAACCAATTAACGTTGAAATCAAGACCTTAACGAAATCGGACT 1296

Qy 1081 GCTAACCTTTCAAAGTATGTTTCAAAATATAGATACGAAATATCATACAGTTGAGCAACG 1140

Db 1297 GCTAACCTTTCAAAGTATGTTTCAAAATATAGATACGAAATATCATACAGTTGAGCAACG 1356

Qy 1141 ATTTATATTAACCTTTCCGTTATTTCCGCAAGGAACCAATGTTAAATTTTCAGGGAAT 1200

Db 1357 ATTTATATTAACCTTTCCGTTATTTCCGCAAGGAACCAATGTTAAATTTTCAGGGAAT 1416

Qy 1201 GGTGATGAAGGTTCAACCAATATAGACGATAGCAATAATTAAGTTTATAAGGTTTGA 1260

Db 1417 GGCATGAAGGTTTCAACCAATATAGACGATAGCAATAATTAAGTTTATAAGGTTTGA 1476

Qy 1261 GATAATCAAAATTTTCAAGATAGTAAACAGAAATTTATGATTAAGTGAATATGAAGATGTC 1320

Db 1477 GATAATCAAAATTTTCAAGATAGTAAACAGAAATTTATGATTAAGTGAATATGAAGATGTC 1536

Qy 1321 ACAAATGATGATTTATGCCCATTAGGAATATATATGATGATGATTAATTTTGGTAAAT 1380

Db 1537 ACAAATGATGATTTATGCCCATTAGGAATATATATGATGATGATTAATTTTGGTAAAT 1596

Qy 1381 ATAGATTTCAACCATATATTTAAAGTTTATAGTAAATATGACCCCTTAATGAAGATGATTAC 1440

Db 1597 ATAGATTTCAACCATATATTTAAAGTTTATAGTAAATATGACCCCTTAATGAAGATGATTAC 1656

Qy 1441 ACGCTATACAGCAAACTGTGACAACTGACAACTGACAACTGACAACTGACAACTGACAACTG 1500

Db 1657 ACGACGATACAGCAAACTGTGACAACTGACAACTGACAACTGACAACTGACAACTGACAACTG 1716

Qy 1501 AGAACAGATCCTCTATGATTAATCAAACTGCTTTCTTCAAACTGCTTTCAAACTGCTTTCAAACTG 1560

Db 1717 AGAACAGATCCTCTATGATTAATCAAACTGCTTTCTTCAAACTGCTTTCTTCAAACTGCTTTCAAACTG 1776

Qy 1561 GACTTGCTCTCTGAAAACTTATAAATCGGAGATTAACGATCGGAGATTAACGATCGGAGATTAACGAT 1620

Db 1777 GACTTGCTCTCTGAAAACTTATAAATCGGAGATTAACGATCGGAGATTAACGATCGGAGATTAACGAT 1836

Qy 1621 GATGCTATTCAAAATACAAATGATTAATGAAAAACCGCTTAGTATGATTAATGATTAATGATTAATG 1680

Db 1837 GATGCTATTCAAAATACAAATGATTAATGAAAAACCGCTTAGTATGATTAATGATTAATGATTAATG 1896

Qy 1681 ACGTATCCTGATGAACCTTCAAAATCAGTCAGAACAGATGAAGATGAAGATGAAGATGAAGATGAAG 1740

Db 1897 ACGTATCCTGATGAACCTTCAAAATCAGTCAGAACAGATGAAGATGAAGATGAAGATGAAGATGAAG 1956

Qy 1741 GATGG 1745

Db 1957 GATGG 1961

RESULT 11

BD245130

LOCUS

DEFINITION BD245130 2976 bp DNA linear PAT 17-JUL-2003

Polypeptides and polynucleotides derived from coagulase-negative staphylococci.

ACCESSION BD245130

VERSION BD245130.1 GI:33054900

KEYWORDS JP 2002528055-A/2.

SOURCE Staphylococcus epidermidis

ORGANISM Staphylococcus epidermidis

REFERENCE 1 (bases 1 to 2976)

AUTHORS Bacteria; Firmicutes; Bacillales; Staphylococcus.

1 (bases 1 to 2976)

Foster, T.J., Hook, M., Davis, S., Hartford, O., McCrea, K. and Eidhin, D.N.

TITLE Polypeptides and polynucleotides derived from coagulase-negative staphylococci

JOURNAL Patent: JP 2002528055-A 2 03-SEP-2002;

THE PROVOST FELLOWS AND SCHOLARS OF THE COLLEGE OF THE HOLY AND UNDIVIDED OF HIGHER EDUCATION TRINITY OF QUEEN ELIZABETH NEAR DUBLIN, THE TEXAS A AND M UNIVERSITY SYSTEM

COMMENT OS Staphylococcus epidermidis

PN JP 2002528055-A/2

PD 03-SEP-2002

PF 31-AUG-1999 JP 2000567676

PR 31-AUG-1998 US 60/098443, 25-JAN-1999 US 60/117119 PI

TMOTHY J FOSTER, MAGNUS HOOK, STACY DAVIS, ORLA HARTFORD, KIRK PI

MCCREA, PI

DEIDRE NI EIDHIN

PC C12N15/09, C12N15/09, A61K39/00, A61K39/085, A61K39/395, A61K39/395, PC

A61K48/00, A61L27/00, A61L27/00, A61L29/00, A61L31/00, A61P9/00, A61P17/02, PC

A61P19/00,

PC A61P31/04, C07K14/31, C07K16/12, C12Q1/02, G01N33/15, G01N33/50, PC

G01N33/569//

PC C12N15/09, C12R1:45), (C12Q1/02, C12R1:44), C12N15/00, C12N15/00,

PC A61K37/02, C12R1:45)

PC C12N15/00, C12R1:45)

CC Polypeptides and polynucleotides derived from coagulase- CC

negative

CC staphylococci

Key Location/Qualifiers

FT CDS (3)..(2975).

1. .2976

/organism="Staphylococcus epidermidis"

/mol\_type="genomic DNA"

FEATURES

source



University System; Dublin;  
IEX; Location/Qualifiers  
source 1..2976  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 92.4%; Score 1613.8; DB 2; Length 2976;  
Best Local Similarity 95.7%; Pred. No. 0;  
Matches 1670; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 1 TCTAGTGATGAAGAAAGATGATGATCAATAATATCACTCAATAAAGACCCAGCAT 60  
DB 318 TCAGTAAATGAAGAAAGATGATGATCAATAATATGATGATCAATAAAGACCCAGCAT 377  
QY 61 AATAACCAATAATATTAAGAAAGAAAGATGATGATCAATAATATCACTCAATAAAGACCCAGCAT 120  
DB 378 GATAACCAATAA--AATAAGAAAGAAAGATGATGATCAATAAAGACCCAGCAT 434  
QY 121 GAAGATGAAGACAGATCAACAATAATGATGATGAAGAAAGAAAGACCCAGCAT 180  
DB 435 AAGATATATACAGATCAACAATAATGATGATGAAGAAAGAAAGACCCAGCAT 494  
QY 181 ACCCTCAAGATATATCTCATCTTACAGAAAGAGAGTAAAGAAATCCTCATCATCGAA 240  
DB 495 ACCCTCAAGATATATCTCATCTTAAAGAAAGAGTAAAGAAATCCTCATCATCGAA 554  
QY 241 TCTCAAAATTCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 555 TCTCAAAATTCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 614  
QY 301 GAATCTGTTCAACAAAGTATATGATGATGATGATGATGATGATGATGATGATGAT 360  
DB 615 GCATCTATTCACAAAGTATATGATGATGATGATGATGATGATGATGATGATGAT 674  
QY 361 AAAATAAGAGAGTAACTCAATCTGTTAAAGAGAGTAACTCAATGATGATGATGAT 420  
DB 675 AAAATAAGAGAGTAACTCAATCTGTTAAAGAGAGTAACTCAATGATGATGATGAT 734  
QY 421 AAGTAAAGAGAGTAACTCAATCTGTTAAAGAGAGTAACTCAATGATGATGATGAT 480  
DB 735 AAGTAAAGAGAGTAACTCAATCTGTTAAAGAGAGTAACTCAATGATGATGATGAT 794  
QY 481 ATTCAAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
DB 795 ATTCAAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 854  
QY 541 CCATTTATCAACATCTGCCCAACATGATGATGATGATGATGATGATGATGATGAT 600  
DB 855 CCGTTATCTCAACATCTGCCCAACATGATGATGATGATGATGATGATGATGATGAT 914  
QY 601 CGGGAACAGGTTTCAAGTATTAACATTTAAATTAAGTATTAAGTATTAAGTATTA 660  
DB 915 GCAGAAACAGGTTTCAAGTATTAACATTTAAATTAAGTATTAAGTATTAAGTATTA 974  
QY 661 GGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
DB 975 GGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1034  
QY 721 GTAACCTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
DB 1035 GTAACCTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1094  
QY 781 AAGAATACAGTTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
DB 1095 AAGAATACAGTTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154  
QY 841 TCTGAGAAATCATCGCTACAGGTACTTATGATGATGATGATGATGATGATGATGAT 900  
DB 1155 TCTGAGAAATCATCGCTACAGGTACTTATGATGATGATGATGATGATGATGATGAT 1214  
QY 901 TTTACAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960

DB 1215 TTTACAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1274  
QY 961 ATTGATAAATCAAAAGGTTCCAAATAATAATACCAAGTTAGATGATGATGATGATGAT 1020  
DB 1275 ATTGATAAATCAAAAGGTTCCAAATAATAATACCAAGTTAGATGATGATGATGATGAT 1334  
QY 1021 CTTTCATCAGTAAATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080  
DB 1335 CTTTCATCAGTAAATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1394  
QY 1081 GCTAACCTTCAAAAGTATGTTTCAAAATATATATATATATATATATATATATATATATAT 1140  
DB 1395 GCTAACCTTCAAAAGTATGTTTCAAAATATATATATATATATATATATATATATATATAT 1454  
QY 1141 ATTTATATTAACCTTCTGTTTATTCAGCCAGGAAACAAATGTAATATATTTTCAAGGAAAT 1200  
DB 1455 ATTTATATTAACCTTCTGTTTATTCAGCCAGGAAACAAATGTAATATATTTTCAAGGAAAT 1514  
QY 1201 GGTGATGAAGTTTCAACAAATTTATAGACGATGATGATGATGATGATGATGATGATGAT 1260  
DB 1515 GGTGATGAAGTTTCAACAAATTTATCGACGATGATGATGATGATGATGATGATGATGAT 1574  
QY 1261 GATTAATCAAAATTTTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320  
DB 1575 GATTAATCAAAATTTTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1634  
QY 1321 ACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
DB 1635 ACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1694  
QY 1381 ATAGATTCACCATATATTTTAAAGTTTATGATGATGATGATGATGATGATGATGATGAT 1440  
DB 1695 ATAGATTCACCATATATTTTAAAGTTTATGATGATGATGATGATGATGATGATGATGAT 1754  
QY 1441 ACAGTATACAGCAAACTGTGACAACTGTGACAACTGTGACAACTGTGACAACTGTGAC 1500  
DB 1755 ACAGTATACAGCAAACTGTGACAACTGTGACAACTGTGACAACTGTGACAACTGTGAC 1814  
QY 1501 AGAACAGATCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
DB 1815 AGAACAGATCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1874  
QY 1561 GACTTGCTCTGAAAAAATTTTAAATTCGAGATTTACGATGATGATGATGATGATGATGAT 1620  
DB 1875 GACTTGCTCTGAAAAAATTTTAAATTCGAGATTTACGATGATGATGATGATGATGATGAT 1934  
QY 1621 GATGTTATTCAAAATACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
DB 1935 GATGTTATTCAAAATACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1994  
QY 1681 ACGTATCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
DB 1995 ACGTATCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2054  
QY 1741 GATCG 1745  
DB 2055 GATCG 2059

RESULT 13  
AR482276  
LOCUS AR482276  
DEFINITION Sequence 7 from patent US 6703025.  
ACCESSION AR482276  
VERSION AR482276.1 GI:47244503  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2976)  
AUTHORS Patti, J.M., Foster, T.J. and Hook, M.  
TITLE Multicomponent vaccines

JOURNAL Patent: US 6703025-A 7 09-MAR-2004;  
Inhibitex, Inc., The Provost Fellows and Scholars of the College of  
The Holy and Undivided Trinity of Queen Elizabeth near Dublin and  
The Texas A&M University System; Alpharetta, GA

## FEATURES

source 1..2976  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 92.4%; Score 1613.8; DB 2; Length 2976;  
Best Local Similarity 95.7%; Pred. No. 0;  
Matches 1670; Conservative 0; Mismatches 72; Indels 3; Gaps 1;  
1 TCTAGTGATGAAGAAAGATGATGTGATCAATAATAATCAAGTCAATAAAGACCGACGAT 60  
Db |||||  
318 TCAGTAATGAAGAAAGATGATGTAATCAATAATAGTCAGTCAATAAAGACCGATGAT 377  
Qy 61 AATAACCAATAATTAAGAAAGAGAAAGCAATACTACGATGGCGATAGAAAACGCTCA 120  
Db |||||  
378 GATAACCAATA---AAAAAGAGAAAGCAAGATAGCAAGCGATGCCATAGAAAATCGCTCT 434  
Qy 121 GAAGATAGAACAGAGTCAACACCAATGTAGATGAAGAAAGCAAGCAACATTTTACAAAG 180  
Db |||||  
435 AAGATATAACACAGTCAACACCAATGTAGATGAAGAAAGCAAGCAACATTTTACAAAG 494  
Qy 181 ACCCTCTCAAGATAATACTCATCTTACAGAAAGAGGTAAAGAAATCCCTCATCAGTCGAA 240  
Db |||||  
495 ACCCTCAAGATAATACTCAGCTTAAGAAAGAGGTGTAAGAAACCTCATCAGTCGAA 554  
Qy 241 TCTCAAAATTCATCAATTCATGATGCTGCCAACCAACCATCTCACACCAATAAATAGAGAA 300  
Db |||||  
555 TCTCAAAATTCATCAATTCATGATGCTGCCAACCAACCATCTCACACCAATAAATAGAGAA 614  
Qy 301 GAATCTGTTCAACAGTGAATGTAGAGATTCACAGTATCAGATTTTGTCACTCT 360  
Db |||||  
615 GCATCTATTCAACAGTGAATGTAGAGAAATTTCCCGGTATCAGATTTTGTCACTCT 674  
Qy 361 AAAATAAAGAGAGTAACTCAATCTGTTAAAGAGAGAAATATATAGACCAACCTAAT 420  
Db |||||  
675 AAAATAAGAGAGTAACTCAATCTGTTAAAGAGAGAAATATATAGACCAACCTAAT 734  
Qy 421 AAGTAAAGAGAGTAACTCAACAGTCAAGCGCTCTGGCTATACAAATATAGATGAAAA 480  
Db |||||  
735 AAGTAAAGAGAGTAACTCAACAGTCAACCGCTCTAGCTATATAAATAATAGATGAAAA 794  
Qy 481 ATTTCAAAATCAAGATGAGTATTAATTTACCAATAAATGAATGAATAAAGCTAGA 540  
Db |||||  
795 ATTTCAAAATCAAGATGAGTATTAATTTACCAATAAATGAATGAATAAAGCTAGA 854  
Qy 541 CCATTATCTAACACATCTGCCCAACCATCGATTTAAACGTTAAACCGTAAATCAATTAGCG 600  
Db |||||  
855 CGTTATCTAACACATCTGCCCAACCATCGATTAAGCGTGAACCGTAAATCAATTAGCG 914  
Qy 601 GCGGAACAAGGTTGCAATGTTAAACCAATTTAAAGTTTACTGATCAAAAGTATTACTGAA 660  
Db |||||  
915 GCAGAAACAAGGTTGCAATGTTAAATCAATTTAAAGTTTACTGATCAAAAGTATTACTGAA 974  
Qy 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Db |||||  
975 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1034  
Qy 721 GTAACCTTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
Db |||||  
1035 GTAACCTTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1094  
Qy 781 AAGAATACAGTTCCATCAGATTTAAACCGATAGCTTTTACAAATACCAAAATAAAGATAT 840  
Db |||||  
1095 AAGAATACAGTTCCATCAGATTTAAACCGATAGCTTTTACAAATACCAAAATAAAGATAT 1154  
Qy 841 TCTGGAGAAATCATCGCTACAGTACTTATGATTAACAAATAAACAATACCTTACT 900  
Db |||||  
1155 TCTGGAGAAATCATCGCTACAGTACTTATGATTAACAAATAAACAATACCTTACT 1214

Qy 901 TTTACAGATTATGTAGATAAGTATGAAAAATATTAAAGCACACCTTAAATTAACGTATAC 960  
Db |||||  
1215 TTTACAGATTATGTAGATAAATATGAAATATTAAAGCGCACCTTAAATTAACATATAC 1274  
Qy 961 ATTGATAAATCAAGGTTCCAAATATAATATACAAAGTTAGATGTAGAAATATAAAACGGCC 1020  
Db |||||  
1275 ATTGATAAATCAAGGTTCCAAATATAATACACATAGTTAGATGTAGAAATATAAGACGGCC 1334  
Qy 1021 CTTTCATCAGTAAATAAACAATTTACGGTTGAATATCAAGACCTTAACGAAATCCGACT 1080  
Db |||||  
1335 CTTTCATCAGTAAATAAACAATTTACGGTTGAATATCAAAACCTTAACGAAATCCGACT 1394  
Qy 1081 GCTAACCTTTCAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAAAACG 1140  
Db |||||  
1395 GCTAACCTTTCAAAGTATGTTTACAAACATAGATACGAAAAACCATACAGTTGAGCAAAACG 1454  
Qy 1141 ATTTATATTAACCTCTTCGTTTATTCAGCCAAAGGAAACAAATGTAAATATTTTCAGGGAAT 1200  
Db |||||  
1455 ATTTATATTAACCTCTTCGTTTATTCAGCCAAAGGAAACAAATGTAAATATTTTCAGGGAAT 1514  
Qy 1201 GGTGATGAGGTTCAACAATTTAGACGATAGCACAAATATAAGTTTATAGGTTGGA 1260  
Db |||||  
1515 GGTGATGAGGTTCAACAATTTAGACGATAGTACAAATATCAATCATTTAAAGTTTATAGGTTGGA 1574  
Qy 1261 GATAATCAAAATTTTACAGATAGTAAACAGAAATTTATGATTTACAGTGAATATGAAGATGC 1320  
Db |||||  
1575 GATAATCAAAATTTTACAGATAGTAAACAGAAATTTATGATTTACAGTGAATATGAAGATGC 1634  
Qy 1321 ACAATGATGATTTATGCCAATTTAGGAAATAATAATGATGTGAATATTAATTTTGGTAAAT 1380  
Db |||||  
1635 ACAATGATGATTTATGCCAATTTAGGAAATAATAATGATGTGAATATTAATTTTGGTAAAT 1694  
Qy 1381 ATAGATTTACCATATATTTATTAAGTTTATAGTAAATATGACCTTAATAGGATGATAC 1440  
Db |||||  
1695 ATAGATTTACCATATATTTATTAAGTTTATAGTAAATATGACCTTAATAGGATGATAC 1754  
Qy 1441 ACAGCTATACAGCAAACTGTGCAATTCAGACGACTATATAATGAGTATATCTGTTGAGTTT 1500  
Db |||||  
1755 ACAGCTATACAGCAAACTGTGCAATTCAGACGACTATATAATGAGTATATCTGTTGAGTTT 1814  
Qy 1501 AGAACAGCATCTTATGATAATAACAATTTGCTTTCTCTACAAGTTTCAGGTCAAGGACAAGGT 1560  
Db |||||  
1815 AGAACAGCATCTTATGATAATAACAATTTGCTTTCTCTACAAGTTTCAGGTCAAGGACAAGGT 1874  
Qy 1561 GACTTGCCTCTGGAAGAACTTATAAATCGAGATTACGTATGGAAGATCTAGATAA 1620  
Db |||||  
1875 GACTTGCCTCTGGAAGAACTTATAAATCGGAGATTACGTATGGAAGATCTAGATAA 1934  
Qy 1621 GATGTTATTTCAAAATACAAATGATATGAAAAACCGCTTTAGTAAATGTTTGGTAACTTTG 1680  
Db |||||  
1935 GATGTTATTTCAAAATACAAATGATATGAAAAACCGCTTTAGTAAATGTTTGGTAACTTTG 1994  
Qy 1681 AGTATCTGATGGAACCTTTCAAAATCAGTCAAGACAGATGAAGATGGGAAATATCAATTT 1740  
Db |||||  
1995 AGTATCTGATGGAACCTTTCAAAATCAGTCAAGACAGATGAAGATGGGAAATATCAATTT 2054  
Qy 1741 GATGG 1745  
Db 2055 GATGG 2059

RESULT 14  
CP000029\_02  
WFCOMMENT

Sequence split into 27 fragments LOCUS CP000029 Accession CP000029

Fragment Name	Begin	End
CP000029_00	1	110000
CP000029_01	100001	210000
CP000029_02	200001	310000
CP000029_03	300001	410000
CP000029_04	400001	510000
CP000029_05	500001	610000







```
RESULT 15
AR484931
LOCUS AR484931 837 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 2699 from patent US 6703492.
ACCESSION AR484931
VERSION AR484931.1 GI:47248034
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
  1 (bases 1 to 837)
AUTHORS Kimmerly, W.J.
TITLE Staphylococcus epidermidis nucleic acids and proteins
JOURNAL Patent: US 6703492-A 2699 09-MAR-2004;
  SmithKline Beecham Corporation; Philadelphia, PA
FEATURES
  Location/Qualifiers
    source
      1..837
        /organism="unknown"
        /mol_type="genomic DNA"
ORIGIN
Query Match 29.0%; Score 507.2; DB 2; Length 837;
Best Local Similarity 97.5%; Pred. No. 6.5e-140;
Matches 515; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 TCTAGTGATGAAGAAAGATGATGTGATCAATAATAATCAAGTCAATAAACCACCGACGAT 60
Db |||||||
QY 223 TCTAGTGATGAAGAGAGATGATGTATTAATTAATATCACTCAATAAAGTCTGATGAT 282
Db |||||||
QY 61 AATAACCAATAATTAATAAAGAAAGAAACGAATAACTACGATGGCATAGAAAACGCTCA 120
Db |||||||
QY 283 AATAACCAATAATTAATAAAGAAAGAAACGAATAACTACGATGGTATAGAAAAGCTCA 342
Db |||||||
QY 121 GAAGATAGACAGAGTCACACAAATGTAGATGAACGAGAGCAACATTTTACAAAG 180
Db |||||||
QY 343 GAAGATAGAACAGAGTCACACAAATGTAGATGAACGAGAGCAACATTTTACAAAG 402
Db |||||||
QY 181 ACCCTCTCAAGATAATACTCTTACAGAAAGAGAGTAAAGAAATCCCTCATCAGTCGAA 240
Db |||||||
QY 403 TCCCTCAAGATAATACTCTTACAGAAAGAGAGTAAAGAAATCCCTCATCAGTCGAA 462
Db |||||||
QY 241 TCCTCAAAATTCATCAATTGATATCTGCCCAACCAACCATCTCAACCAATAAATAGAGAA 300
Db |||||||
QY 463 TCCTCAAAATTCATCAATTGATATCTGCCCAACCAACCATCTCAACCAATAAATAGAGAA 522
Db |||||||
QY 301 GAATCTGTTCAACAGTGATATGTAGAGATTACACGATATCAGATTTTGTAACTCT 360
Db |||||||
QY 523 GAATCTGTTCAACAGTGATATGTAGAGATTACACGATATCAGATTTTGTAACTCT 582
Db |||||||
QY 361 AAAATAAAGAGAGTAACACTGAATCTGGTAAAGAGAGTAATCTATAGAGCAACCTAAT 420
Db |||||||
QY 583 AAAATAAAGAGAGTAACACTGAATCTGGTAAAGAGAGTAATCTATAGAGCAACCTAAT 642
Db |||||||
QY 421 AAAGTAAAGAGAGTTCAACAAAGTCAGCGCTCTGGCTATACAAATATAGATGAAAAA 480
Db |||||||
QY 643 AAAGTAAAGAGAGTTCAACAAAGTCAGCGCTCTGGCTATACAAATATAGATGAAAAA 702
Db |||||||
QY 481 ATTTCAATCAAGATGAGTTATTAATTTTACCATAAATGAATATGAA 528
Db |||||||
QY 703 ATTTCAATCAAGATGAGTTATTAATTTTACCATAAATGAATATGAA 750
Db |||||||
```

Search completed: August 14, 2006, 06:35:41  
Job time : 10157 secs

**This Page Blank (uspto)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2006, 03:31:25 ; Search time 1154 Seconds  
(without alignments)  
10549.000 Million cell updates/sec

Title: US-10-806-288-12

Perfect score: 1746

Sequence: 1 tctggtgatgaagaaga.....ggaaatatcaattgatgga 1746

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_8.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*
- 15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1746	100.0	3600	2	AaV04279
2	1613.8	92.4	2676	8	ACA46427
3	1613.8	92.4	2676	13	ADS20620
4	1613.8	92.4	2793	6	ABN93014
5	1613.8	92.4	2793	13	ADS02242
6	1613.8	92.4	2976	3	AAZ93534
7	1613.8	92.4	2976	3	AAZ51202
8	1448.4	83.0	1680	10	ACF80624
9	929	53.2	1030	10	ACF80625
10	866	49.6	951	10	ACF80626
11	618.2	35.4	2010	8	ACA46390
12	507.2	29.0	837	4	AAH53653
13	507.2	29.0	3236	4	AAH54128
14	364.4	20.9	3498	2	AAH77594
15	362.8	20.8	3498	8	ABT14929
16	362.6	20.8	3426	8	ACA46197
17	130.6	7.5	1300	12	ADP85917
18	126	7.2	3945	2	AAH77593

19	126	7.2	4047	4	AAS52261
20	126	7.2	4047	8	ACF73996
21	126	7.2	4050	4	AAS55402
22	126	7.2	4143	8	ABT14918
23	122.2	7.0	3619	4	AH54793
24	121.6	7.0	1806	2	AAT83975
25	110.4	6.3	1000	12	ADQ62833
26	110.4	6.3	1000	12	ADQ62832
27	110.2	6.3	2957	4	AH54771
28	110.2	6.3	3132	4	AH54091
29	110.2	6.3	3465	4	AH53193
30	110.2	6.3	4899	8	ACA46383
31	108.6	6.2	5406	3	AAZ93533
32	108.6	6.2	5406	3	AAZ51201
33	108.4	6.2	4158	8	ACA20270
34	104.6	6.0	6668	6	ABL33697
35	103.6	5.9	3683	8	ABZ10199
36	103.2	5.9	6292	4	AAS46735
37	102	5.8	4985	6	ABQ75107
38	102	5.8	4985	10	ACF79720
39	101	5.8	2886	8	ACA19724
40	100.8	5.8	969	6	ABQ39490
41	100.8	5.8	969	6	ABQ39491
42	100.6	5.8	4660	14	ADZ70902
43	100.4	5.8	7442	4	AAS46686
44	99	5.7	2796	4	AAS51941
45	99	5.7	2799	4	AAS54703

ALIGNMENTS

RESULT 1

AAV04279

ID AAV04279 standard; DNA; 3600 BP.

XX AC AAV04279;

XX 17-OCT-2003 (revised)

DT 22-JUN-1998 (first entry)

XX Staphylococcus epidermidis fibrinogen binding protein fig gene.

KW Fibrinogen binding protein; fig gene; aggregation; infection;

KW coagulase-negative Staphylococcus; therapy; diagnosis; immunisation;

KW vaccine; ss.

XX Staphylococcus epidermidis; strain HB.

XX Key Location/Qualifiers

FT RBS 22..27

FT CDS /tag= a

FT sig\_peptide 33..3311

FT mat\_peptide /tag= b

FT repeat\_region 33..185

FT repeat\_unit /tag= c

FT repeat\_unit /tag= d

FT repeat\_unit /tag= e

FT repeat\_unit /tag= f

FT repeat\_unit /tag= g

FT repeat\_unit /tag= h

FT repeat\_unit /tag= i

FT repeat\_unit /tag= j

FT repeat\_unit /tag= k

FT repeat\_unit /tag= l

FT repeat\_unit /tag= m

FT repeat\_unit /tag= n

FT repeat\_unit /tag= o

FT repeat\_unit /tag= p

FT repeat\_unit /tag= q

FT repeat\_unit /tag= r

FT repeat\_unit /tag= s

FT repeat\_unit /tag= t

FT repeat\_unit /tag= u

FT repeat\_unit /tag= v

FT repeat\_unit /tag= w

FT repeat\_unit /tag= x

FT repeat\_unit /tag= y

FT repeat\_unit /tag= z



CC	also as a DNA vaccine to protect humans and animals against coagulase-
CC	negative Staphylococcus infection. Probes based on the fig gene can be
CC	used to identify S. epidermidis; fig is present in all strains of this
CC	species but not in other staphylococci. Probes can also be used to
CC	fingerprint strains (e.g. to identify a source of infection) and to
CC	isolate similar genes from other species. (Updated on 17-OCT-2003 to
CC	standardise OS field)
XX	
SQ	Sequence 3600 BP; 1418 A; 554 C; 665 G; 963 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1746; DB 2; Length 3600;
	Best Local Similarity 100.0%; Pred. No. 1.1e-307;
	Matches 1746; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 TCTAGTGATGAAGAAAGATGATGTGATCAATAATACAGTCAATAAACAACCGACGAT 60
DB	255 TCTAGTGATGAAGAAAGATGATGTGATCAATAATACAGTCAATAAACAACCGACGAT 314
QY	61 AATAACCAATTAATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB	315 AATAACCAATTAATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 374
QY	121 GAAGATAGAACAGAGTCAACAACAATGTAGATGAAGAAAGAAAGAAAGAAAGAAAG 180
DB	375 GAAGATAGAACAGAGTCAACAACAATGTAGATGAAGAAAGAAAGAAAGAAAGAAAG 434
QY	181 ACCCTCTCAAGATAATACTCATCTTACAGAAAGAGAGGTAAAGAAATCCCTCATCAGTCGAA 240
DB	435 ACCCTCTCAAGATAATACTCATCTTACAGAAAGAGAGGTAAAGAAATCCCTCATCAGTCGAA 494
QY	241 TCCTCAAAATTCATTAATTGATACCTGCCCAACCAACCATCTCAACAACAATAATAGAGAA 300
DB	495 TCCTCAAAATTCATTAATTGATACCTGCCCAACCAACCATCTCAACAACAATAATAGAGAA 554
QY	301 GAATCTGTTTCAACAAGTGATTAATGTAGAGATTCACAGTATCAGATTTTCTTAACCTCT 360
DB	555 GAATCTGTTTCAACAAGTGATTAATGTAGAGATTCACAGTATCAGATTTTCTTAACCTCT 614
QY	361 AAAATAAAGAGAGTAAACACTGAATCTGGTAAAGAGAGAAATCTATAGAGCAACTAAT 420
DB	615 AAAATAAAGAGAGTAAACACTGAATCTGGTAAAGAGAGAAATCTATAGAGCAACTAAT 674
QY	421 AAGTAAAGAGAGTTCACAAACAAGTCAAGCGCTCTGGCTATACAAATATAGATGAAAAA 480
DB	675 AAGTAAAGAGAGTTCACAAACAAGTCAAGCGCTCTGGCTATACAAATATAGATGAAAAA 734
QY	481 ATTTCAAAATCAGATGAGTTTAAATTTACCAATAAATGAATATGAAAAATAGGCTAGA 540
DB	735 ATTTCAAAATCAGATGAGTTTAAATTTACCAATAAATGAATATGAAAAATAGGCTAGA 794
QY	541 CCATTATCTACAAACATCTGCCCAACCATCGATTAAACGTTAAACCGTAAATCAATTAGCG 600
DB	795 CCATTATCTACAAACATCTGCCCAACCATCGATTAAACGTTAAACCGTAAATCAATTAGCG 854
QY	601 GCGGAACAAGGTTTCAAGTGTAAACCAATTTAAAGTTTACTGTATCAAAAGTATTACTGAA 660
DB	855 GCGGAACAAGGTTTCAAGTGTAAACCAATTTAAAGTTTACTGTATCAAAAGTATTACTGAA 914
QY	661 GGATATGATGATGATGAGGTTTATTAAGACACATGATGCTGAAAACTTAATCTATGAT 720
DB	915 GGATATGATGATGATGAGGTTTATTAAGACACATGATGCTGAAAACTTAATCTATGAT 974
QY	721 GTAACCTTTTGAAGTATGATGAAGGTGAATCTGTTGATACCATGACAGTGTGATATAGAT 780
DB	975 GTAACCTTTTGAAGTATGATGAAGGTGAATCTGTTGATACCATGACAGTGTGATATAGAT 1034
QY	781 AAGAATACAGTTTCCATCAGATTAAACCGTAGCTTTTACAAATACCAAAATAAAGATAAT 840
DB	1035 AAGAATACAGTTTCCATCAGATTAAACCGTAGCTTTTACAAATACCAAAATAAAGATAAT 1094
QY	841 TCTGAGAAATCATCGCTACAGGTACTTATGATTAACAAATAAACAATAATCACTTACT 900
DB	1095 TCTGAGAAATCATCGCTACAGGTACTTATGATTAACAAATAAACAATAATCACTTACT 1154

QY	901 TTTTACAGATTATGTAGATAAGTATGAAATATTTAAAGCACACCTTTAAATTAACGTCATAC 960
DB	1155 TTTTACAGATTATGTAGATAAGTATGAAATATTTAAAGCACACCTTTAAATTAACGTCATAC 1214
QY	961 ATTGATAAATCAAAAGGTTCCAAATTAATAATACAAAGTTAGATGTAGAAATATAAAACGGCC 1020
DB	1215 ATTGATAAATCAAAAGGTTCCAAATTAATAATACAAAGTTAGATGTAGAAATATAAAACGGCC 1274
QY	1021 CTTTCATCAGTAAATAAACAATTAACGGTTGAATATCAAGACCTTAACCAAAATCCGACT 1080
DB	1275 CTTTCATCAGTAAATAAACAATTAACGGTTGAATATCAAGACCTTAACCAAAATCCGACT 1334
QY	1081 GCTAACCTTTCAAAGTATGTTTACAATATAGATAGCAAAAAATCATACAGTTGAGCAAAACG 1140
DB	1335 GCTAACCTTTCAAAGTATGTTTACAATATAGATAGCAAAAAATCATACAGTTGAGCAAAACG 1394
QY	1141 ATTTATATTAACCCCTCTTCGTTTATTCAGCCAAAGGAAACAAATGTAAATATTTACGGAAAT 1200
DB	1395 ATTTATATTAACCCCTCTTCGTTTATTCAGCCAAAGGAAACAAATGTAAATATTTACGGAAAT 1454
QY	1201 GGTGATGAGGTTTCAACAATTAATAGCAGTACCAATTAATTAAGTTTATAAGTTTGA 1260
DB	1455 GGTGATGAGGTTTCAACAATTAATAGCAGTACCAATTAATTAAGTTTATAAGTTTGA 1514
QY	1261 GATAATCAAAATTTTACCAGATAGTAAACAGAAATTTTATGATTACAGTCAATATGAAGATGTC 1320
DB	1515 GATAATCAAAATTTTACCAGATAGTAAACAGAAATTTTATGATTACAGTCAATATGAAGATGTC 1574
QY	1321 ACAATATGATGATTATGCCCAATTTAGGAAATAATAATATGATGTGAATATTAATTTGGTAAAT 1380
DB	1575 ACAATATGATGATTATGCCCAATTTAGGAAATAATAATATGATGTGAATATTAATTTGGTAAAT 1634
QY	1381 ATAGATTCCACCATATATTTAAAGTTTATAGTAAATATGACCCCTTAATAGGATGATTAC 1440
DB	1635 ATAGATTCCACCATATATTTAAAGTTTATAGTAAATATGACCCCTTAATAGGATGATTAC 1694
QY	1441 ACGACTATACAGCAAACTGTGCAATGCAGACGACTATAAATGAGTATACTGCTGAGTTT 1500
DB	1695 ACGACTATACAGCAAACTGTGCAATGCAGACGACTATAAATGAGTATACTGCTGAGTTT 1754
QY	1501 AGAACAGCATCTATGATAATAACAATTCCTTTCTCAAAAGTTCAAGGTCAGGACAAGGT 1560
DB	1755 AGAACAGCATCTATGATAATAACAATTCCTTTCTCAAAAGTTCAAGGTCAGGACAAGGT 1814
QY	1561 GACTTGCTCTCTGAAAAAATTTAAATCGGAGATTACGTTATCGGAGATGTAGATAAA 1620
DB	1815 GACTTGCTCTCTGAAAAAATTTAAATCGGAGATTACGTTATCGGAGATGTAGATAAA 1874
QY	1621 GATGGTATTTCAAAATACAAATGATAATGAAAAACCGCTTTAGTAAATGTTTGTAACTTTG 1680
DB	1875 GATGGTATTTCAAAATACAAATGATAATGAAAAACCGCTTTAGTAAATGTTTGTAACTTTG 1934
QY	1681 ACGTATCTGTATGGAACTTCAAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT 1740
DB	1935 ACGTATCTGTATGGAACTTCAAAATCAGTCAGAACAGATGAAGATGGGAAATATCAATTT 1994
QY	1741 GATGGA 1746
DB	1995 GATGGA 2000

RESULT 2  
ACR46427  
ID ACR46427 standard; DNA; 2676 BP.  
XX  
ACR46427;  
XX AC  
XX AC  
DT 19-JUN-2003 (first entry)  
XX  
DE Prokaryotic essential gene #28084.  
XX  
KW Antisense; ds; prokaryotic essential gene; cell proliferation;



XX	(INTE-) INTERCELL AG.
PA	
XX	Mainke A, Min Bui D, Nagy E;
PI	WPI; 2004-729219/71.
XX	P-PSDB; AD820651.
DR	
DR	New nucleic acid molecules encoding hyperimmune serum reactive antigens from Staphylococcus epidermidis, useful for diagnosing, preventing or treating S. epidermidis infections.
XX	
PT	Claim 1; SEQ ID NO 21; 196pp; English.
XX	
CC	The invention relates to a novel isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or its fragment. Staphylococci are commonly associated with human disease. Both Staphylococcus epidermidis and Staphylococcus aureus have become resistant to many commonly used antibiotics, most importantly methicillin (MRSA) and vancomycin (VISA).
CC	Drug resistance is an increasingly important public health concern and novel therapies to combat staphylococci infection must be developed in preparation for a time when such infections may be untreatable by antibiotics. The molecules of the invention demonstrate antibacterial activity and may be useful for manufacturing a medicament, such as a vaccine, for treating or preventing S. epidermidis infections, possibly via gene therapy. The antigen or its fragment may also be used for generating an anticline peptide binding to the hyperimmune serum reactive antigen or fragment, for manufacturing a functional nucleic acid, such as an aptamer or spiegelmer and for manufacturing a functional ribonucleic acid, such as a ribozyme, antisense nucleic acid or siRNA (short interfering RNA). The current sequence is that of a Staphylococcus epidermidis hyperimmune serum reactive antigen DNA of the invention.
XX	
SQ	Sequence 2676 BP; 1091 A; 408 C; 484 G; 693 T; 0 U; 0 Other;
	Query Match            92.4%; Score 1613.8; DB 13; Length 2676;
	Best Local Similarity 95.7%; Pred. No. le-283;
	Matches 1670; Conservative 0; Mismatches 72; Indels 3; Gaps 1
QY	1 TCTAGTGTGAAGAAAGAATGATGTGATCAATAATTAATCAGTCAATAAACAACCGACGAT 60
Db	103 TCAGTAATGAAGAANAAGANTGTGTATCATTAATTAATAGTCAGTCAATAAACCCGATGAT 162
QY	61 AATAACCAAATATTAAAAAAGAGAAAACGAATTAATCAGATGCATAGAAAAACGCTCA 120
Db	163 GATNACCAAATA--AAAAAGAGNAACGAATAGCAACGATGCCATAGAAAATCGCTCT 219
QY	121 GAAGATAGAACAGAGTGCAACAACAAAATGTAGATGAAAAACGAAGCAACATTTTTCAAAAAG 180
Db	220 AAAGATATAACACAGTCAACAACAAAATGTAGATGAAAAACGAAGCAACATTTTTCAAAAAG 279
QY	181 ACCCTCTCAGATATACTCATCTTACAGNAGAGAGGTAAAGNATCCTCATCAGTCGAA 240
Db	280 ACCCTCTCAGATATATCTCACGCTTAAAGAGAGAGTGGTAAAGAACCCCTCATCAGTCGAA 339
QY	241 TCTCTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCACAAACAATAAATAGAGAA 300
Db	340 TCTCTCAATTCATCAATGATCTGCCCAACCAACCATCTCATACNACNATAAATAGTAGAA 399
QY	301 GAATCTGTTCAAAACGAAGTGAATAATGTAGAGAGATTACACGATATCAGATTTTGTCTAACTCT 360
Db	400 GCATCTATTCAAAACGAAGTGAATAATGAAGAAAAATTCGCCGCTATCAGATTTTGTCTAACTCT 459
QY	361 AAAATAAAGAGAGTAAACACTGAATCTGGTAAAGAGAGAAATACTATAGAGCAACCTAAT 420
Db	460 AAAATAAAGAGAGTAAACACTGAATTCCTAAATAAAGAGAGAAATACTATAGAGCAACCTAAC 519
QY	421 AAAGTAAAGAGAGATTCAACAAACAAGTCACCGCTCTGGCTTATCAAAATATAGATGAAAAA 480
Db	520 AAAGTAAAGAGAGATTTCATTAACCAAGTCAACCGCTCTAGCTTATTAATAATATAGATGAAAAA 579
QY	481 ATTTTCAAATCAAGATGAGTTATTAATTTTACCATAAATGAATATGAAATTAAGAGGCTAGA 540





Db 277 GATAACCAATA--AAAAAGAGAAACGAATAGCAACGATGCCATAGAAAAATCGCTCT 333  
QY 121 GAAGATAGACACAGAGTCAACAAATGTAGATGAAACGAAACCAACATTTTACAAAAG 180  
Db 334 AAAGATATAACACAGTCAACAAATGTAGATGAAACGAAACCAACATTTTACAAAAG 393  
QY 181 ACCCTCAAGATTAATCTCTTACAGAAGAGAGGTAAAGAAATCTCATCAGTCGAA 240  
Db 394 ACCCTCAAGATTAATCTCTTACAGAAGAGAGGTAAAGAAATCTCATCAGTCGAA 453  
QY 241 TCCTCAAAATTCATCAATTCATCTGCCCCAACCAACCTCTCACACAACAATAAATAGAA 300  
Db 454 TCCTCAAAATTCATCAATTCATCTGCCCCAACCAACCTCTCATACAACAATAAATAGAA 513  
QY 301 GAATCTGTTCAAAACAAAGTGATTAATGTAGAAAGTTTACAGTATCAGATTTTGTAACTCT 360  
Db 514 GCATCTATTCAAAACAAAGTGATTAATGAAGAAATTCCTCGGTATCAGATTTTGTAACTCT 573  
QY 361 AAAATAAAGAGAGTAACTGAATCTGTTAAAGAGAGAGATTAATCTATAGAGCAACCTAAT 420  
Db 574 AAAATAAAGAGAGTAACTGAATCTGTTAAAGAGAGAGATTAATCTATAGAGCAACCTAAT 633  
QY 421 AAAGTAAAGAGAGATTAATCAACCAAGTCAAGCTCTGCTGTATACAAATAGATGAATA 480  
Db 634 AAAGTAAAGAGAGATTAATCAACCAAGTCAAGCTCTGCTGTATACAAATAGATGAATA 693  
QY 481 ATTTCAAATCAAGATGAGTTATTAATTTTACCAATAAATGAATATGAAATAGAGGTAGA 540  
Db 694 ATTTCAAATCAAGATGAGTTATTAATTTTACCAATAAATGAATATGAAATAGAGGTAGA 753  
QY 541 CCAATATCTAACAATCTGCCCAACCAATCGATTAACCGTGTAAACCGTAAATCAATPAGCG 600  
Db 754 CCGTTATCTACAAATCTGCCCAACCAATCGATTAACCGTGTAAACCGTAAATCAATPAGCG 813  
QY 601 GCGGAACAAGGTTTCAATGTTTAACTTAAATTTAAAGTTTACTGATCAAAAGTATTACTGAA 660  
Db 814 GCGGAACAAGGTTTCAATGTTTAACTTAAATTTAAAGTTTACTGATCAAAAGTATTACTGAA 873  
QY 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Db 874 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 933  
QY 721 GTAACCTTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
Db 934 GTAACCTTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 993  
QY 781 AAGAATACAGTTTCCATCAGATTTTAAACCGTATGATGATGATGATGATGATGATGATGAT 840  
Db 994 AAGAATACAGTTTCCATCAGATTTTAAACCGTATGATGATGATGATGATGATGATGATGAT 1053  
QY 841 TCTGGAGAAATCATCGCTACAGTACTTATGATTAACAAAAATAAACAAATCACTTACT 900  
Db 1054 TCTGGAGAAATCATCGCTACAGTACTTATGATTAACAAAAATAAACAAATCACTTACT 1113  
QY 901 TTACAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960  
Db 1114 TTACAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1173  
QY 961 ATTGATAATCAAGGTTCCAAATTAATTAACCAAGTATGATGATGATGATGATGATGATGATGAT 1020  
Db 1174 ATTGATAATCAAGGTTCCAAATTAATTAACCAAGTATGATGATGATGATGATGATGATGATGAT 1233  
QY 1021 CTTTTCATCAAGTAAATAAACAAATTAAGGTTGATATCAAGACCTTAACGAAATCGGACT 1080  
Db 1234 CTTTTCATCAAGTAAATAAACAAATTAAGGTTGATATCAAGACCTTAACGAAATCGGACT 1293  
QY 1081 GCTAACCTTTCAAAGTATGTTTCAAAATATAGATGATGATGATGATGATGATGATGATGATGAT 1140  
Db 1294 GCTAACCTTTCAAAGTATGTTTCAAAATATAGATGATGATGATGATGATGATGATGATGATGAT 1353  
QY 1141 ATTTATATTAACCTCTTCTGTTTATTCAGCCAAAGGAAACAAATGTTAAATTTTCAGGGAAT 1200  
Db 1354 ATTTATATTAACCTCTTCTGTTTATTCAGCCAAAGGAAACAAATGTTAAATTTTCAGGGAAT 1413

QY 1201 GGTGATGAAGGTTCAACAATTTATAGACGATAGCACAAATTAATTAAGTTTATTAAGTTTGA 1260  
Db 1414 GCGGATGAAGGTTCAACAATTTATAGACGATAGCACAAATTAATTAAGTTTATTAAGTTTGA 1473  
QY 1261 GATAATCAAAATTTACAGATAGTAAACAGAAATTTATGATTTACAGTGAATATGAAGATGTC 1320  
Db 1474 GATAATCAAAATTTACAGATAGTAAACAGAAATTTATGATTTACAGTGAATATGAAGATGTC 1533  
QY 1321 ACAATGATGATTTATGCCCCAATTTAGGAAATTAATGATGATGATGATGATGATGATGATGAT 1380  
Db 1534 ACAATGATGATTTATGCCCCAATTTAGGAAATTAATGATGATGATGATGATGATGATGATGAT 1593  
QY 1381 ATAGATTTACCATATATTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTTAT 1440  
Db 1594 ATAGATTTACCATATATTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTTATTAAGTTTAT 1653  
QY 1441 AGCACTATACAGAAATCTGTGCAATGACAGACGACTATTAATGATGATGATGATGATGATGATGATGAT 1500  
Db 1654 AGCACTATACAGAAATCTGTGCAATGACAGACGACTATTAATGATGATGATGATGATGATGATGATGAT 1713  
QY 1501 AGAAGAGCATCTTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
Db 1714 AGAAGAGCATCTTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1773  
QY 1561 GACTTGCCTCTCTGAAAAAACTTTATAAAAATCGGAGATTAATGATGATGATGATGATGATGATGATGAT 1620  
Db 1774 GACTTGCCTCTCTGAAAAAACTTTATAAAAATCGGAGATTAATGATGATGATGATGATGATGATGATGAT 1833  
QY 1621 GATGATTTCAAAATCAAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
Db 1834 GATGATTTCAAAATCAAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1893  
QY 1681 AGCTATCTGATGAACTTCAAAATCAAGTACAGACGATGATGATGATGATGATGATGATGATGATGAT 1740  
Db 1894 AGCTATCTGATGAACTTCAAAATCAAGTACAGACGATGATGATGATGATGATGATGATGATGATGAT 1953  
QY 1741 GATGG 1745  
Db 1954 GATGG 1958

RESULT 5  
ADS02242

ID ADS02242 standard; DNA; 2793 BP.

AC ADS02242;

XX 04-NOV-2004 (first entry)

XX Staphylococcus epidermis polynucleotide seqid 1537.

DE antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;  
KW recombinant expression vector; infection; computer readable medium;  
KW computer based system; gene; ds.

XX Staphylococcus epidermidis.

XX US2004147734-A1.

XX 29-JUL-2004.

XX 01-DEC-2003; 2003US-00724972.

XX 08-NOV-1997; 97US-0064964P.

PR 13-AUG-1998; 98US-00134001.

PR 29-NOV-1999; 99US-00450969.

XX (DOUC/) DOUCETT-B-STAMM L.

XX (BUSH/) BUSH D.

XX Doucette-Stamm L, Bush D;



Db 1774 GACTTCCCTCCGAAATAATGATAATGATAATGCGGAGATTACGTATGCGAAGATGTAGATAAA 1833  
Qy 1621 GATGGTATTCAAAATACAAATGATAATGATAATGATAATGCGGAGATTACGTATGCGAAGATGTAGATAAA 1680  
Db 1834 GATGGTATTCAAAATACAAATGATAATGATAATGATAATGCGGAGATTACGTATGCGAAGATGTAGATAAA 1893  
Qy 1681 ACGTATCCTGATGGAAGTCTCAAAATCAGTCAGAACAGATGGAAGATGGAAGATGGAAGATGGAAGATGGAAGAT 1740  
Db 1894 ACGTATCCTGATGGAAGTCTCAAAATCAGTCAGAACAGATGGAAGATGGAAGATGGAAGATGGAAGATGGAAGAT 1953  
Qy 1741 GATGG 1745  
Db 1954 GATGG 1958

RESULT 6  
AAZ93534  
ID AAZ93534 standard; DNA; 2976 BP.  
XX AAZ93534;  
XX  
DT 24-JUL-2000 (first entry)  
XX  
DE Cell wall protein SdrG coding sequence.  
XX  
KW SdrF; SdrG; SdrH; coagulase negative; staphylococcus; septicemia;  
KW osteomyelitis; endocarditis; immune response; vaccine; graft; stent;  
KW intravenous catheter; heart valve; cardiac; ss.  
XX  
OS Staphylococcus sp.

Key Location/Qualifiers  
FT 1. .2976  
FT CDS /tag= a  
FT /label= SdrG cell wall protein  
FT 42. .44  
FT /tag= b  
FT /transl\_except= TAG stop codon  
FT 99. .101  
FT /tag= c  
FT /transl\_except= TGA stop codon  
FT 2892. .2894  
FT /tag= e  
FT /transl\_except= TAA stop codon  
FT 2940. .2942  
FT /tag= d  
FT /transl\_except= TAG stop codon  
FT 2967. .2969  
FT /tag= f  
FT /note= "TAA stop codon"

WO200012689-A1.  
XX  
XX 09-MAR-2000.  
XX  
XX 31-AUG-1999; 99WO-US019728.  
XX  
XX 31-AUG-1998; 98US-0098443P.  
XX 25-JAN-1999; 99US-0117119P.  
XX  
XX (QURE-) QUEEN ELIZABETH COLLEGE DUBLIN.  
PA (TEXA ) UNIV TEXAS A & M SYSTEM.  
XX  
XX Foster TJ, Hook M, Davis S, Hartford O, Mccrea K, Ni Eidhin D;  
XX WPI; 2000-256637/22.  
DR P-PSDB; AAY83171.  
XX  
XX Recombinant or synthetic proteins from coagulase-negative staphylococci  
XX useful for prevention, treatment and diagnosis of staphylococcal  
XX infections bind soluble and immobilized fibrinogen.

PS Claim 9; Fig 3; 104pp; English.  
XX  
CC Isolated Staphylococcus Sdr cell wall proteins which bind both soluble  
CC and immobilized fibrinogen are useful for treating or preventing  
CC coagulase-negative staphylococcal infection such as septicemia,  
CC osteomyelitis or endocarditis, and for inducing immune responses in  
CC patients. The cell wall proteins are also useful for reducing coagulase-  
CC negative staphylococci infection of indwelling medical devices such as  
CC vascular grafts, vascular stents, intravenous catheters, artificial heart  
CC valves and cardiac assist devices. The cell wall associated proteins are  
CC able to inhibit staphylococcal adhesion to immobilised extracellular  
CC matrix or host cells present on the surface of implanted biomaterials  
XX  
SQ Sequence 2976 BP; 1225 A; 439 C; 526 G; 786 T; 0 U; 0 Other;  
Query Match 92.4%; Score 1613.8; DB 3; Length 2976;  
Best Local Similarity 95.7%; Pred. No. ie-283;  
Matches 1670; Conservative 0; Mismatches 72; Indels 3; Gaps 1;  
Qy 1 TCTAGTGTGAGAAAGAAAGATGATGTGATCAATAATAATCAAGTCAATAAACACCGACGAT 60  
Db 318 TCCAGTAAATGAAGAAAGAAAGATGATGTGATCAATAATAATCAAGTCAATAAACACCGATGAT 377  
Qy 61 AATAACCAATAATTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120  
Db 378 GATAACCAATAATAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 434  
Qy 121 GAAGTAGACAGAGTCAACACAAATGATGTGATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180  
Db 435 AAGATATAACACAGTCAACAAATGATGTGATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 494  
Qy 181 ACCCTCTCAAGATAATACTCATCTTACAGAAAGAGAGTAAAGAAAGTCCATCATCAGTCGAA 240  
Db 495 ACCCTCTCAAGATAATACTCATCTTACAGAAAGAGAGTAAAGAAAGTCCATCATCAGTCGAA 554  
Qy 241 TCCTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCTCAACAATAAATAGTGAA 300  
Db 555 TCCTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCTCAACAATAAATAGTGAA 614  
Qy 301 GAATCTGTTCAACCAAGTGATAATGTAGAGAGTTCACACGATATCAGATTTTCTCAACTCT 360  
Db 615 GCATCTATTCAACCAAGTGATAATGTAGAGAGTTCACACGATATCAGATTTTCTCAACTCT 674  
Qy 361 AAAATAAAGAGAGTAAACACTGAATCTCGTAAAGAGAGAGTAAATATATAGACCAACTAAT 420  
Db 675 AAAATAAAGAGAGTAAACACTGAATCTCGTAAAGAGAGAGTAAATATATAGACCAACTAAT 734  
Qy 421 AAGTAAAGAGAGTAAACCAACCAAGTCAAGCGCTGCGCTATACAAATATAGATGAAAA 480  
Db 735 AAGTAAAGAGAGTAAACCAACCAAGTCAAGCGCTGCGCTATACAAATATAGATGAAAA 794  
Qy 481 ATTTCAAAATCAAGAGTGTATTAATTTTCAAAATCAAGAGTGTATTAATTTTCAAAATCAAGAGTGTATTA 540  
Db 795 ATTTCAAAATCAAGAGTGTATTAATTTTCAAAATCAAGAGTGTATTAATTTTCAAAATCAAGAGTGTATTA 854  
Qy 541 CCATTATCTACAACTCTGCCCAACCAAGTCAAGCGTAAAGAGAGTAAATCAATCAATTAGCG 600  
Db 855 CCGTTATCTACAACTCTGCCCAACCAAGTCAAGCGTAAAGAGAGTAAATCAATCAATTAGCG 914  
Qy 601 GCGGAAACAAAGTTTCAAGTTTAAACCAATTAATTAAGTTTCTGATCAAGATTAATTAAGTTTCTGAT 660  
Db 915 GCAGAAACAAAGTTTCAAGTTTAAATCAATTTAAAGTTTCTGATCAAGATTAATTAAGTTTCTGAT 974  
Qy 661 GGATATGAT 720  
Db 975 GGATATGAT 1034  
Qy 721 GTAACCTTTTGAAGTAGATGATAAGTGAATCTCGTGTATGATGATGATGATGATGATGATGATGATGAT 780  
Db 1035 GTAACCTTTTGAAGTAGATGATAAGTGAATCTCGTGTATGATGATGATGATGATGATGATGATGATGAT 1094  
Qy 781 AAGATACAGTTCCATCAGATTTTAAACCGATGATTTTAAACCGATGATTTTAAACCGATGATTTTAAACCGAT 840

Db 1095 AAGAATACAGTTCCATCAGATTTCACCGATAGTTTTCACATACCAAAATAAAGATAAT 1154  
Qy 841 TCTGAGAAATCATCGCTACAGTACTTATGATTAACAAAAATAAACAATACCTATACT 900  
Db 1155 TCTGAGAAATCATCGCTACAGTACTTATGACAAACAAAAATAAACAATACCTACT 1214  
Qy 901 TTTACAGATTATGTAGATAAGTATGAGAAATATTTAAAGCACACCTTAAATTAACGTCATAC 960  
Db 1215 TTTACAGATTATGTAGATAAATATGAGAAATATTTAAAGCGCACCTTAAATTAACATCATAC 1274  
Qy 961 ATTGATAAATCAAGGTTCCAAATTAATAATACCAAGTTAGATGTAGATAATAAAACGGCC 1020  
Db 1275 ATTGATAAATCAAGGTTCCAAATTAATAATACCAAGTTAGATGTAGATAATAAGCGCC 1334  
Qy 1021 CTTTCATCAGTAATAAACAATTAACGTTGAATATCAAGACCTTAACGAAAAATCGGACT 1080  
Db 1335 CTTTCATCAGTAATAAACAATTAACGTTGAATATCAAGACCTTAACGAAAAATCGGACT 1394  
Qy 1081 GCTAACCTTTCAAGTATGTTTACAATATAGATACGAAATATCATACAGTTTGACCAACG 1140  
Db 1395 GCTAACCTTTCAAGTATGTTTACAACATAGATACGAAATATCATACAGTTTGAGCAACG 1454  
Qy 1141 ATTTATATTAACCTCTTCGTTATTCAGCCAGGAAACAAATGTAAATATTTTCAGGGAAT 1200  
Db 1455 ATTTATATTAACCTCTTCGTTATTCAGCCAGGAAACAAATGTAAATATTTTCAGGGAAT 1514  
Qy 1201 GGTGATGAAGGTTCAACATTTATAGACGATAGCAACAATAATTAAGTTTATAAGTTTGA 1260  
Db 1515 GCGGATGAAGGTTCAACATTTATCGCATAGTACAATCATTAAGTTTATAAGTTTGA 1574  
Qy 1261 GATTAATCAAAATTTACCAAGATAGTAAACAGATTTATGATTAACGTTGAATATGAAGATGTC 1320  
Db 1575 GATTAATCAAAATTTACCAAGATAGTAAACAGATTTATGATTAACGTTGAATATGAAGATGTC 1634  
Qy 1321 ACAATGATGATTTATGCCCAATTAGGAAATTAATATGATGTGAATATTAATTTTGGTAAT 1380  
Db 1635 ACAATGATGATTTATGCCCAATTAGGAAATTAATATGATGTGAATATTAATTTTGGTAAT 1694  
Qy 1381 ATAGATTCACCATATATTTAAAGTTATAGTAAATATGATGATGATGATGATGATGATGAT 1440  
Db 1695 ATAGATTCACCATATATTTAAAGTTATAGTAAATATGATGATGATGATGATGATGAT 1754  
Qy 1441 ACGACTATACAGCAAACTGACATGACAGTACGATGATGATGATGATGATGATGATGATGAT 1500  
Db 1755 ACGAGATACAGCAAACTGACATGACAGTACGATGATGATGATGATGATGATGATGATGAT 1814  
Qy 1501 AGAAGAGATCCTATGATAAATCAATTCCTTCTCTCAAGTTCAAGGTCAGGCAAGGT 1560  
Db 1815 AGAAGAGATCCTATGATAAATCAATTCCTTCTCTCAAGTTCAAGGTCAGGCAAGGT 1874  
Qy 1561 GACTTGCTCTGAAAAAATTTAATAATCGAGATTCAGTATGCGGAAGATGTAGATAA 1620  
Db 1875 GACTTGCTCTGAAAAAATTTAATAATCGAGATTCAGTATGCGGAAGATGTAGATAA 1934  
Qy 1621 GATGATTTCAAAATACAAATGATTAATCAAAACCGCTTAGTAAATGATGATGATGATGATGAT 1680  
Db 1935 GATGATTTCAAAATACAAATGATTAATCAAAACCGCTTAGTAAATGATGATGATGATGATGAT 1994  
Qy 1681 ACGTATCCTGATGGAACCTTCAAAATCAGTACAGAACAGATGAGGAAATATCAATTT 1740  
Db 1995 ACGTATCCTGATGGAACCTTCAAAATCAGTACAGAACAGATGAGGAAATATCAATTT 2054  
Qy 1741 GATGG 1745  
Db 2055 GATGG 2059

## RESULT 7

AAZ51202

ID AAZ51202 standard; DNA; 2976 BP.

XX

AC AAZ51202;

XX

06-JUN-2000 (first entry)  
Staph. epidermidis serine-aspartate repeat region protein SdrG gene.  
Multicomponent vaccine; immunostimulatory; antibacterial; MSCRAMM;  
microbial surface components recognising adhesive matrix molecules;  
collagen binding protein; CBP; CNA; fibrinogen binding protein;  
Clumping factor A; ClfA; Clumping factor B; ClfB; PnBP;  
fibrinectin binding protein; Staphylococcus infection;  
serine-aspartate repeat region protein; SDR protein; SdrG; ds.  
Staphylococcus epidermidis.  
Key Location/Qualifiers  
CDS 3..2975  
FT /\*tag= a  
FT /product= "SdrG protein"  
FT /transl\_except= (pos:42..44, aa:Xaa)  
FT /transl\_except= (pos:99..101, aa:Xaa)  
FT /transl\_except= (pos:2892..2894, aa:Xaa)  
FT /transl\_except= (pos:2940..2942, aa:Xaa)  
FT /transl\_except= (pos:2967..2969, aa:Xaa)  
FT /note= "The coding region does not include stop codon."  
FT xaa corresponds to in-frame stop codon"  
FT /partial  
XX  
PN WO200012131-A1.  
XX  
XX 09-MAR-2000.  
XX 31-AUG-1999; 99WO-US019727.  
XX 31-AUG-1998; 98US-0098439P.  
XX (INH-) INHIBITEX INC.  
XX (TEXA-) UNIV TEXAS A & M SYSTEM.  
XX (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.  
XX Patti JM, Foster TJ, Hook M;  
XX WPI; 2000-237781/20.  
XX P-PSDB; AAY70120.  
XX Composition used for generating immune response or for inhibiting  
XX microbial colonization in an animal comprises antibodies that bind  
XX collagen binding protein, fibrinogen binding protein and, optionally,  
XX fibrinectin binding protein.  
XX Disclosure; Fig 4; 115pp; English.  
XX The patent discloses multicomponent vaccines containing selected  
XX combinations of bacterial binding proteins termed MSCRAMM (microbial  
XX surface components recognising adhesive matrix molecules) or their  
XX antibodies. A vaccine composition is provided that includes collagen  
XX binding protein or peptide, e.g. CNA, a fibrinogen binding protein  
XX preferably Clumping factor A (ClfA) or Clumping factor B (ClfB), and  
XX optionally a fibrinectin binding protein e.g. PnBP-A. The vaccines are  
XX useful for imparting protection against a broad spectrum of  
XX Staphylococcal strains and for inhibiting microbial colonisation,  
XX especially of Staphylococcus aureus, in an animal. The combinations can  
XX also be used to select donor blood pools for the preparation of purified  
XX blood products for passive immunisation. The present sequence is a gene  
XX encoding serine-aspartate repeat region protein, SdrG from Staphylococcus  
XX epidermidis. The Sdr protein is useful in vaccine preparation in  
XX combination with specific bacterial binding proteins. These vaccines can  
XX be used to treat a broad spectrum of bacterial infections, including  
XX those arising from both coagulase-positive and coagulase-negative  
XX bacteria  
XX  
XX Sequence 2976 BP; 1225 A; 439 C; 526 G; 786 T; 0 U; 0 Other;  
Query Match 92.4%; Score 1613.8; DB 3; Length 2976;  
Best Local Similarity 95.7%; Pred. No. 1e-283;

Matches 1670; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

Qy	1	TCTAGTGTGATGAAGAAAAGAAATGATGTGATCAATTAATTAATCAGTCAATAAACCACGACGAT	60
Db	318	TCCAGTAATGAAGAAAAGAAATGATGTGATCAATTAATTAATCAGTCAATAAACCACGACGAT	377
Qy	61	AATAACCAAAATAATTAAAAAAGAGAAGAACGAAATTAACACGATGCATAGCAAGAAAACGCTCA	120
Db	378	GATTAACCAAAATA---AAAAAAGAGAAGAACGAAATTAACGATGCATAGCAAGAAAACGCTCT	434
Qy	121	GAAGATAGAAACAGAGTCAACCAACAAATGTAGATCAAAACGAAAGCAACATTTTACAAAAG	180
Db	435	AAAGATATAACACAGTCAACCAACAAATGTAGATGAAGAAAGCAACATTTTACAAAAG	494
Qy	181	ACCCCTCAAGATAATATCTATCTTTACAGAAGAGAGGTAAAGAATCTCTCATCAGTGGAA	240
Db	495	ACCCCTCAAGATAATATCTCAGCTTTAAAGAAGAGGTAAAGAACCTCTCATCAGTGGAA	554
Qy	241	TCCTCAAAATTCATCAATTTGATACCTGCCCAACCAACCATCTCACAAACAATTAATAGAGAA	300
Db	555	TCCTCAAAATTCATCAATTTGATACCTGCCCAACCAACCATCTCATACAACAATAATAGTGA	614
Qy	301	GAATCTCTTCAAAACAAGTGAATAATGTAGAAGATTACACAGGTATCAGATTTTGTCTAACTCT	360
Db	615	GCATCTATTCAACACAGTGAATAATGAAGAAATTTCCCGGTATCAGATTTTGTCTAACTCT	674
Qy	361	AAAATAAAGAGAGTAAACACTGTAATCTGTAAAGAAGAGAATACTATAGAGCAACCTAAT	420
Db	675	AAAATAATAGAGTAAACACTGTAATCCAATAAAGAAGAGAATACTATAGAGCAACCTAAT	734
Qy	421	AAAGTAAAGAAGATTCAACAACAAGTCAGCGTCTGGCTATACAAATATAGATGAAGAAA	480
Db	735	AAAGTAAAGAAGATTCAATAACAAGTCAACCGTCTAGCTATAAAAATATAGATGAAGAAA	794
Qy	481	ATTTCAAAATCAAGATGAGTTATTAATTTTACCATAAATGAATATGAATATAGGCTAGA	540
Db	795	ATTTCAAAATCAAGATGAGTTATTAATTTTACCATAAATGAATATGAATATAGGCTAGA	854
Qy	541	CCATTATCTACAAACATCTGCCCAACCATCGAATTAACGCTGAACCGTAAATCAATTAGCG	600
Db	855	CCGTTATCTACACATCTGCCCAACCATCGATGAAGCGGTGAACCGTAAATCAATTAGCG	914
Qy	601	CGCGAAACAAGTTCGAATGTTTAAACATTTAAAGTTACTGATCAAAAGTATTAATCTGAA	660
Db	915	CGCGAAACAAGTTCGAATGTTTAAATCAATTTAAAGTTACTGATCAAAAGTATTAATCTGAA	974
Qy	661	GGATATGATGATGAGTGAAGTGTATTTAAAGCACATGATGCTGAAAACCTTAAATCTATGAT	720
Db	975	GGATATGATGATGATGATGATTTATTTAAAGCACATGATGCTGAAAACCTTAAATCTATGAT	1034
Qy	721	GTAATTTTGAAGTGAATGATTAAGTGAATCTCGTGAATCGATGACAGTGGATATAGAT	780
Db	1035	GTAATTTTGAAGTGAATGATTAAGTGAATCTCGTGAATCGATGACAGTGGATATAGAT	1094
Qy	781	AAGAATAACAGTTCATCAGATTTTAAACCGATAGCTTTTAAATACCAAAAAATAAAGATAAT	840
Db	1095	AAGAATAACAGTTCATCAGATTTTAAACCGATAGCTTTTAAATACCAAAAAATAAAGATAAT	1154
Qy	841	TCGGAGAAATCATCGCTACAGGTACTTTATGAATGAAGAAAATAAACAATCACTATACT	900
Db	1155	TCGGAGAAATCATCGCTACAGGTACTTTATGACAAACAATAAACAATCACTATACT	1214
Qy	901	TTTACAGATATGTAGATAAGTATGAATAATTAAGCACACCTTTAAATTAAGCTATAC	960
Db	1215	TTTACAGATATGTAGATAAGTATGAATAATTAAGCGCACCTTTAAATTAAGCTATAC	1274
Qy	961	ATTGATAAATCAAAAGTTTCCAAAATAAATACCAAGTTTATGATGATGAATAATAAAGCGCC	1020
Db	1275	ATTGATAAATCAAAAGTTTCCAAAATAAATACCAAGTTTATGATGATGAATAATAAAGCGCC	1334
Qy	1021	CTTTTCATCAGTAAATAAACAATTAACGGTTGAATATCAAGAGACTTAACGAAAATCGGACT	1080
Db	1335	CTTTTCATCAGTAAATAAACAATTAACGGTTGAATATCAAGAGACTTAACGAAAATCGGACT	1394

Qy	1081	GCTAACCTTCAAAGTATGTTTACAATATATAGATACGAAAAATCATACAGTTGAGCAAAACG	1141
Db	1395	GCTAACCTTCAAAGTATGTTTACAACAATAGATACGAAAAACCATACAGTTGAGCAAAACG	1454
Qy	1141	ATTTTATATTAACCCCTCTTCGTTATTCAGCCAAAGGAACAATATGTTTAAATATTTTCAGGGAAT	1200
Db	1455	ATTTTATATTAACCCCTCTTCGTTATTCAGCCAAAGGAACAATATGTTTAAATATTTTCAGGGAAT	1514
Qy	1201	GGTGATGAAGGTTTCAACAATTTATAGACGATAGCACCAATTAATTAAGAGTTTATAAGGTTTGA	1260
Db	1515	GGCGATGAAGTTCACAACATTCATCGACGATAGTACAAATCAATTAAGGTTTATAAGGTTTGA	1574
Qy	1261	GATTAATCAAAATTTTACAGATAGTAAACAGAAATTTATGATTTACAGTGAATGAAGATGTC	1320
Db	1575	GATAATCAAAATTTTACAGATAGTAAACAGAAATTTATGATTTACAGTGAATGAAGATGTC	1634
Qy	1321	ACAAATGATGATATATGCCCAATTTAGGAAATAATAATGATGCTGAATATTAATTTTGGTAAAT	1380
Db	1635	ACAANTGATGATATATGCCCAATTTAGGAAATAATAATGATGCTGAATATTAATTTTGGTAAAT	1694
Qy	1381	ATAGATTCAACCATATATTTATTAAGTTTATTTAGTAAATATGACCTTAATTAAGGATGATTAC	1440
Db	1695	ATAGATTCAACCATATATTTATTAAGTTTATTTAGTAAATATGACCTTAATTAAGGATGATTAC	1754
Qy	1441	ACGACTATACAGCAAACTGTGACAATGACGACGACATATAAATGAGTATATCTGGTGAGTTT	1500
Db	1755	ACGACGATACAGCAAACTGTGACAATGCAAAACGACTATAAATGAGTATATCTGGTGAGTTT	1814
Qy	1501	AGAACACATCTCTATGATAATACAAATTTGCTTTCTCTACAAGTTTCAGTCAAGGACAAGGT	1560
Db	1815	AGAACACATCTCTATGATAATACAAATTTGCTTTCTCTACAAGTTTCAGTCAAGGACAAGGT	1874
Qy	1561	GACTTGCTCTCTGAAAAAATTTATAAATCGGAGATTCAGTATGGGAAGATGTAGATAAA	1620
Db	1875	GACTTGCTCTCTGAAAAAATTTATAAATCGGAGATTCAGTATGGGAAGATGTAGATAAA	1934
Qy	1621	GATGGTATTCAAAATACAAATGATATGAATAAACCCTTAGTAAATGTTTGGTAACTTTG	1680
Db	1935	GATGGTATTCAAAATACAAATGATATGAATAAACCCTTAGTAAATGTTTGGTAACTTTG	1994
Qy	1681	ACGTATCTCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGAAATATCAATTT	1740
Db	1995	ACGTATCTCTGATGGAACCTTCAAAATCAGTCAGAACAGATGAAGATGGAAATATCAATTT	2054
Qy	1741	GATGG 1745	
Db	2055	GATGG 2059	
RESULT 8			
ACF80624			
ID	ACF80624	standard; DNA; 1680 BP.	
XX			
AC	ACF80624;		
XX			
DT	15-JAN-2004	(first entry)	
XX			
DE	Staphylococcus epidermidis	SdrG N1N2N3 domain coding sequence.	
XX			
KW	SdrG; surface protein; infection; antibacterial; vaccine; gene; ss.		
XX			
OS	Staphylococcus epidermidis.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..1680	
FT		/*tag= a	
FT		/partial	
FT		/product= "SdrG N1N2N3 domain"	
FT		/note= "No stop codon"	
XX			
XX	WO2003076470-A1.		



SdrG; surface protein; infection; antibacterial; vaccine; gene; ss.



OS	Staphylococcus epidermidis.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..951
FT		/*tag= a
FT		/product= "SdrG TR2 protein"
XX		
FN	WO2003076470-A1.	
XX		
PD	18-SEP-2003.	
XX		
PF	05-MAR-2003; 2003WO-US006415.	
XX		
PR	05-MAR-2002; 2002US-0361324P.	
XX		
PA	(INH1-) INHIBITEX INC.	
PA	(TEXA ) UNIV TEXAS A & M SYSTEM.	
XX		
PI	Patti JM, Hutchins JT, Hall A, Domanski P, Patel P, Hook M;	
PI	Robbins J, Vernachio J, Bowden MG;	
XX		
DR	WPI; 2003-722324/68.	
DR	P-PSDB; ABW79017.	
XX		
PT	New antibody recognizing a Staphylococcus epidermidis protein comprising	
PT	SdrG N1N2N3, SdrG N2N3 or SdrGTR2 useful for preparing a composition for	
PT	treating or preventing a coagulase-negative staphylococcal infection.	
XX		
PS	Claim 30; Page 26; 78pp; English.	
XX		
CC	The present sequence is that of a polynucleotide encoding the truncated	
CC	TR2 protein (amino acids 273-577) of the SdrG surface protein of	
CC	coagulase-negative staphylococcus epidermidis. A claimed antibody	
CC	recognises a protein selected from SdrG N1N2N3, N2N3 and TR2. The	
CC	antibody may be a monoclonal antibody, including a chimeric, murine,	
CC	humanized, human or single chain monoclonal antibody, which prevents a	
CC	coagulase-negative staphylococcal infection in a human or animal by	
CC	inhibiting binding of staphylococcus bacteria to fibrinogen. Such	
CC	antibodies can be used to treat or prevent staphylococcal infections	
CC	including nosocomial coagulase-negative staphylococcal infections in low	
CC	birth weight infants. A claimed vaccine comprises the isolated SdrG	
CC	N1N2N3, N2N3 or TR2 protein	
XX		
SQ	Sequence 951 BP; 389 A; 140 C; 155 G; 267 T; 0 U; 0 Other;	
	Query Match 49.6%; Score 866; DB 10; Length 951;	
	Best Local Similarity 96.7%; Pred. No. 5.9e-148;	
	Matches 884; Conservative 0; Mismatches 30; Indels 0; Gaps 0;	
Qy	602 CGGAACAAGGTTGGAATGTTAACCAATTTAAATTAAGTTACTGATCAAAAGTATTACTGAAG 661	
Db	35 CCGACAAGGTTGGAATGTTAATCAATTTAAATTAAGTTACTGATCAAAAGTATTACTGAAG 94	
Qy	662 GATATGATGATAGTGAAGTGTTATTAAAGCACATGATGCTGAAACCTTAATCTATGATG 721	
Db	95 GATATGATGATAGTGAAGTGTTATTAAAGCACATGATGCTGAAACCTTAATCTATGATG 154	
Qy	722 TAACTTTTGAAGTAGATGATAGGTCAAATCTGGTGATACGATGACAGTGGATATAGATA 781	
Db	155 TAACTTTTGAAGTAGATGATAGGTCAAATCTGGTGATACGATGACAGTGGATATAGATA 214	
Qy	782 AGAATACAGTTCATCAGATTAAACCGATAGCTTTTACAAATACCAAAATATAAAGATAATT 841	
Db	215 AGAATACAGTTCATCAGATTAAACCGATAGCTTTTTCGAATACCAAAATATAAAGATAATT 274	
Qy	842 CTGGAGAATCATCGCTCAGCTACTTATGATAACAAAATATAAACAATCACTACTATT 901	
Db	275 CTGGAGAATCATCGCTCAGCTACTTATGATAACAAAATATAAACAATCACTACTATT 334	
Qy	902 TTACAGATTATGATAGTAAATGATAATTTAAAGCACACCTTAAATTAAGCTCATACA 961	
Db	335 TTACAGATTATGATAGTAAATGATAATTTAAAGCGCAGCTTAAATTAACATCATACA 394	

Qy	962 TTGATAATCAAAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATATAAAACGGCCC 1021	
Db	395 TTGATAATCAAAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATATAAAACGGCCC 454	
Qy	1022 TTTTCATCAGTAATAATAAAACCAATTACGGTTGAAATATCAAAAGACCTTAACGAAAATCGGACTG 1081	
Db	455 TTTTCATCAGTAATAATAAAACCAATTACGGTTGAAATATCAAAAGACCTTAACGAAAATCGGACTG 514	
Qy	1082 CTAACCTTCAAAAGTATGTTTACAAATATAGATACGAAATAATATATATGAGTGGAGCAACGA 1141	
Db	515 CTAACCTTCAAAAGTATGTTTACAAACATAGATACGAAATAATATATATGAGTGGAGCAACGA 574	
Qy	1142 TTTTATATTAACCCCTCTTCGTTATTTCAGCCAAAGAAACAAATGTAATAATTTTCAGGGAATG 1201	
Db	575 TTTTATATTAACCCCTCTTCGTTATTTCAGCCAAAGAAACAAATGTAATAATTTTCAGGGAATG 634	
Qy	1202 GTGATGAAGGTTTCAACAATATATAGACGATACACATAATTAATTAAGTTTGGAG 1261	
Db	635 GCGATGAAGGTTTCAACAATATATCGCGATAGTACATCATTAAGTTTGGAG 694	
Qy	1262 ATAATCAAAATTTTACCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGCA 1321	
Db	695 ATAATCAAAATTTTACCAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGCA 754	
Qy	1322 CAAATGATGATTATGCCCAATTTAGGAAATATAATGATGTAATAATTTTGGTAATA 1381	
Db	755 CAAATGATGATTATGCCCAATTTAGGAAATATAATGATGTAATAATTTTGGTAATA 814	
Qy	1382 TAGATTCAACATATATTATTAAAGTTATTAGTAAATATGACCTTAATAAGGATGATTACA 1441	
Db	815 TAGATTCAACATATATTATTAAAGTTATTAGTAAATATGACCTTAATAAGGATGATTACA 874	
Qy	1442 CGACTATACAGCAAACTGTGCAATGACAGACGACTATAAATGAGTATACTGGTGAATTTA 1501	
Db	875 CGAGCATACAGCAAACTGTGCAATGCAAACTGCAAACTATAAAATGAGTATACTGGTGAATTTA 934	
Qy	1502 GAACAGCATCTCTAT 1515	
Db	935 GAACAGCATCTCTAT 948	
	RESULT 11	
ID	ACA46390 standard; DNA; 2010 BP.	
XX	ACA46390;	
XX	AC	
XX	19-JUN-2003 (first entry)	
DT	Prokaryotic essential gene #28047.	
DE	Antisense; db; prokaryotic essential gene; cell proliferation;	
XX	drug design; gene.	
KW	Staphylococcus epidermidis.	
XX	WO20027183-A2.	
OS	03-OCT-2002.	
XX	21-MAR-2002; 2002WO-US009107.	
PF	21-MAR-2001; 2001US-00815242.	
XX	06-SEP-2001; 2001US-00948993.	
PR	25-OCT-2001; 2001US-0342923P.	
PR	08-FEB-2002; 2002US-00072851.	
PR	06-MAR-2002; 2002US-0362699P.	
XX	(ELIT-) ELITRA PHARM INC.	
PA	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen K, Zykend JW;	
PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;	
XX		



DR WPI; 2003-029926/02.  
 XX P-PSDB; ABU42520.  
 PT New antiseptic nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 XX  
 PS Claim 14; SEQ ID NO 34260; 1766pp; English.  
 CC  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antiseptic sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antiseptic  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antiseptic nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antiseptic nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
 CC prokaryotic essential genes. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 2010 BP; 723 A; 340 C; 419 G; 528 T; 0 U; 0 Other;  
 SQ  
 Query Match 35.4%; Score 618.2; DB 8; Length 2010;  
 Best Local Similarity 98.2%; Pred. No. 6.2e-103;  
 Matches 639; Conservative 0; Mismatches 3; Indels 9; Gaps 1;  
 QY 1096 ATGTTTCAAAATATAGATACGAAATAATCATACAGTTGACCAACCGATTATTAACCTT 1155  
 DB 1 ATGTTTCAAAATATAGATACGAAATAATCATACAGTTGACCAACCGATTATTAACCTT 60  
 QY 1156 CTTTCGTTATTCAGCAAGCAACCAATGTAAATATTTTCAGGCAATGGTGATCAAGTTCA 1215  
 DB 61 CTTTCGTTATTCAGCAAGCAACCAATGTAAATATTTTCAGGCAATGGTGATCAAGTTCA 120  
 QY 1216 ACAATATAGATACGATACGCAATATTAAGTTTGAAGATTAATCAAAATTTA 1275  
 DB 121 ACAATATAGATACGATACGCAATATTAAGTTTGAAGATTAATCAAAATTTA 180  
 QY 1276 CCAGATAGTAACAGAAATTTATGATTAAGTATGAAGATGTCAAAATGATGATTAT 1335  
 DB 181 CCAGATAGTAACAGAAATTTATGATTAAGTATGAAGATGTCAAAATGATGATTAT 240  
 QY 1336 GCCCAATAGGAATAATATATGATGATTAATATTTTGGTAAATATAGATTCACCATAT 1395  
 DB 241 GCCCAATAGGAATAATATATGATGATTAATATTTTGGTAAATATAGATTCACCATAT 300  
 QY 1396 ATTATTAAAGTTATTAGTAAATATGACCTTAATAGGATGATTACACGACTATACGCA 1455  
 DB 301 ATTATTAAAGTTATTAGTAAATATGACCTTAATAGGATGATTACACGACTATACGCA 360  
 QY 1456 ACTGTGACAAATGACGACGACTATAATAGATGATCTGGTGGAGTTTGAAGACGATCCCTAT 1515

Db 361 ACTGTGACAAATGACGACGACTATAATAGATGATCTTTTGA-----AGCATCTAT 411  
 QY 1516 GATAATACAAATGCTTTCTCTCAAGTTTCAGGTCAAGGACAAAGTCACTTGCCTCTGAA 1575  
 Db 412 GATAATACAAATGCTTTCTCTCAAGTTTCAGGTCAAGGACAAAGTCACTTGCCTCTGAA 471  
 QY 1576 AAAAATTTATAAATCGGAGATTACGTTATCGGAAGATGTAGATAAAGATGTTATTTCAAAAT 1635  
 Db 472 AAAAATTTATAAATCGGAGATTACGTTATCGGAAGATGTAGATAAAGATGTTATTTCAAAAT 531  
 QY 1636 ACAATGATAATGAAAAACCGCTTAGTATGTTTGGTAACTTTGACGTTATCTGATGGA 1695  
 Db 532 ACAATGATAATGAAAAACCGCTTAGTATGTTTGGTAACTTTGACGTTATCTGATGGA 591  
 QY 1696 ACTTCAAAATCAGTCAGAACAGATGAAGATGGGAATATCAATTTTCATGGA 1746  
 Db 592 ACTTCAAAATCAGTCAGAACAGATGAAGATGGGAATATCAATTTTCATGGA 642  
 RESULT 12  
 AAH53653  
 ID AAH53653 standard; DNA; 837 BP.  
 XX  
 AC AAH53653;  
 XX  
 DT 03-SEP-2001 (first entry)  
 DE  
 DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:2699.  
 XX  
 KW Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;  
 KW endocarditis; ds.  
 XX  
 XX Staphylococcus epidermidis.  
 XX  
 PN WO200134809-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 XX 09-NOV-2000; 2000WO-US030782.  
 XX  
 XX 09-NOV-1999; 99US-0164258P.  
 XX  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX  
 XX Kimmerly WJ;  
 XX  
 DR WPI; 2001-316495/33.  
 XX P-PSDB; AAG82803.  
 PT  
 PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,  
 PT useful for vaccinating against infections, e.g. endocarditis.  
 XX  
 PS Claim 8; Page 705; 2188pp; English.  
 CC  
 CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides  
 CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I)  
 CC and (II) can have antibacterial activity and therefore can be used in  
 CC vaccination. The nucleic acids (I) may be used to produce the S.  
 CC epidermidis polypeptides (II) via the production of vectors containing  
 CC them which are used to produce host cells which express the  
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be  
 CC used to vaccinate subjects and to raise antibodies against the bacteria.  
 CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the  
 CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to  
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH55091 to AAH55098  
 CC represent oligonucleotide sequences and primers which are used in the  
 CC exemplification of the present invention. N.B. The present invention  
 CC specifically claims all the polynucleotide sequences given in the  
 CC sequence listing of the present specification, however the sequence  
 CC listing only goes up to SEQ ID NO:4454 so even though sequences are given  
 CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present

```
CC for SEQ ID NO:4455 to 4464
XX Sequence 837 BP; 375 A; 124 C; 126 G; 212 T; 0 U; 0 Other;
SQ

Query Match      29.0%; Score 507.2; DB 4; Length 837;
Best Local Similarity 97.5%; Pred. No. 8.2e-83;
Matches 515; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TCTAGTGAAGAAAGAGATGATGATGATCAATTAATATCAATGATCAATTAATCAACCGACGAT 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
223 TCTAGTGAAGAAAGAGATGATGATGATCAATTAATATCAATGATCAATTAATCAACCGAT 282
Qy 61 AATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
283 AATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 342
Qy 121 GAAGATAGACAGAGTCAACCAACCAATAGATGAAAGCAAGCAACCAATTTTACAAAAG 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
343 GAAGATAGACAGAGTCAACCAACCAATAGATGAAAGCAAGCAACCAATTTTACAAAAG 402
Qy 181 ACCCTCAAGATATATCTATCTTACAGAGAGGTAAGAAATCTCTATCAGTCGAA 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
403 TCCCTCAAGATATATCTATCTTACAGAGAGGTAAGAAATCTCTATCAGTCGAA 462
Qy 241 TCCTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCACACAACTAATATAGAA 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
463 TCCTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCACACAACTAATATAGAA 522
Qy 301 GAATCTGTTCAAAACAAAGTAAATGTAGAAGATTCACACGATATCAGATTTTGCTAACTCT 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
523 GAATCTGTTCAAAACAAAGTAAATGTAGAAGATTCACACGATATCAGATTTTGCTAACTCT 582
Qy 361 AAAATAAAGAGAGTAAACACTGAATCTGTGTAAGAGAGATATCTATATAGAGCAACCTAAT 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
583 AAAATAAAGAGAGTAAACACTGAATCTGTGTAAGAGAGATATCTATATAGAGCAACCTAAT 642
Qy 421 AAGTAAAGAGAGATTCACACAGATCAGCGCTCTGGCTATACAAATATAGATGAAAA 480
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
643 AAGTAAAGAGAGATTCACACAGATCAGCGCTCTGGCTATACAAATATAGATGAAAA 702
Qy 481 ATTTCAAAATCAAGATGAGTTTAAATTTTACCAATAAATGAATATGAA 528
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
703 ATTTCAAAATCAAGATGAGTTTAAATTTTACCAATAAATGAATATGAA 750

RESULT 13
AAH54128
ID AAH54128 standard; DNA; 3236 BP.
XX
AC AAH54128;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3492.
XX
KW Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US030782.
XX
PR 09-NOV-1999; 99US-0164258P.
XX
PA (GLAX ) GLAXO GROUP LTD.
XX
PI Kimmerly WJ;
XX
WPI; 2001-316495/33.
XX
DR

Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
useful for vaccinating against infections, e.g. endocarditis.
Claim 8; Page 1063-1064; 2188pp; English.
AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
(II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I)
and (II) can have antibacterial activity and therefore can be used in
vaccination. The nucleic acids (I) may be used to produce the S.
epidermidis polypeptides (II) via the production of vectors containing
them which are used to produce host cells which express the
polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
used to vaccinate subjects and to raise antibodies against the bacteria.
The polypeptides may also be used to assay for other inhibitors of their
activity and therefore identify compounds that may be used for the
treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
AAH55090 represent specifically claimed S. epidermidis genomic DNA
polynucleotide sequences from the present invention. AAH55091 to AAH55098
represent oligonucleotide sequences and primers which are used in the
exemplification of the present invention. N.B. The present invention
specifically claims all the polynucleotide sequences given in the
sequence listing of the present specification, however the sequence
listing only goes up to SEQ ID NO:4454 so even though sequences are given
in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present
for SEQ ID NO:4455 to 4464
SQ Sequence 3236 BP; 1223 A; 432 C; 500 G; 1081 T; 0 U; 0 Other;
Query Match      29.0%; Score 507.2; DB 4; Length 3236;
Best Local Similarity 97.5%; Pred. No. 9.1e-83;
Matches 515; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 TCTAGTGAAGAAAGAGATGATGATCAATTAATATCAATGATCAATTAATCAACCGACGAT 60
Db 1807 TCTAGTGAAGAAAGAGATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1866
Qy 61 AATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 120
Db 1867 AATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1926
Qy 121 GAAGATAGACAGAGTCAACCAACCAATGTAGATGAAAGCAAGCAACCAATTTTACAAAAG 180
Db 1927 GAAGATAGACAGAGTCAACCAACCAATGTAGATGAAAGCAAGCAACCAATTTTACAAAAG 1986
Qy 181 ACCCTCAAGATATATCTATCTTACAGAGAGAGGTAAGAAATCTCTATCAGTCGAA 240
Db 1987 TCCCTCAAGATATATCTATCTTACAGAGAGAGGTAAGAAATCTCTATCAGTCGAA 2046
Qy 241 TCCTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCACACAACTAATATAGAGAA 300
Db 2047 TCCTCAAAATTCATCAATTTGATCTGCCCAACCAACCATCTCACACAACTAATATAGAGAA 2106
Qy 301 GAATCTGTTCAAAACAAAGTAAATGTAGAAGATTCACACGATATCAGATTTTGCTAACTCT 360
Db 2107 GAATCTGTTCAAAACAAAGTAAATGTAGAAGATTCACACGATATCAGATTTTGCTAACTCT 2166
Qy 361 AAAATAAAGAGAGTAAACACTGAATCTGTGTAAGAGAGATATCTATATAGAGCAACCTAAT 420
Db 2167 AAAATAAAGAGAGTAAACACTGAATCTGTGTAAGAGAGATATCTATATAGAGCAACCTAAT 2226
Qy 421 AAGTAAAGAGAGATTCACACAGATCAGCGCTCTGGCTATACAAATATAGATGAAAA 480
Db 2227 AAGTAAAGAGAGATTCACACAGATCAGCGCTCTGGCTATACAAATATAGATGAAAA 2286
Qy 481 ATTTCAAAATCAAGATGAGTTTAAATTTTACCAATAAATGAATATGAA 528
Db 2287 ATTTCAAAATCAAGATGAGTTTAAATTTTACCAATAAATGAATATGAA 2334

RESULT 14
AAH77594
ID AAX77594 standard; DNA; 3498 BP.
```





Qy	430	GAAGATTCAACAACAGCTCAGCCGCTGGCTGTATACAAATATAGATGAAAAAATTTTCCAAT	489
Db	649	CCAGTAAATGTGTCAAAAGAGAAATCTTAAAAAAATCTCGAGAAATTTAAAGAAATTCGGTT	708
Qy	490	CAAGATGAGTATTATTAATTTTACCATAAAATGAAATATGAAAAATAGGGCTAGACCAATATCT	549
Db	709	AGAAATGATAGCAATA CAGATCATTTCAACTTAACCCAGTTGCTACAGCTCCACAGAGTTT	768
Qy	550	ACAACTCTGCCCCAACCATCGATTAAACGGTGTAAACCGTAAATCAATTAATTTAGCGGCGGAACAA	609
Db	769	GCACCAAAACGTTGTAAACGCAAAATCGCTTTCAGTTGCACAAACGACGACGATGCT	828
Qy	610	GGTTTCGAATGTTAACCAATTTAAATTTAAAGTTTACTGATCAAAAGTATTAATCTGAAGAGATATGAT	669
Db	829	TCAACAATGTTAAATGATTTAAATTTAAAGTGCAGCAAGCAAAACAATCA --- AAGTTGGCGAT	885
Qy	670	GATAGTGAAGGTGTTATTAAAGCACATGATGCTCGAAAACCTTAATCTATGATGTAACTTTT	729
Db	886	GGTAAAGATTAATGTGGCAGCAGCCGATGACGGTAAAGATATTGAATATGATACAGAGTTT	945
Qy	730	GAAGTAGATGAATAAGGTCAAAATCTGGTGTACATACGATGACAGTGGGATATAGATAAGAAATACA	789
Db	946	ACAAATGACAATAAGTCAAAAAGGCGATACATGACGATTAATTAATGATAGATGAATGA	1005
Qy	790	GTTCCTCATGAGTTAAACCGATAGCTTTTACAATACCAAAAATAAAGATAAATCTGGAGAA	849
Db	1006	ATTCCTTTCGGATTTAAACAGATAAAAATGATCTCTATCGATATTACTGATCCATCAGGAGAG	1065
Qy	850	ATCATCGCTACAGTACTTATGATTAACAAAATAAACAANAATCACTTATACCTTTTACAGAT	909
Db	1066	GTCAATGCTTAAAGGAAACATTTGATTAAGCAAACTAAAGCAAAATCAATATACATTTACAGAC	1125
Qy	910	TATGTAGATAAGTATGAAAAATTTAAAGCACACCTTAAATTTAAAGCTCATACATTTGATAAA	969
Db	1126	TATGTAGATAAATATGAAGATATAAATCAGCTTAATCTCTATTTTCGTATATTTGATAAA	1185
Qy	970	TCAAAGGTTCCAAATAATAATACAAAGTTAGATGTAGAATATAAAAACGGCCCTTTTCATCA	1029
Db	1186	AAAAACAGTTCCA --- AATGAGACAAGTTTGAATTTTAACTTTGCTACAGCAGGTAAAGAA	1242
Qy	1030	GTAAATAAACAATTTAGCTTGAATATCAAAAGACCTTAACGAAAATCGGACTGCTAACCTT	1089
Db	1243	ACAAGCCAAAATGTCTGTTGATATATCAAGATCCAAATGGTCCATGGTGAATCAAAACATTT	1302
Qy	1090	CAAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTCGAGCAAAACGATTTATATT	1149
Db	1303	CAATCTATCTTTACAAAATTTAGATGAAGATAGCAAACTATTGACAAACAAATTTATGTT	1362
Qy	1150	AACCTCTTCGTTATTTCAGCCAAAGGAAACAAATGTAAATATTTTCAGGGAATGGTGATG --	1207
Db	1363	AACCCATTGAAAAAATCAGCAACCAACACTAAAGTTTGATATAGCTGGTAGTCAAGTAGAT	1422
Qy	1208	-----AAGTTTCAACAATTTATAGACGATGACCAATTAATT	1242
Db	1423	GATTATGGAATAATTAACCTAGGAATGGTAGCACCATTATTGACCAAAATACAGAAATA	1482
Qy	1243	AAAGTTTATAAGGTTGGAGATATAAAAAATTTTACAGATAGTACGAAATTTATGATTAC	1302
Db	1483	AAGTTTATAAGGTTTAACTCTGATCAACAATGGCTCAAAAGTAATAGAACTCTATGATTTT	1542
Qy	1303	AGTGAATATGAAGATGTCAAAAATGA --- TGATTTATGCCCAAATTTAGGAAATAATAATATGAT	1359
Db	1543	AGTCAATACGAAGATGTAAACAAGTCAATTTTGATAATAAAAAATCAATTTAGTAAATATGA	1602
Qy	1360	GTGAATATTAAATTTTGGTAAATATAGATTTCCCATATATTAATTAAGGTTATTAGTAAATAT	1419
Db	1603	GCAACATTTGGATTTTGGTGATTTAAATTTACGCTTATATTACAAAGTTGTTAGTAAATAT	1662
Qy	1420	GACCTTAATAAGGATGATTACACGCTATACACGCAACTGTGCAATGCAGACGACTATA	1479
Db	1663	ACACCTACATCAGATGGCGAACTAGATATTTGGCCCAAGGTACTAGTATGAGAAACAACT	1719
Qy	1480	AATGAGTATACTGGTGAGTTTAGAAACAGCACTCTATGATAATAACAAATGCTTTCTCTACA	1539

**This Page Blank (uspto)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 12, 2006, 08:10:16 ; Search time 12.7 Seconds  
(without alignments)  
3610.121 Million cell updates/sec

Title: US-10-806-288-12  
Perfect score: 3026  
Sequence: 1 tctagtgtatgaagaagaa.....ggaaatatcaattgtatgga 1746

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 1301182

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-O=/abs/ABSSWEB/spool/US10806288/runat\_11082006\_163411\_21225/app.query.fasta\_1  
-DB=Issued\_Patents\_AA -QPMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0  
-LIST=45 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-MODE=LOCAL -OUTFMT=ptc -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15  
-HOST=abss02p -USR=US10806288 @CGN 1.1 84 @runat\_11082006\_163411\_21225  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5 COMB.pcp.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pcp.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7 COMB.pcp.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB.pcp.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS COMB.pcp.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pcp.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/baCkfile01.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3013	99.6	593	2	US-09-147-405B-11
2	3013	99.6	1092	2	US-09-147-405B-15
3	3007	99.4	582	2	US-09-147-405B-13
4	2810.5	92.9	930	2	US-09-134-001C-5314
5	2810.5	92.9	930	2	US-09-386-962C-10
6	1144.5	37.8	1166	2	US-09-200-650E-7
7	857	28.3	278	2	US-09-710-279-2700
8	576	19.0	1315	2	US-09-200-650E-5
9	499	16.5	1742	2	US-09-386-962C-4
10	499	16.5	1742	2	US-09-386-959-4
11	497	16.4	1155	2	US-09-710-279-1780
12	455	15.0	930	2	US-09-200-650E-3
13	454	15.0	936	2	US-08-956-171E-5249
14	454	15.0	936	2	US-08-781-986A-5249
15	452	14.9	933	2	US-08-293-728-2
16	452	14.9	933	2	US-09-421-868-2
17	452	14.9	933	2	US-09-679-643-2
18	443.5	14.7	520	2	US-10-056-052A-2
19	396	13.1	918	2	US-09-200-650E-1
20	349	11.5	331	2	US-10-056-052A-4
21	349	11.5	345	2	US-08-856-253-7
22	300.5	9.9	1027	2	US-08-956-171E-5254
23	300.5	9.9	1027	2	US-08-781-986A-5254
24	259.5	8.6	1112	1	US-08-714-402-2
25	259.5	8.6	1161	2	US-09-327-536-2
26	226	7.5	52	2	US-09-386-959-41
27	220.5	7.3	3696	2	US-03-134-001C-5080
28	215.5	7.1	1279	2	US-09-710-279-3188
29	212	7.0	44	2	US-09-386-959-46
30	209	6.9	630	2	US-08-973-462-9
31	208.5	6.9	251	2	US-08-956-171E-5252
32	208.5	6.9	251	2	US-08-781-986A-5252
33	204.5	6.8	1177	2	US-09-134-001C-5106
34	203.5	6.7	2504	2	US-09-328-352-5821
35	203	6.7	368	2	US-09-134-000C-4597
36	203	6.7	5024	2	US-09-710-279-2964
37	202	6.7	676	2	US-09-134-001C-4318
38	199.5	6.6	709	2	US-09-248-796A-19045
39	199	6.6	1306	2	US-09-134-000C-6670
40	197	6.5	2314	2	US-09-268-347-49
41	195	6.4	1335	2	US-09-134-001C-3716
42	195	6.4	10182	2	US-09-134-001C-3159
43	194.5	6.4	1435	1	US-08-568-459A-4
44	194.5	6.4	1435	1	US-08-487-826B-4
45	194.5	6.4	1435	2	US-09-210-288-4

#### ALIGNMENTS

##### RESULT 1

US-09-147-405B-11  
; Sequence 11, Application US/09147405B  
; Patent No. 6733758  
; GENERAL INFORMATION:  
; APPLICANT: Guss, Bengt  
; APPLICANT: Nilsson, Martin  
; APPLICANT: Frykberg, Lars  
; APPLICANT: Flock, Jan-Ingmar  
; APPLICANT: Lindberg, Martin  
; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from  
; FILE REFERENCE: Coagulase-Negative Staphylococcus  
; CURRENT APPLICATION NUMBER: US/09147405  
; CURRENT FILING DATE: 1999-04-11  
; PRIOR APPLICATION NUMBER: PCT/SE97/10191  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: SE 9602496-3  
; PRIOR FILING DATE: 1996-06-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-147-405B-11

Alignment Scores:  
Pred. No.: 6.66e-212 Length: 593  
Score: 3013.00 Matches: 582  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 99.6% Indels: 0  
DB: 2 Gaps: 0

```
US-10-806-288-12 (1-1746) x US-09-147-405B-11 (1-593)
QY 1 TCTAGTGTGATGAGAAAGAAATGATGTGATCAATAATAATCAGTCAATAATAACACCGGCGAT 60
Db 8 SerSerAspGluGluLysAsnAspValIleAsnAsnAsnGlnSerIleAsnThrAspAsp 27
QY 61 AATAACCAATAATTAATAAAGAAAGAAACCAATAACTTACGATGCGCATAGAAAACGCTCA 120
Db 28 AsnAsnGlnIleIleLysLysGluGluThrAsnAsnTyrAspGlyIleGluLysArgSer 47
QY 121 GAAGATAGAACAGAGTCAACCAACAATGTAGATGAAACGAAGCAACATTTTACAAAAG 180
Db 48 GluAspArgThrGluSerThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 67
QY 181 ACCCTCAAGATTAATCTCATCTTACAGAAGAGAGTAAGAATCCTCATCGTCGAA 240
Db 68 ThrProGlnAspAsnThrHisLeuThrGluGluValLysGluSerSerSerValGlu 87
QY 241 TCTCTCAAAATTCATCAATTGATCTGCCCAACCACTCTCACACAATAAATATAGAA 300
Db 88 SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrIleAsnArgGlu 107
QY 301 GAATCTGTTCAACCAAGTGAATAATGTAGAAAGATTCACACGTATCAGATTTTGTAACTCT 360
Db 108 GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer 127
QY 361 AAAATAAAGAGAGTAACTGAATCTGTGAAGAAGAGAGAAATCTATAGAGCAACCTAAT 420
Db 128 LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn 147
QY 421 AAAGTAAAGCAAGATTCACCAACAGTCAGCGCTCGGCTATACAAATATAGATGAAAAA 480
Db 148 LysValLysGluAspSerThrThrSerGlnProSerGlyThrAsnIleAspGluLys 167
QY 481 ATTTCAAAATCAAGATGAGTTATTAATTTTACCAATAAATGAATATGAAATTAAGGCTAGA 540
Db 168 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluThrGluAsnLysAlaArg 187
QY 541 CCATTATCTACACATCTGCCCAACCATCGATTAAACGGTGTAACCGTAATCAATTAGCG 600
Db 188 ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla 207
QY 601 GCGGAACAAGTTTCAAGTGTAACTTAAATTAAGTTACTCATCAAGTATTTACTGAA 660
Db 208 AlaGluGlnGlySerAsnValAsnHisLeuLysValThrAspGlnSerIleThrGlu 227
QY 661 GGATATGATGATGATGAGGTGTTATTAAAGCACATGATGCTGAAACCTTAATCTATGAT 720
Db 228 GlyTyrAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 247
QY 721 GTAACCTTTTCAAGTAGATGATAGGTGAATCTGGTGATACGATGACAGTGGATATAGAT 780
Db 248 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAspIleAsp 267
QY 781 AAGCAATACAGTTCATCAGATTTAAACCGATAGCTTTACATACCAATAAATAAAGATAAT 840
Db 268 LysAsnThrValProSerAspLeuThrAspSerPheThrIleProLysIleLysAspAsn 287
QY 841 TCTGGAGAAATCATCGCTACAGTACTTATGATAACAAAAATAACAAATCACTTACT 900
Db 288 SerGlyGluIleAlaThrGlyThrTyrAspAsnLysAsnLysGlnIleThrTyrThr 307
QY 901 TTTACAGATTATGATAGTAAGTATGAATAATATTAAAGCACACCTTTAAATTAACGTCTATC 960
Db 308 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 327
QY 961 ATTGATAAATCAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATAATAAAGCGCC 1020
Db 328 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 347
QY 1021 CTTTCATCAGTAATAAACAATTTACGGTTGAAATATCAAGACCTTAACGAAATCCGACT 1080
Db 348 LeuSerSerValAsnLysThrIleThrValGluTyrGlnArgProAsnGluAsnArgThr 367
```

---

```
QY 1081 GCTAACCTTCAAGATATGTTTACAAATATAGATACGAAAAATCATACAGTTGACCAACG 1140
Db 368 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 387
QY 1141 ATTTATATTAAACCTCTTCGTTATTTCAGCAAGAAACAAATGTAATATTTTCAGGGAAT 1200
Db 388 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 407
QY 1201 GGTGATGAAGTTCAACAAATTATAGACGATAGCACAAATAATTAAGATTTTATAAGTTGGA 1260
Db 408 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 427
QY 1261 GATAATCAAAATTTACCAGATAGTAACAAATTTATGATACAGTCAAGTAATGAGAGTGC 1320
Db 428 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 447
QY 1321 ACAAAATGATGATTATGCCCAATTAGGAAATAATAATGATGTGAATATTAAATTTTGTAAAT 1380
Db 448 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 467
QY 1381 ATAGATTCCCATATATATTAAAGTTATTAGTAAATATGACCTTAATAAGGATGATTAC 1440
Db 468 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 487
QY 1441 AGCATATACAGCAAACTGTGACAAATGACAGCACTATAAATCAGTATATCTGCTGAGTTT 1500
Db 488 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 507
QY 1501 AGAACAGCATCTCTATGATAATAACAAATGCTTCTCTACAAAGTTTCAGGTCAAAGCAAGGT 1560
Db 508 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 527
QY 1561 GACTTGCTCTCTGAAAAAATCTTATAAAATCGAGATTACGTATGGGAAGATGTAGATAAA 1620
Db 528 AspLeuProGluLysThrTyrLysIleGlyAspTyrValTyrGluAspValAspLys 547
QY 1621 GATGCTATTCAAAATACAAATGATATGAAACCGCTTAGTAATCTATTGTTAACTTTG 1680
Db 548 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 567
QY 1681 ACCTATCTCTGATGGAATCTTCAAAATCAGTCAGAACAGATGGAAGATGGAATATCAATTT 1740
Db 568 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluAspGlyLysTyrGlnPhe 587
QY 1741 GATGGA 1746
Db 588 AspGly 589
```

RESULT 2  
US-09-147-405B-15  
; Sequence 15, Application US/09147405B  
; Patent No. 6733758  
; GENERAL INFORMATION:  
; APPLICANT: Guss, Bengt  
; APPLICANT: Nilsson, Martin  
; APPLICANT: Frykberg, Lars  
; APPLICANT: Flock, Jan-Ingmar  
; APPLICANT: Lindberg, Martin  
; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from  
; FILE REFERENCE: Coagulase-Negative Staphylococcus  
; CURRENT APPLICATION NUMBER: US/09/147,405B  
; CURRENT FILING DATE: 1999-04-11  
; PRIOR APPLICATION NUMBER: PCT/SE97/10191  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: SE 9602496-3  
; PRIOR FILING DATE: 1996-06-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 1092  
; TYPE: PRT



ORGANISM: Staphylococcus epidermidis  
US-09-147-405B-15

Alignment Scores:  
Pred. No.: 7,07e-212 Length: 1092  
Score: 3013.00 Matches: 582  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 99.6% Indels: 0  
DB: 2 Gaps: 0

US-10-806-288-12 (1-1746) x US-09-147-405B-15 (1-1092)

```

Qy 1 TCTAGTGAAGAAAAGAAATGATGTGATCAATAATATCAAGTCAATAAAACACCGACGAT 60
Db 75 SerSerAspGluGluLysAsnAspValIleAsnAsnAsnGlnSerIleAsnThrAspAsp 94

Qy 61 AATAACCAAAATAATTAAGAAAGAAACGAAATCACTACGATGCGATAGAAAACGGCTCA 120
Db 95 AsnAsnGlnIleIleLysLysGluGluThrAsnAsnTyrAspGlyIleGluLysArgSer 114

Qy 121 GAAGATGAACAGAGTCAACAAACAAATGTAGATCAAAACGAAGCAACATTTTACAAAAG 180
Db 115 GluAspArgThrGluSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 134

Qy 181 ACCCTCAAGATAATACATCTTACAGAAAGAGAGGTAAAGAAATCCTCATCAGTCGAA 240
Db 135 ThrProGlnAspAsnThrHisLeuThrGluGluGluValLysGluSerSerSerValGlu 154

Qy 241 TCCTCAAAATTCATCAATGTACTGCCCAACCAACCATCTCCACACAACTAATATAGAGAA 300
Db 155 SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrThrIleAsnArgGlu 174

Qy 301 GAATCTGTCAAAACAAAGTAAATGTAGAAATTCACACGATCATCAGATTTTGTAACTCT 360
Db 175 GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer 194

Qy 361 AAAATAAAGAGAGTAACTGAATCTCGTAAAGAGAGATATCTATAGAGCAACCTAAT 420
Db 195 LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn 214

Qy 421 AAAGTAAAGAGATTCAACACAAAGTCAGCCGCTCGCTATACAAATATAGATGAAGAAA 480
Db 215 LysValLysGluAspSerThrThrSerGlnProSerGlyTyrThrAsnIleAspGluLys 234

Qy 481 ATTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATGAATAAAGCTAGA 540
Db 235 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysAlaArg 254

Qy 541 CCATTATCTCAACATCTGCCCAACCATCGAATTAACCGTGAACCGTAAATCAATTAGCG 600
Db 255 ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla 274

Qy 601 GCGAACAAGGTTCCGAATTTAACTTAATTAAGTTACTGATCAAGATTAATCTGAA 660
Db 275 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 294

Qy 661 GGATATGATGATGAGGTTATTAAAGCACATCATGCTGAAACTTAATCTATGAT 720
Db 295 GlyTyrAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 314

Qy 721 GTAACTTTGAAGTAGATGAATGAAGTGAATCTCGTGATACGATCAGATGGATATAGAT 780
Db 315 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAspIleAsp 334

Qy 781 AAGAAATCAGTTCATCAGATTAAACCGATAGCTTTTACATACCACAAAATAAAGATAAT 840
Db 335 LysAsnThrValProSerAspLeuThrAspSerPheThrIleProLysIleLysAspAsn 354

Qy 841 TCTGAGAAATCATCGGTACAGGTACTATGATACAAAATTAACAAATCAACCTACTACT 900
Db 355 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnLysAsnLysGlnIleThrTyrThr 374

```

```

Qy 901 TTTACAGATTATGTAGATAAGTATGAAAAATATTAAAGCACACCTTAAATTAACGTCATAC 960
Db 375 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 394

Qy 961 ATTGATAAATCAAGGTTCCAAATAATAATACCAAGTTAGATGTAGATATAAAACGGCC 1020
Db 395 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyrLysThrAla 414

Qy 1021 CTTTCATCAGTAAATAAAACAAATTAACGTTGAAATATCAAGACCTTAACGAAAAATCGGACT 1080
Db 415 LeuSerSerValAsnLysThrIleThrValGluTyrGlnArgProAsnGluAsnArgThr 434

Qy 1081 GCTTAACCTTCAAAAGTATGTTTACAAATATAGATACGAAAAATCATACAGTTGAGCAACG 1140
Db 435 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 454

Qy 1141 ATTTATATTAACCTCTCTCGTTATTACGCCAAGCAAAACAAATGTAATATTATTCAGGGAAT 1200
Db 455 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 474

Qy 1201 GGTGATCAAGGTTCAACAAATTAAGACGATAGCAACAATAATTAAGTTTATAAGGTTGGA 1260
Db 475 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 494

Qy 1261 GATAATCAAAATTTACAGATAGTAAACAGAAATTTATGATTACAGTGAATATGAAGATGC 1320
Db 495 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 514

Qy 1321 ACAATGATGATTTATGCCCCTTAGGAAATAATAATGATGTAATATATTTTGGTAAAT 1380
Db 515 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn 534

Qy 1381 ATAGATTCACCATATATTATAAGTTATTAGTAAATATGACCCCTAATAAGGATGATTAC 1440
Db 535 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 554

Qy 1441 ACGATATACAGCAAACTGTGACAATCGACACGACTATAAATAGATGATCTACTGGTGGTTT 1500
Db 555 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 574

Qy 1501 AGAACAGATCCTATGATAATACAAATTCCTTCTCAAGTTTCAGTCAAGGCAAGGT 1560
Db 575 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 594

Qy 1561 GACTTGCTCTCGAAAAAATCTTATAAATCGAGATTACGATATCGGGAAGATGTAGATAAA 1620
Db 595 AspLeuProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys 614

Qy 1621 GATGGTATTCAAAATACAAAATGATAATGAAAAACCGCTTAGTATGATTTTGGTAACTTTG 1680
Db 615 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 634

Qy 1681 ACGTATCCTGATGAACTTCAAAATCAAGTCAAGACAGATGAAGATGGGAAATATCAATTT 1740
Db 635 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluAspGlyLysTyrGlnPhe 654

Qy 1741 GATGGA 1746
Db 655 AspGly 656

```

# RESULT 3

US-09-147-405B-13  
; Sequence 13, Application US/09147405B  
; Patent No. 6733758  
; GENERAL INFORMATION:  
; APPLICANT: Gues, Bengt  
; APPLICANT: Nilsson, Martin  
; APPLICANT: Frykberg, Lars  
; APPLICANT: Flock, Jan-Ingmar  
; APPLICANT: Lindberg, Martin  
; TITLE OF INVENTION: Fibrinogen Binding Protein Originating from  
; TITLE OF INVENTION: Coagulase-Negative Staphylococcus  
; FILE REFERENCE: guss 09/147405

```
; CURRENT APPLICATION NUMBER: US/09/147,405B
; CURRENT FILING DATE: 1999-04-11
; PRIOR APPLICATION NUMBER: PCT/SE97/10191
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: SE 9602496-3
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-147-405B-13

Alignment Scores:
Pred. No.: 1.82e-211 Length: 582
Score: 3007.00 Matches: 582
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 99.4% Indels: 0
DB: 2 Gaps: 0

US-10-806-288-12 (1-1746) x US-09-147-405B-13 (1-582)
QY 1 TCTAGTGATGAAGAAAGAAATGTGATCAATAAATCAGTCAATAAACAACCGACGAT 60
DB 1 SerSerAspGluGluLysAsnAspValIleAsnAsnAsnGlnSerIleAsnThrAspAsp 20
QY 61 AATAACCAATAATTTAAAAAGAGAAACGAATACTACGATGGCATAGAAAAACGCTCA 120
DB 21 AsnAsnGlnIleIleLysLysGluGluThrAsnAsnTyrAspGlyIleGluLysArgSer 40
QY 121 GAAGATAGACAGAGTCAACAACAATGTAGATGAACAACAACAACAATTTTACAAG 180
DB 41 GluAspArgThrGluSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 60
QY 181 ACCCTCAAGATAATCTCATCTTACAGAAGAGAGGTAAAGAAATCCTCATCAGTCGAA 240
DB 61 ThrProGlnAspAsnThrHisLeuThrGluGluGluValLysGluSerSerValGlu 80
QY 241 TCCTCAAAATTCATCAATTTGATCTGCCCAACAACCATCTCACACAACAATAATAGAGAA 300
DB 81 SerSerAsnSerSerIleAspThrAlaGlnGlnProSerHisThrThrIleAsnArgGlu 100
QY 301 GAATCTGTTCAACAAGTGAATATAGAGATTTCACAGTATCAGATTTTGTAACTCT 360
DB 101 GluSerValGlnThrSerAspAsnValGluAspSerHisValSerAspPheAlaAsnSer 120
QY 361 AAAATAAAAGAGAGTAACACTGAATCTGGTAAAGAGAGAAATACTATAGAGCAACCTAAT 420
DB 121 LysIleLysGluSerAsnThrGluSerGlyLysGluGluAsnThrIleGluGlnProAsn 140
QY 421 AAAGTAAAGAGAGATTCAACAACAAGTCAGCCGTCTGGCTATACAAATATAGATGAAAAA 480
DB 141 LysValLysGluAspSerThrThrSerGlnProSerGlyTyrThrAsnIleAspGluLys 160
QY 481 ATTTCAAAATCAAGATGAGTTTAAATTTACCAATTAATGAATATGAATAAAGGCTAGA 540
DB 161 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyrGluAsnLysAlaArg 180
QY 541 CCATTATCTACAACATCTGCCCAACCATCGATTAAACGTTAAACGTTAAATCAATTAGCG 600
DB 181 ProLeuSerThrThrSerAlaGlnProSerIleLysArgValThrValAsnGlnLeuAla 200
QY 601 GCGGAACAAGGTTTCAAGTGTAACTTAAATTTAAAGTTTACTGATCAAAAGTATTACTGAA 660
DB 201 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 220
QY 661 GGATATGATGATAGTAGAGTGTTATTAAAGCACATGATGCTGAAACCTTAATCTATGAT 720
DB 221 GlyTyrAspAspSerGluGlyValIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 240
QY 721 GTAACTTTTGAAGTAGATGATAGGTGAAATCTGGTGATACGATGACAGTGGATATAGAT 780
```

RESULT 4

US-09-134-001C-5314

```

; Sequence 5314, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5314
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-5314

Alignment Scores:
Pred. No.: 3,99e-197 Length: 930
Score: 2810.50 Matches: 545
Percent Similarity: 96.2% Conservative: 15
Best Local Similarity: 93.8% Mismatches: 21
Query Match: 92.9% Indels: 1
DB: 2 Gaps: 1

US-10-806-288-12 (1-1746) x US-09-134-001C-5314 (1-930)

Qy 1 TCTAGTATGAAGAAAGATGTGATCAATTAATCAATAGTCAATAAACCACGAGAT 60
Db 73 SerSerAsnGluGluLysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 92
Qy 61 AATAACCAATAATTAATAAAGAGAAACGAAATCACTACGATGCGATGAGAAACGCTCA 120
Db 93 AsnGln-----IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer 111
Qy 121 GAAGATAGACAGAGTCAACAAACAAATGTAGATGAAACGAAACGAAATTTTACAAAG 180
Db 112 LysAspIleThrGlnSerThrThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 131
Qy 181 ACCCTCAAGATAATCTCATCTTACAGAGAGAGGTAAAGAAATCTCATAGTCGAA 240
Db 132 ThrProGlnAspAsnThrGlnLeuLysGluGluValLysGluProSerSerValGlu 151
Qy 241 TCCTCAAAATTCATCAATTTGATCTGCCCAACCACTCTCACACAAATAAATAGAGAA 300
Db 152 SerSerAsnSerSerMetAspThrAlaGlnGlnProSerHisThrThrIleAsnSerGlu 171
Qy 301 GAATCTGTTCACAAAGTGATAATGTAGAGATTCACACGATPATCAGATTTTGTCTAACTCT 360
Db 172 AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer 191
Qy 361 AAAATAAAGAGAGTAACTGAATCTGTGTAAGAGAGAAATATCTATAGAACACCTAAT 420
Db 192 LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn 211
Qy 421 AAAGTAAAGAGATTCACAAACAGTCAGCGCTCGCTATACAAATATAGATGAAAAA 480
Db 212 LysValArgGluAspSerIleThrSerGlnProSerSerThrLysAsnIleAspGluLys 231
Qy 481 ATTTCAAATCAAGATGAGTTATTAATTAATTAACAAATTAATGAATTAAGAAATAGAGCTAGA 540
Db 232 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluThrGluAsnLysValArg 251
Qy 541 CCATTATCTAACATCTGCCCAACCATCGATTAAACGCTGTAACCGTAAATCAATTAGCG 600
Db 252 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 271
Qy 601 GCGAACAAGGTTTCAATTTGAATTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
Db 272 AlaGluGlnGlySerAsnValAsnHisLeuIleLysValThrAspGlnSerIleThrGlu 291

```

```

Qy 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 292 GlyTyrAspAspSerAspGlyIleIleLysAlaHisAspAlaGluAsnLeuIleTyrAsp 311
Qy 721 GTAATCTTTGAGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 312 ValThrPheGluValAspAspLysValLysSerGlyAspThrMetThrValAsnIleAsp 331
Qy 781 AAGAATACAGTTCATCAGATTTAAACCATAGCTTTTAAATACCAATACCAATACCAATAC 840
Db 332 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 351
Qy 841 TCTGAGAAATCATCGCTACAGGTACTTATGATTAACAAATAAATAAATAAATAAATAA 900
Db 352 SerGlyGluIleIleAlaThrGlyThrTyrAspAsnThrAsnLysGlnIleThrThr 371
Qy 901 TTTACAGATTTATGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT 960
Db 372 PheThrAspTyrValAspLysTyrGluAsnIleLysAlaHisLeuLysLeuThrSerTyr 391
Qy 961 ATTGATAAATCAAAAGTTTCCAAATAATAATAACCAAGTTAGATGATAGATAGATAGAT 1020
Db 392 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluThrLysThrAla 411
Qy 1021 CTTTCATCAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1080
Db 412 LeuSerSerValAsnLysThrIleThrValGluThrGlnLysProAsnGluAsnArgThr 431
Qy 1081 GCTAACCTTCAAGATGTTTCAAAATATAGATAGATAGATAGATAGATAGATAGATAGAT 1140
Db 432 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 451
Qy 1141 ATTTATATTAACCTCTTCGTTATTCAGCCAGGAAACAAATGTAATATTTTCAGGGAT 1200
Db 452 IleTyrIleAsnProLeuArgTyrSerAlaLysGluThrAsnValAsnIleSerGlyAsn 471
Qy 1201 GGTGATGAAGGTTTCAACAAATTTATAGACGATAGCAACAATAATAAAGTTTATAAG 1260
Db 472 GlyAspGluGlySerThrIleIleAspAspSerThrIleIleLysValTyrLysValGly 491
Qy 1261 GATAATCAAAATTTACAGATAGTAAACAGATTTTATGATGATGATGATGATGATGATGAT 1320
Db 492 AspAsnGlnAsnLeuProAspSerAsnArgIleTyrAspTyrSerGluTyrGluAspVal 511
Qy 1321 ACAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 512 ThrAsnAspAspTyrAlaGlnLeuGlyAsnAsnAsnAspValAsnIleAsnPheGlyAsn 531
Qy 1381 ATAGATTCACCATATATTTAAAGTTTATTAAGTATGATGATGATGATGATGATGATGAT 1440
Db 532 IleAspSerProTyrIleIleLysValIleSerLysTyrAspProAsnLysAspAspTyr 551
Qy 1441 ACAGATATACAGCAAACTGTGACATGACAGCACTATATAATAGATGATGATGATGATGAT 1500
Db 552 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyrThrGlyGluPhe 571
Qy 1501 AGAACGATCCTCATGATATCAATGCTTCTCTACAGATTCAGCTCAGGCAAGGT 1560
Db 572 ArgThrAlaSerTyrAspAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 591
Qy 1561 GACTTGCTCTCAAAACCTTATAAATCGAGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 592 AspLeuProProGluLysThrTyrLysIleGlyAspTyrValTrpGluAspValAspLys 611
Qy 1621 GATGGTATTCAAATACAAATGATTAATAAAGCCGCTTAGTATGATGATGATGATGATGAT 1680
Db 612 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 631
Qy 1681 ACGTATCCTGATCGAATTCAAATTCAGTACAGACAGATGAGATGAGATGAGATGAGATGAT 1740
Db 632 ThrTyrProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyrGlnPhe 651

```

```
QY 1741 GATGGA 1746
Db 652 AspGly 653

RESULT 5
US-09-386-962C-10
; Sequence 10, Application US/09386962C
; Patent No. 6635473
; GENERAL INFORMATION:
; APPLICANT: FOSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLOCOCCUS
; FILE REFERENCE: P06335US2/BAS
; CURRENT APPLICATION NUMBER: US/09/386,962C
; CURRENT FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-386-962C-10

Alignment Scores:
Pred. No.: 3,99e-197 Length: 930
Score: 2810.50 Matches: 545
Percent Similarity: 96.2% Conservative: 15
Best Local Similarity: 93.6% Mismatches: 21
Query Match: 92.9% Indels: 1
DB: 2 Gaps: 1

US-10-806-288-12 (1-1746) x US-09-386-962C-10 (1-930)

QY 1 TCTAGTGATCAAGAAAGAAATGATGATCAATAATAATCAGTCAATAAACACCGCAT 60
Db 73 SerSerAsnGluGluysAsnAspValIleAsnAsnSerGlnSerIleAsnThrAspAsp 92
QY 61 AATAACCAATAATTAATAAAGAAAGAAACGAATAACTACGATGGCATAGAAAACGCTCA 120
Db 93 AspAsnGln--IleLysLysGluGluThrAsnSerAsnAspAlaIleGluAsnArgSer 111
QY 121 GAAGATAGACAGAGTCAACAAACAAATGTAGATGAAACGAACCAACATTTTACAAAG 180
Db 112 LysAspIleThrGlnSerThrAsnValAspGluAsnGluAlaThrPheLeuGlnLys 131
QY 181 ACCCCTCAAGATAACTACTCATCTTACAGAAAGAGAGTAAAGAAATCCTCATCAGTCGAA 240
Db 132 ThrProGlnAspAsnThrGlnLeuLysGluGluValValysGluProSerSerValGlu 151
QY 241 TCTCAAAATTCATCAATTGATCTGCCCAACAAACCATCTCACAAACAATAATAGAGAA 300
Db 152 SerSerAsnSerSerMetAspThrAlaGlnProSerHisThrThrIleAsnSerGlu 171
QY 301 GAATCTGTTCAACAGTGTATGTAGAGATTCAACGATATCAGATTTTGCTACTCT 360
Db 172 AlaSerIleGlnThrSerAspAsnGluGluAsnSerArgValSerAspPheAlaAsnSer 191
QY 361 AAAATAAAGAGAGTAAACCTGAATCTGGTAAAGAGAGAAATACTATAGAGCAACCTAAT 420
Db 192 LysIleIleGluSerAsnThrGluSerAsnLysGluGluAsnThrIleGluGlnProAsn 211
QY 421 AAAGTAAAGAGATTCAACAAACAGTCAGCCGCTCTGGCTATACAATAATAGATGAAAAA 480
Db 212 LysValArgGluAspSerIleThrSerGlnProSerSerTyLysAsnIleAspGluLys 231
QY 481 ATTTCAATCAAGATGATGATTAATAATTTACCAATAAATCAATATCAAAATAGGCTAGA 540
Db 232 IleSerAsnGlnAspGluLeuLeuAsnLeuProIleAsnGluTyArgGluAsnLysValArg 251
QY 541 CCATTATCTCAACATCTGCCCAACCATCGATTTAAACGTTAAACCGTAAATCAATTAGCG 600
```

```
Db 252 ProLeuSerThrThrSerAlaGlnProSerSerLysArgValThrValAsnGlnLeuAla 271
QY 601 GCGGAA CAAGGTTT CGAATGTTAA CCAATTTAAATTTAAAGTTTACTGATCAAAAGTATTACTGAA 660
Db 272 AlaGluGlnGlySerAsnValAsnHieLeuLysValThrAspGlnSerIleThrGlu 291
QY 661 GGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 292 GlyTyAspAspSerAspGlyIleIleLysAlaHieAspAlaGluAsnLeuIleTyAsp 311
QY 721 GTAACCTTTTGAAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 312 ValThrPheGluValAspAspLysValLysSerGlyAspThrMecThrValAsnIleAsp 331
QY 781 AAGAATACAGTTTCCATCAGATTTAA CCGATAGCTTTTCAATACCAAAAAATAAAAAAGATAAT 840
Db 332 LysAsnThrValProSerAspLeuThrAspSerPheAlaIleProLysIleLysAspAsn 351
QY 841 TCTGGAGAAATCATCGCTACAGTACTTATGATAACAAAAATAAAAAATCAACATCACCCTACTACT 900
Db 352 SerGlyGluIleAlaThrGlyThrTyAspAsnThrAsnLysGlnIleThrTyThr 371
QY 901 TTTTACAGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 372 PheThrAspTyArgValAspLysTyArgLysIleLysAlaHieLysLysLeuThrSerTyThr 391
QY 961 ATTGATAAATCAAGGTTCCAAATATAATACCAAGTTAGATGTAGATAATAAAACGGCC 1020
Db 392 IleAspLysSerLysValProAsnAsnAsnThrLysLeuAspValGluTyLysThrAla 411
QY 1021 CTTTCATCAGTAATAAATAAACAATTACGGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 412 LeuSerSerValAsnLysThrIleThrValGluTyArgLysProAsnGluAsnArgThr 431
QY 1081 GCTAACCTTTCAAGATGATGTTTACAAATATAGATATACGAAAAATCATACAGTTAGCAAAACG 1140
Db 432 AlaAsnLeuGlnSerMetPheThrAsnIleAspThrLysAsnHisThrValGluGlnThr 451
QY 1141 ATTTATATTAAACCTCTTCGTTATTACGCAAGGAAACAAATGTAATATTTTTCAGGGAAT 1200
Db 452 IleTyIleAsnProLeuArgTyArgSerAlaLysGluThrAsnValAsnIleSerGlyAsn 471
QY 1201 GGTGATGAGGTTCAACAATATTAGACGATACACACAATAATTAAGTTTATAGGTTGGA 1260
Db 472 GlyAspGluGlySerThrIleIleAspAspSerThrIleLysValTyLysValGly 491
QY 1261 GATAATCAAAATTTACAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGTC 1320
Db 492 AspAsnGlnAsnLeuProAspSerAsnArgIleTyAspTyArgSerGluTyArgAspVal 511
QY 1321 ACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 512 ThrAsnAspAspTyArgAlaGlnLeuGlyAsnAsnAspValAsnIleAsnPheGlyAsn 531
QY 1381 ATGATGTTCCACATATATTATTAAGTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 532 IleAspSerProTyArgIleIleLysValIleSerLysTyArgProAsnLysAspAspTyArg 551
QY 1441 AGCACTATACACCAAACTGTGCAATGACAGACGACTATAAATCAGTATATCTGCTGAGTTT 1500
Db 552 ThrThrIleGlnGlnThrValThrMetGlnThrThrIleAsnGluTyArgGlyGluPhe 571
QY 1501 AGAACAGCATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Db 572 ArgThrAlaSerTyArgAsnThrIleAlaPheSerThrSerSerGlyGlnGlyGlnGly 591
QY 1561 GACTTGCCCTCCGAAAAAATCTTATAAATCGAGATTTAGTATGCGAAGATGATGATGATGATGATGAT 1620
Db 592 AspLeuProGluLysThrTyArgLysIleGlyAspTyArgTrpGluAspValAspLys 611
QY 1621 GATGTTTCAAAATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
```

Db 612 AspGlyIleGlnAsnThrAsnAspAsnGluLysProLeuSerAsnValLeuValThrLeu 631  
 Qy 1691 AGCTATCTGATGGAACTTCAAAATCAGTCAGAAACAGATGAGGAAATATCAATTT 1740  
 Db 632 ThrTyProAspGlyThrSerLysSerValArgThrAspGluGluGlyLysTyGlnPhe 651  
 Qy 1741 GATGGA 1746  
 Db 652 AspGly 653

RESULT 6  
 US-09-200-650E-7  
 ; Sequence 7, Application US/09200650E  
 ; Patent No. 6860195  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fatti, Joseph M.  
 ; APPLICANT: Foster, Timothy J.  
 ; APPLICANT: Hook, Magnus A.O.  
 ; APPLICANT: Eidhinn, Deirdre Ni  
 ; APPLICANT: Perkins, Samuel L.  
 ; TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus aureus  
 ; FILE REFERENCE: P06283US2/BAS  
 ; CURRENT APPLICATION NUMBER: US/09/200,650E  
 ; PRIORITY FILING DATE: 1998-11-25  
 ; PRIOR APPLICATION NUMBER: 60/066,815  
 ; PRIOR FILING DATE: 1997-11-26  
 ; PRIOR APPLICATION NUMBER: 60/098,427  
 ; PRIOR FILING DATE: 1998-08-31  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 1166  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus aureus  
 US-09-200-650E-7

Alignment Scores:  
 Pred. No.: 1,07e-75 Length: 1166  
 Score: 1144.50 Matches: 263  
 Percent Similarity: 60.1% Conservative: 108  
 Best Local Similarity: 42.6% Mismatches: 191  
 Query Match: 37.8% Indels: 55  
 DB: 2 Gaps: 18

US-10-806-288-12 (1-1746) x US-09-200-650E-7 (1-1166)

Qy 1 TCTAGTGATGAAGAAAGATGTGTGATCAATAATATCATGCTCAATAAACACCGACAT 60  
 Db 66 AlaThrThrSerAspAsnLysGluValSerGluThrGluAsnAsnSerThrThrGlu 85  
 Qy 61 AATAACCAATA-----ATTAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 114  
 Db 86 AsnAsnSerThrAsnProIleLysLysGlu-----ThrAsnThrAspSerGlnProGlu 103  
 Qy 115 CGCTCAGAAAGATGAAGATCAACAAATGTAGATGAAAGAAAGAAAGAAAGAAATTTTA 174  
 Db 104 AlaLysLysGluSerThrSerSerSerThrGlnLysGlnAsnAsnValThrAlaThr 123  
 Qy 175 CAAAAGACCCCTCAGATAAATCTCATCTTACAGAGAGAGAGAGAGAGAGAGAGATCC----- 228  
 Db 124 ThrGluThrLysProGlnAsn-----IleGluLysGluAsnValLysProSerThrAsp 141  
 Qy 229 ---TCATCAGTCGAACTCTCAAAATTCATCAATTTGATCTGCCCAACACCATCTCACACA 285  
 Db 142 LysThrAlaThrGluAspThrSerValIleLeuGluLysLysAlaProAsnAsnThr 161  
 Qy 286 ACAATAAATAGAGAAGATCTGTTCAAAACAAAGATGATATGTAGAAGATTCACAGTATCA 345  
 Db 162 -----AsnAsnAspValThrThrLysProSer-----ThrSer 172  
 Qy 346 GATTTGCTAACTCTAAATTAAGAGAGATTAACACT-----GAATCTGGTAAAGAA 396  
 Db 173 GluProSerThrSerGluIleGlnThrLysProThrThrProGlnGluSerThrAsnIle 192

Qy 397 GAGAAATCTATAGAGCAACCTTAATAAAGTAAAGAAATTCACAAACAAGTCAGCGTCT 456  
 Db 193 GluAsnSerGlnProGlnProThrProSerLysValAsp-----AsnGlnValThr 209  
 Qy 457 GGCTATACAAATATAGATGAAAAAATTTCA---AATCAAGATGAGTTTAAATTTACCA 513  
 Db 210 AspAlaThrAsnProLysGluProValAsnValSerLysGluLysGluLeuLysAsnAsnPro 229  
 Qy 514 -----ATAAATGAATATGAAATAAGCTAGACCATTA 546  
 Db 230 GluLysLeuLysGluLeuValArgAsnAspSerAsnThrAspHisSerThrLysProVal 249  
 Qy 547 TCTCAACATCTGCCCAACCATCGATTAAACGTGTA-----ACCGTA 588  
 Db 250 AlaThrAlaProThrSerValAlaProLysArgValAsnAlaLysMetArgPheAlaVal 269  
 Qy 589 AATCAATTAGCGCGGGAACAAGTTTCAATGTTTAAACCAATTAATTAAGTTTACTGATCAA 648  
 Db 270 AlaGlnProAlaAlaValAlaSerAsnAsnValAsnAspLeuIleLysValThrLysGln 289  
 Qy 649 AGTATTACTGAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708  
 Db 290 ThrIleLysValGly---AspGlyLysAspAsnValAlaAlaLysAspGlyLysAsp 308  
 Qy 709 TTAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768  
 Db 309 IleGluTyThrAspThrGluPheThrIleAspAsnLysValLysLysGlyAspThrMetThr 328  
 Qy 769 GTGATATAGATAAGATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828  
 Db 329 IleAsnTyThrAspLysAsnValIleProSerAspLeuThrAspLysAsnAspProIleAsp 348  
 Qy 829 ATAAAGATTAATCTCGAGGAATCATCGTACAGTACTTATGATTAACAAAAATAACAA 888  
 Db 349 IleThrAspProSerGlyGluValIleAlaLysGlyThrPheAspLysAlaThrLysGln 368  
 Qy 889 ATCACTATATCTTTTACAGATTTATGATAGATTAAGTATGAAATATTAAGACCACTTAAA 948  
 Db 369 IleThrTyThrPheThrAspTyThrValAspLysTyThrGluAspLysLeuAspArgLeuThr 388  
 Qy 949 TTAACGTATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008  
 Db 389 LeuTyThrTyThrIleAspLysLysThrValPro---AsnGluThrSerLeuAsnLeuThr 407  
 Qy 1009 TATAAAGCGCCCTTTTCAATCAGTAAATAAACAATTAAGTTCAGTTGATTAACAAAGACCTAAC 1068  
 Db 408 PheAlaThrAlaGlyLysGluThrSerGlnAsnValThrValAspTyThrGlnAspProMet 427  
 Qy 1069 GAAATCGGACTGCTAACTTCAAAAGTATGTTTACAAATATAGATACGAAAAATCATACA 1128  
 Db 428 ValHisGlyAspSerAsnIleGlnSerIlePheThrLysLeuAspGluAspLysGlnThr 447  
 Qy 1129 GTTGAGCAACGATTTATATTAACCTCTTCCTGTTTATTCAGCAAGGAAACAAATGTAAAT 1188  
 Db 448 IleGluGlnGlnIleTyThrValAsnProLysLysSerAlaThrAsnThrLysValAsp 467  
 Qy 1189 ATTTCAGGAATGCT-----GATGAAGTTTCAACATTT 1221  
 Db 468 IleAlaGlySerGlnValAspAspTyThrGlyAsnIleLysLeuGlyAsnGlySerThrIle 487  
 Qy 1222 ATAGACCATAGCAACAATAATTAAGTTTATAAGTTTGGAGATAATCAAAATTTTACCAGAT 1281  
 Db 488 IleAspGlnAsnThrGluIleLysValTyLysValAsnSerAspGlnGlnLeuProGln 507  
 Qy 1282 AGTAACAGAAATTTATGATACAGTGAATATGAAGATCTCAAAATGAT---GATTATGCC 1338  
 Db 508 SerAsnArgIleTyThrAspPheSerGlnTyThrGluAspValThrSerGlnPheAsnLys 527  
 Qy 1339 CAATTAGCAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1398  
 Db 528 LysSerPheSerAsnAsnValAlaThrLeuAspPheGlyAspIleAsnSerAlaTyIle 547



```

Db      115 SerValGlnSerThrThrGlyAsnLysValGluValSerThrAlaLysSerAspGluGln 134
Qy      229 TCATCAGTCGAATCTCAAAATTCATCAATTCATGATCGCCCAACCAACATCTCACACACA 288
Db      135 AlaSerProLysSerThrAsnGluAspLeuAsnThrLysGln-----Thr 149
Qy      289 ATAATAGAGAAGAAATCTGTTCAACAAGTAGATATGTAAGATTCACACGTCATCAGAT 348
Db      150 IleSerAsnGlnGluAlaLeuGln---ProAspLeuGlnGluAsnLysSerValValAsn 168
Qy      349 TTTCGCTAACTCTAAATAAAGAGAGAGTAACTGAATCTGCTGTAAGAGAGAAATCTATA 408
Db      169 -----ValGlnProThrAsnGluGluAsnLysLysValAsp----- 180
Qy      409 GAGCAACCTAATAAAGTAAGAAGATTCACAACAAGTCAGCCGCTCGGCTATACAAAT 468
Db      181 -----AlaLysThrGluSerThr-----LeuAsn 189
Qy      469 ATA---GATGAAAAATTTCAAAATCAAGATCAGTTATTA-----AATTTACCAATAAAT 519
Db      190 VallysSerAspAlaIleLysSerAsnAspGluThrLeuValAspAsnAsnSerAsnSer 209
Qy      520 GAATATGAATAGGCTAGACCATTATCTACAACATCTGCCCAACCA----- 567
Db      210 AsnAsnGluAsnAsnAlaAspIleLeuProLysSerThrAlaProLysAArgLeuAsn 229
Qy      568 TCGATTAAACGTTAAACCGTAAATCAATTCACGCGGGAACAAGTTCGAATGTTAAACCAT 627
Db      230 ThrArgMetArgIleAlaValGlnProSerSerThrGluAlaLysAsnValAsnAsp 249
Qy      628 TTAATTAAGATTACTGATCAAAAGTATTACTGAAGGATATGATGATGAAGGTGTTATT 687
Db      250 LeuIleThrSerAsnThrThrLeuThrValValAspAlaAspLysAsnAsnLysIleVal 269
Qy      688 AAACCATGATGCTGAAACTTAATCTATGATGTAATCTTTGAAGTAGATGATAAGGTG 747
Db      270 ProAlaGlnAspTyrLeuSerLeuLysSerGlnIleThr-----ValAspAspLysVal 287
Qy      748 AAATCTGCTGATACGATCAGATCAGATGATATAGATATAGATATAGATATAGATAT 792
Db      288 LysSerGlyAspTyrPheThrIleLysTyr---SerAspThrValGlnValThrGlyLeu 306
Qy      793 ---SCATCAGATTAAACCGATAGCTTTACATACCAAAAATAAAGAT---AATCTCGGA 846
Db      307 AsnProGluAspIleLysAsn-----IleGlyAspIleLysAspProAsnAsnGly 323
Qy      847 GAAATCATCGCTCAGGTACTTATGATAACAAAATAAACAATCACTACTACTACTTTTACA 906
Db      324 GluThrIleAlaThrAlaLysHisAspThrAlaAsnAsnLeuIleThrTyrThrPheThr 343
Qy      907 GATTATCTAGATAGTATGAAATATTAAGACCAACCTTAATTAAGTCATCATATTGAT 966
Db      344 AspTyrValAspArgPheAsnSerValGlnMetGlyIleAsnTyrSerIleTyrMetAsp 363
Qy      967 AAATCAAAAGGTTCCAAATAATAATACCAAGTTAGATAGATATATAAAGCCGCTTTCA 1026
Db      364 AlaAspThrIlePro-----ValSerIleAsnAspValGluPheAsnValThrIleGly 381
Qy      1027 TCAGTAAATAAACAATTCAGGTTGAATATCAAAAGACCTTAAC-----GAAAATCGGACT 1080
Db      382 AsnThrThrThrLysThrThrAlaAsnIleGlnTyrProAspTyrValValAsnGluLys 401
Qy      1081 GCTAACCTTCAAGTATGTTTACAAATATAGATACGAAAATATCATACA----- 1128
Db      402 AsnSerIleGlySerAlaPheThr-----GluThrValSerHisValGlyAsnLysGlu 419
Qy      1129 -----GTTGAGCAACCATTTATATTAACCTCTCTGTTATTTCAGCCCAAGGAA 1176
Db      420 AsnProGlyTyrTyrLysGlnThrIleTyrValAsnProSerGluAsnSerLeuThrAsn 439
Qy      1177 ACAATGTAAATATV-----TCAGGGGAATGGTGATGAAGGTTCAACAATATATA 1224

```

```

Db      440 AlaLysLeuLysValGlnAlaTyrHisSerSerTyrProAsnAsnIleGlyGlnIleAsn 459
Qy      1225 GACCATAGCAACAATAATTAAGTTTATAAGTTTCGAGATATCAAAATTTTACCAGATAGT 1284
Db      460 LysAspValThrAspIleLysIleTyrGlnValProLysGlyTyrThrLeu----- 476
Qy      1285 AACAGAAATTTATGATTACAGT-----GAATATATGAAGATGTCAAAAATGATGATTATGCC 1338
Db      477 AsnLysGlyTyrAspValAsnThrLysGluLeuThrAspValThrAsn---GlnTyrLeu 495
Qy      1339 CAA-----TTAGGAATAATAATGAATGATGAATTAATTTTGGTAAATATAGATTCA 1389
Db      496 GlnLysIleThrTyrGlyAspAsnAsnSerAlaValIleAspPheGlyAsnAlaAspSer 515
Qy      1390 CCATATATTAATAAGTTTATTAGTAAATATGACCTTAATAAGGATGATTACACGACTATA 1449
Db      516 AlaTyrValValMetValAsnThrLysPheGlnTyrThrAsnSerGluSerProThrLeu 535
Qy      1450 CAGCAAACTGTGCAATCGACGACGATATAAATGAGTATATCTGCTGAGTTTAGAACACA 1509
Db      536 ValGlnMetAlaThrLeuSerSerThrGlyAsn-----LysSerVal 549
Qy      1510 TCCTATGATATCAATGCTTTCTCTCAAGTTCAGGTCAAGCAAGGTGACTTGCCCT 1569
Db      550 SerThrGlyAsnAlaLeuGlyPheThrAsnAsnGlnSerGlyGlyAlaGly----- 566
Qy      1570 CCTGAAAAAATCTATAAAATCGGAGATTCAGTATGCGAAGATGTAGATAAAGATGGTATT 1629
Db      567 ---GlnGluValTyrLysIleGlyAsnTyrValTyrGluAspThrAsnLysAsnGlyVal 585
Qy      1630 CAAATAACAATGATATGAAATGAAACCCCTTAGTAATGTTGTTAACTTTTGACGTATCCT 1689
Db      586 GlnGluLeu-----GlyGluLysGlyValGlyAsnValThrValThrVal---PheAsp 602
Qy      1690 GATGGAACCTCAAAATCAGTCAGA-----ACAGATGAAGATGGGAATAT 1734
Db      603 AsnAsnThrAsnThrLysValGlyGluAlaValThrLysGluAspGlySerTyr 620

RESULT 9
US-09-386-962C-4
; Sequence 4, Application US/09386962C
; Patent No. 6635473
; GENERAL INFORMATION:
; APPLICANT: FOSTER, Timothy
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLO
; FILE REFERENCE: P0633502/BAS
; CURRENT APPLICATION NUMBER: US/09/386,962C
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/098,443
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/117,119
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1742
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-386-962C-4

Alignment Scores:
Pred. No.: 1,23e-28 Length: 1742
Score: 499.00 Matches: 168
Percent Similarity: 43.9% Conservative: 104
Best Local Similarity: 27.1% Mismatches: 275
Query Match: 16.5% Indels: 72
DB: 2 Gaps: 25

US-10-806-288-12 (1-1746) x US-09-386-962C-4 (1-1742)
Qy      1 TCTAGTATGAAGAAAAGATGATGTCATCAATAATATCAATCAATCAATCAATCAATCAAT 60
Db      157 ThrSerThrThrGlnGlnAspSerThrGluLysAsnAsnProSerLeuLysAspAsnLeu 176

```



Qy	61	AATAACCAAAATAATTA	AAAAAGAAACGAATAA	CTACGATGCATAGAAAA	ACGCTCA	120
Db	177	AanSerSerThrThr	SerLysGluSerLysThr	AspGluHisSerThrLys	GlnAla	196
Qy	121	GAGATAGACAGAGTCA	CAACAACAATGTGTAG	TAGAAACGAACA	---ACATTTTACAA	177
Db	197	GlnMetSerThr---	AenLysSerAenLeu	AspThrAenAepSerPro	ThrGlnSerGlu	215
Qy	178	AAGACC---CCTCAAG	ATAACTCATCTTAC	AGAAGAAGAGGTAA	AAAGAACTCTCATCA	234
Db	216	LysThrSerSerGln	AlaAenAenAepSer	ThrAepAenGlnSer	AlaProSerLysGln	235
Qy	235	GTCCAAATCCTCAAA	TTCA-----TCA	ATTGATCTACTGCC	267	
Db	236	LeuAepSerLysPro	SerGluGlnLysVal	ThrLysThrLysPhe	AenAepGluProThr	255
Qy	268	CAACAACATCTCTCA	CAACAACAATAAAT	---AGAGAAGAACT	CTGTCTCAACAACAG	TGATAAT 324
Db	256	GlnAepValGluHis	ThrThrThrLysLeu	LysThrProSerValSer	ThrAepSerSer	275
Qy	325	GTAGAAGNTTCA	CACCGTATCAGATTT	TGCTAACTTAAATA	AAAGAGAGATTAAC	CTGAA 384
Db	276	ValAenAepLys---	GlnAepTyrThr	ArgSerAlaVal-----	AlaSer 289	
Qy	385	TCTGTTAAAGAA	GAATACTATATAG	ACACCTAATAAAGT	AAAGAGATTCAACA	CAACA 444
Db	290	LeuGlyValAepSer	AenGluThrGluAla	lleThrAenAlaVala	ArgAepAenLeuAep	309
Qy	445	AGTCAGCGCTGCT	TATACAAATATATAG	ATGAAAAAAT	-----	483
Db	310	LeuLysAlaAeSer	ArgGluGlnAenGlu	AlaAlaAlaAlaAla	LeuLysLys 329	
Qy	484	-----TCAAATCA	AGATGAGTTAATA	TTTATACCA-----	ATAATGATGATAA	AT 531
Db	330	AepPheSerAenPro	AepTyrGlyValAep	ThrProLeuAlaLeu	AenAenArgSerGln	Ser 349
Qy	532	AAGCTAGACCAT	TATCTACAACATCTG	CCCAACCATCGAT	TAAACCTGTAACCG	TAAAT 591
Db	350	LysAenSerPro---	HisLysSerAlaSer	Pro-----Arg	MetAenLeuMet 364	
Qy	592	CAATTAGCGCGGAA	-----CAAGTTT	CGAATCTTAACCAT	TTTAATTAAGTTACT	GAT 645
Db	365	SerLeuAlaAlaGlu	ProAenSerGlyLys	AenValAenAepLys	ValLysIleThrAen	384
Qy	646	CAA-----AGTATT	ACTGAAGGATATGAT	GATAGTAGTGTTAT	TAAAGCACATGAT	699
Db	385	ProThrLeuSerLeu	AenLysSerAenAen	HisAlaAenAenVal	IleTyrProThrSer 404	
Qy	700	GCTCAAACTTAAT	CTATGTTAACTTTT	CGAATGATAGTAAG	TGAAGTAATCTGGT	TGAT 759
Db	405	AenGluGlnPheAen	LeuLysAlaAenTyr	GluLeuAepSerIle	LysGluGlyAep 424	
Qy	760	ACGATGACAGTGG	ATATAGATAAGAATA	CAGTTCATCAGATTT	TAACCGATAGCTTT	TACA 819
Db	425	ThrPheThrIleLys	TyrGlyTyrIleArg	ProGlyLysLeuGlu	LeuProAlaIle 444	
Qy	820	ATACCAAAATAAA	AGATAATCTTGGGA	AAATCATCGCTACAG	GTACTTATGATAACA	AAA 879
Db	445	LysThrGlnLeuA	ArgSerLysAepGly	SerIleValAlaAen	GlyValTyrAepLys	Thr 464
Qy	880	AATAAACAAATC	CACTTACTTTTACAG	ATTATCTAGTAA	TAGTAATATAATTA	AAAGCA 939
Db	465	ThrAenThrThr	ThrTyrThrPheThr	AenTyrValAepGln	TyrGlnAenIleThr	Gly 484
Qy	940	CACCTTAAATTA	ACGTATACATTTG	ATAAAATCAAAAGG	TTCCAAAATAATA	TACCAAGTTA 999
Db	485	SerPheAepLeu	IleAlaThrProLys	ArgGluThrAlaIle	LysAepAenGlnAen	Tyr 504
Qy	1000	GATGTAGATA	TAAACCGCCCTT	TCATCAGTAATA	TAAACAAATTCG	GTGAATATCAA 1059
Db	505	ProMetGluVal	ThrIleAlaAenGlu	ValValLysLysAep	PheIleValAepTyr	Gly 524

Qy	1060	AGACCTAACGAAATCGGACTGCTAAACCTTCAAGATGTATTTTCAAAATATAGATACGAAA	1119
Db	525	AsnLysAspAspThrThrThr-----AlaAlaValAlaAsnValAspAsnVal	541
Qy	1120	AATCATACAGTTGAGCAACGATTTATTAACCCCTCTTCGTTATTACGCCACCGAAGAAC	1179
Db	542	AsnAsnLysHisAsnGluValValTyrLeuAsnGlnAsnAsnGlnAsnProLysTyrAla	561
Qy	1180	AATGTAAATATTTTCAGGAATGCTGAAGGTTTCAACAAATATAGACGATAGCAACA	1239
Db	562	LysTyr-----PheSerThrValLysAsnGlyGluPheIle	573
Qy	1240	-----ATTAAGTTTATAAGTTGGAGATAATCAAAATTTACAGATAGT---AAC	1287
Db	574	ProGlyGluValLysValTyrGluValThrAspThrAsnAlaMetValAspSerPheAsn	593
Qy	1288	AGAATTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCCAATTA--	1344
Db	594	ProAspLeuAsnSerSerAsnValLysAspValThrSerGlnPheAlaProLysValSer	613
Qy	1345	GGAAATAAATAATGATGTGAATATTAATTTTTTGGTAATATA-----GATTCACCATAT	1395
Db	614	AlaAspGlyThrArgValAspIleAsnPheAlaArgSerMetAlaAsnGlyLysLysTyr	633
Qy	1396	ATTATTAAAGTTATTAGTAAATATGACCCCTAATPAAGGATGATTACACGACTATACAGCAA	1455
Db	634	IleValThrGlnAlaValArgProThrGlyThrGlyAsnValTyrThr-----GluTyr	651
Qy	1456	ACTGTGCAATGCAGACGACTATAAATAGTATACTGGTGAGTTTTAGACAGCATCCTAT	1515
Db	652	TrpLeuThrArgAspGlyThrThrAsn-----ThrAsnAspPheTyrArgGlyThrLys	669
Qy	1516	GATAATAACAATTCGTTCTCTCAAGTTCAAGGTCACAGGACAAGGTGACTTGCCTCCTGAA	1575
Db	670	SerThrThrValThrTyrLeuAsnGlySerSerThrAlaGlnGlyAspAsnPro-----	687
Qy	1576	AAAACTTATAAAATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAAAT	1635
Db	688	---ThrTyrSerLeuGlyAspTyrValTyrLeuAspLysAsnLysAsnGlyValGln--	705
Qy	1636	ACAAATGATTAATGAAAAACCGCTTAGTAATGTATTGGTAACTTTGACGTATCCTGATGA	1695
Db	706	---AspAspAspGluLysGlyLeuAlaGlyValTyrValThrLeu-----LysAspSer	722
Qy	1696	ACTTCAAAATCA-----GTCAGAACAGATGAAGATGGGAAATATCAATTTGAT	1743
Db	723	AsnAsnArgGluLeuGlnArgValThrThrAspGlnSerGlyHisTyrGlnPheAsp	741
RESULT 10			
US-09-386-959-4			
; Sequence 4, Application US/09386959			
; Patent No. 6703025			
; GENERAL INFORMATION:			
; APPLICANT: PATTI, Joseph M.			
; APPLICANT: FOSTER, Timothy J.			
; APPLICANT: HOOK, Magnus			
; TITLE OF INVENTION: MULTICOMPONENT VACCINES			
; FILE REFERENCE: P06333US1/BAS			
; CURRENT APPLICATION NUMBER: US/09/386,959			
; CURRENT FILING DATE: 1999-08-31			
; EARLIER APPLICATION NUMBER: 60/098,439			
; EARLIER FILING DATE: 1999-08-31			
; NUMBER OF SEQ ID NOS: 65			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 4			
; LENGTH: 1742			
; TYPE: PRT			
; ORGANISM: Staphylococcus epidermidis			
US-09-386-959-4			
Alignment Scores:			
Pred. No.:		1.23e-28	Length:
Score:		499.00	Matches:
			168



Percent Similarity:	43.9%	Conservative:	104
Best Local Similarity:	27.1%	Mismatches:	275
Query Match:	16.5%	Indels:	72
DB:	2	Gaps:	25

US-10-806-288-12 (1-1746) x US-09-386-959-4 (1-1742)

	QY	1	TCTAGTGATGAAGAAGAAATGATGTGATCAATAATTATTCAGTCAATTAACACCGCAGAT	60
	Db	157	ThrSerThrThrGlnGlnAspSerThrGluLysAsnAsnProSerLeuLysAspAsnLeu	176
	QY	61	AATAACCAAATAAATAAAAAAGAACAAACGAATAACTACGATGGCATAGAAAACGCATCA	120
	Db	177	AsnSerSerSerThrThrSerLysGluSerLysThrAspGluHisSerThrLysGlnAla	196
	QY	121	GAAATAGAACAGAGTCAACAACAATAATGTAGTAGAAAACGGAACA---ACATTTTTCACAA	177
	Db	197	GlnMetSerThr--AsnLysSerAsnLeuAspThrAsnAspSerProthrGlnSerGlu	215
	QY	178	NAGACC---CCCTCAAGATAACTCATCTTACAGACNAGAGGTAAAAGAATCCTCATCA	234
	Db	216	LysThrSerSerGlnAlaAsnAsnAspSerThrAspAsnGlnSerAlaProSerLysGln	235
	QY	235	GTCCGAATCCTCAAAATCCA-----TCAAATGTAGTACTGCC	267
	Db	236	LeuaspSerLysProSerGluGlnLysValTyrlsThrLysPheAsnAspGluProThr	255
	QY	268	CACAACCACTCTCACACACAATAAAT---AGAGAANAATCTGTTCAAACAGTGATAAT	324
	Db	256	GlnAspValGluHisThrThrLysLeuLysThrProSerValSerThrAspSerSer	275
	QY	325	GTAGAAGATTTCCACGCTATCAGATTTTTGCTAACTCTAAAATAAAAGAGAGTAACACTGAA	384
	Db	276	ValAsnAspLys-----GlnAspTyThrArgSerAlaVal-----AlaSer	289
	QY	385	TCGTGTAAGAAGAGAATACTATAGAGCAACCTAATAAGATAAAAGAGAGTCAACAACA	444
	Db	290	LeuGlyValAspSerAsnGluThrGluAlaIleThrAsnAlaValArgAspAsnLeuasp	309
	QY	445	AGTCAGCGCTCTGGCTATACAAATATAGATGMAAAATTT-----	483
	Db	310	LeuLysAlaAlaSerArgGluGlnIleAsnGluAlaIleIleAlaGluAlaLeuLysLys	329
	QY	484	-----TCAAATCAAGATGAGTTAATTAATTTACCA-----ATAAATGAATATGAAAT	531
	Db	330	AspPheSerAsnProAspTyrlsValAspThrProLeuAlaLeuAsnArgSerGlnSer	349
	QY	532	AAGGCTAGACCATTTCTACAACAATCTGCCCAACCATCGATTAAACGCTGTAACCGTAAAT	591
	Db	350	LysAsnSerPro-----HisLysSerAlaSerPro-----ArgMetAsnLeuMet	364
	QY	592	CAATTAGCGGGCGAA-----CAAGGTTCGAATGTTTAACCAVTTAATTAAGGTACTGAT	645
	Db	365	SerLeuAlaIlaGluProAsnSerGlyLysAsnValAsnAspLysVallysileThrAsn	384
	QY	646	CAA-----AGTATTACTGAAGGATATGATCATAGTCAAGGTCTTATTAAAGCACATGAT	699
	Db	385	ProThrLeuSerLeuAsnLysSerAsnAsnHialaAsnAsnValIleTrpProThrSer	404
	QY	700	GCTGAAACTTAAATCTATGATGTAACCTTTTGAAGTAGATGATGAAGCTGAAATCTGGTAT	759
	Db	405	AsnGluGlnPheAsnLeuLysAlaAsnTyrlsGluLeuAspAspSerileLysGluGlyAsp	424
	QY	760	ACGATGACAGTGGATATAGATAAGAAATACAGTTCATCCATCAGATTTAACCGATAGCTTTTACA	819
	Db	425	ThrPheThrIleLysTyrlsGlyGlnTyrlsEargProGlyGlyLeuLeuProIalaIle	444
	QY	820	ATACC AAAAATAAAGATAAATCTCTGGAGAAATCATCGCTACAGTACTTATGATAACAAA	879
	Db	445	LysThrGlnLeuAspSerLysAspGlySerIleValAlaAsnGlyValTyrlsAspLysThr	464
	QY	880	AATAACAACAAATCACCCTATACCTTTTACAGATATGTTAGATAAGATPATGAAATAATTAAACA	939

465	ThrAsnThrThrThrTyThrThrPheThrAsnTyValAspGlnTyThrGlnAsnIleThrGly	484
940	CACCTTAAATTAACGTCATACATTGATAAATCAAAGGTTCCAAATATAATAATACCAAGTTA	999
485	SerPheAspLeuIleAlaThrProLysArgGluThrAlaIleLysAspAsnGlnAsnTyr	504
1000	GATGTAGAATATAAACCGGCCCTTCATCATAGTAAATAAACAATATACGGTTGGTAATCAA	1059
505	ProMetGluValThrIleAlaAsnGluValValLysLysAspPheIleValAspTyrGly	524
1060	AGACCTAACCAAAATCGAGTCGTAACTTCAAAGTATGTTTCAAAATATAGATACGAAA	1119
525	AsnLysLysAspAsnThrThrThr-----AlaAlaValAlaAsnValAspAsnVal	541
1120	AATCATACATGTGAGCAACAGATTTATTAACCCCTCTTCGTTTATTACGCCAAGGAACA	1179
542	AsnAsnLysHisAsnGluValValTyrLeuAsnGlnAsnAsnGlnAsnProLysTyrAla	561
1180	AATGTTAAATATTTACGGGAATGTTGATGAAGTTCAAGTTTCAACAATTATAGACGATACCAATA	1239
562	LysTyr-----PheSerThrValLysAsnGlyGluPheIle	573
1240	-----ATTAAAGTTTATAAGTTGGAGTAATCAAAATTTTACCAGATAGT---AAC	1287
574	ProGlyGluValLysValTyrGluValThrAspThrAsnAlaMetValAspSerPheAsn	593
1288	AGAATTATGATTACAGTCAGTGAATATGAAGATGTCAAAATGATGATTATGCCCAATTA---	1344
594	ProAspLeuAsnSerSerAsnValLysAspValThrSerGlnPheAlaProLysValSer	613
1345	GGAAATAAATAATGATGTGAATATTAATTTTGGTAAATA-----GATTCACCATAT	1395
614	AlaAspGlyThrArgValAspIleLeuAsnPheAlaArgSerMetAlaAsnGlyLysLysTyr	633
1396	ATTATTAAAGTTATTAGTAAATATGACCCCTAAATAGGATGATTTACAGCTACTATACAGAA	1455
634	IleValThrGlnAlaValArgProThrGlyThrGlyAsnValTyrThr-----GluTyr	651
1456	ACTGTGCACATGCAGCAGCTATAAATGATGATCTGCTGAGTTTAGACAGCATCCTAT	1515
652	TrpLeuThrArgAspGlyThrThrAsn-----ThrAsnAspPheTyrArgGlyThrLys	669
1516	GATAATAACAATTCTTTCTCTACAAGTTCCAGGTCAAGCAAGGTGACATTGCTCTCTGAA	1575
670	SerThrThrValThrTyrLeuAsnGlySerSerThrAlaGlnGlyAspAsnPro-----	687
1576	AAACTTTATAAATCGGAGATTACGTATCGGGAAGATGTAGATAAGATGGTATTCAAAT	1635
688	---ThrTyrSerLeuGlyAspTyrValTrpLeuAspLysAsnLysAsnGlyValGln---	705
1636	ACAAATGATAAATGAAACCGCTTACTGATGATGTTTGGTAACTTTTGACGTATCTGATGCA	1695
706	---AspAspAspGluLysGlyLeuAlaGlyValTyrValThrLeu-----LysAspSer	722
1696	ACTTCAAATCA-----GTCAGAACAGATGAAGATGGAAATATCAATTTGAT	1743
723	AsnAsnArgGluLeuGlnArgValThrThrAspGlnSerGlyHisTyrGlnPheAsp	741

RESULT 11

RESOLUTION 11  
US-09-710-279-1780  
; Sequence 1780, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; CURRENT FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1780

```
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-1780

Alignment Scores:
Pred. No.:      1.65e-28      Length:      1155
Score:          497.00       Matches:    167
Percent Similarity: 43.9%     Conservative: 105
Best Local Similarity: 27.0%   Mismatches: 275
Query Match:      16.4%     Indels:     72
DB:               2         Gaps:       25

US-10-806-288-12 (1-1746) x US-09-710-279-1780 (1-1155)
QY  1  TCTAGTGATGAAGAAGAATAATCATGTGATCAATAATACGTCAATAAACAACCGACGAT 60
    :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  148 ThrSerThrThrGlnAspSerThrGluLysAsnAsnProSerLeuLysAspAsnLeu 167
QY  61  AATAACCAATAATTAAAAAGAAAGAACGAATAACTACGATGGCATTAGAAAACGCCTCA 120
    |||:::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  168 AsnSerSerSerThrThrSerLysGluSerLysThrAspGluHiserThrLysGlnAla 187
QY  121 GAAGATAGACAGAGTCACAACAARAATCTAGATGAAACGAAGCA---ACATTTTTACAA 177
    :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  188 GlnMetSerThr---AsnLysSerAsnLeuAspThrAsnAspSerProThrGlnSerGlu 206
QY  178 AAGACC---CCTCAAGATAATACTCATCTTACAGAAGAAGAGGTAAAAGAAATCCTCATCA 234
    :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  207 LysThrSerSerGlnAlaAsnAsnAspSerThrAspAsnGlnSerAlaProSerLysGln 226
QY  235 GTCGAATCTCCAATTC-----TCAAITGTGACTATGCC 267
    :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  227 LeuAspSerLysProSerGluGlnLysValTyrLysThrLysPheAsnAspGluProThr 246
QY  268 CAACAACCATCTCACACAACAATAAAT---AGAGAAGAATCTGTTTCAAACAAGTGATAAT 324
    :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  247 GluAspValGluHisThrThrThrLysLeuLysThrProSerIleSerThrAspSerSer 266
QY  325 GTAGAAGATTCACAGTATCAGATTTTGGTAACTCTCTAAATATAAAGAGAGTAACACTGAA 384
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  267 ValAsnAspLys-----GlnAspTyrThrArgSerAlaVal-----AlaSer 280
QY  385 TCTGGTAAAGAGAGAATACTATACAGCAACTTAAGGTAAAAGAAGATTCAACAACA 444
    :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  281 LeuGlyValAspSerAsnGluThrGluAlaIleThrAsnAlaValArgAspAsnLeuAsp 300
QY  445 AGTCAGCCGCTCTGGCTATACAATAATATAGATGAAAAAAT-----483
    :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  301 LeuLysAlaAlaSerArgGluGlnIleAsnGluAlaIleIleAlaGluAlaLeuLysLys 320
QY  484 -----TCAATCAAGATGAGTTATTAATTTTACCA-----ATAATGATATGAAAT 531
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  321 AspPheSerAsnProAspTyrGlyValAspThrProLeuAlaLeuAsnThrSerGlnSer 340
QY  532 AAGCGTAGACCATATTCTACACATCTGCCCAACCATCGATTAAACGTGTAACCGTAAAT 591
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  341 LysAsnSerPro-----HisLysSerAlaSerPro-----ArgMetAsnLeuMet 355
QY  592 CAATTAGCGCGGAA-----CAAGGTTCGAATGTTAACCATTTAATTAAGTTACTGAT 645
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  356 SerLeuAlaAlaGluProAsnSerGlyLysAsnValAsnAspLysValLysIleThrAsn 375
QY  646 CAA-----AGTATTACTGAAGGATATGATGATGAGCGGTGTTATTAAAGCACATGAT 699
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  376 ProThrLeuSerLeuAsnLysSerAsnAsnHisAlaAsnAsnValIleTrpProThrSer 395
QY  700 GCTGAAACCTTAATCTATGATGTAATCTTTTGAAGTAGATGATAAGGTGAAATCTGGTGAT 759
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db  396 AsnGluGlnPheAsnLeuLysAlaAsnTvrGluLeuAspAspSerIleLysGluGluValAsp 415
```



Db 530 SerAsnGlyLysGluLeuAspArgThrThrThrAspGluAsnGlyLysTyrGlnPheThr 549

QY 1744 GGA 1746

Db 550 Gly 550

RESULT 13

US-08-956-171E-5249

; Sequence 5249, Application US/08956171E

; Patent NO. 6593114

; GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5249:

SEQUENCE CHARACTERISTICS:

LENGTH: 936 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5249:

US-08-956-171E-5249

Alignment Scores:

Pred. No.: 2,2e-25 Length: 936

Score: 454.00 Matches: 154

Percent Similarity: 44.7% Conservative: 105

Best Local Similarity: 26.6% Mismatches: 234

Query Match: 15.0% Indels: 86

DB: 2 Gaps: 26

US-10-806-288-12 (1-1746) x US-08-956-171E-5249 (1-936)

QY 1 TCTAGTCATGAAGAAAGATGTGTGATCAATAATAATCAGTCAATAAACAACCGAGAT 60

Db 60 SerAsnGluSerLysSerAsnAspSerSerSerValSerAlaAlaProLysThrAspAsp 79

QY 61 AATAACCAATAATTAATAAAGAAAGAAACGAATAACTACGTGCATAGAAAAACGCTCA 120

Db 80 ThrAsnVal-----Ser 83

QY 121 GAAGATAGAACAGAGTCAACAACAATGTAGATGAAGAAACGAACAACATTTTTCACAAAG 180

Db 84 AspThrLysThrSerSerAsnThrAsn-----AsnGlyGluThrSerValAlaGln 100

QY 181 ACCCTCAAGATAATACTCATCTTACAGAAGAGAGTAAAGAAATCCCTCCTCAGTCGAA 240

Db 101 AsnPro-----AlaGlnGlnGluThrThrGlnSerSerThrAsn 114

QY 241 TCCTCAAAATTCATCAATTGATCTGCCCAACCACTCTCACACAACAATAAATAGAGAA 300

Db 115 AlaThrThrGluGluThrProValThrGlyGluAlaThrThrThrThrAsnGlnAla 134

QY 301 GAATCTGTTCAACAAGTGAATATGTAGAAGATTCACAGTATCAGATTTTGTCTACTCT 360

Db 135 AsnThrProAlaThrThrGlnSer-----SerAsnThrAsnAlaGluLeuValAsn--- 152

QY 361 AAAATAAAGAGAGTAAACACTGAATCTGTGAAGAAGAGATACTATAGAGCAACCTAAT 420

Db 153 -----GlnThrSerAsnGluThrThrSerAsnAspThrAsnThrVal----- 166

QY 421 AAAGTAAAAAGAGATTCAACAACAGTCCGCTCTGGCTATACAAATATAGATGAAGAA 480

Db 167 -----SerSerValAsnSerProGlnAsnSerThrAsnAlaGluAsnVal 181

QY 481 ATTTCAAATCAAGATGAGTTTAAAT-----TTACCAATAAATGAATATGAATAAGGCT 537

Db 182 SerThrThrGlnAspThrSerThrGluAlaThrProSerAsn-----AsnGluSer 198

QY 538 AGACCAATTATCTACACATCTGCCCAACCATCGATTAAACGTTAACCGTAAAT----- 591

Db 199 AlaProGlnSerThrAspAlaSerAsnLysAspValValAsnGlnAlaValAsnThrSer 218

QY 592 -----CAATTAGCGCGCGGAAACAAGTTTCGAATGTGTAACCATTTA 630

Db 219 AlaProArgMetArgAlaPheSerLeuAlaAlaValAlaAlaAspAlaProValAlaGly 238

QY 631 ATTAAAGTTACTGATCAA-----AGTATTCTGAAGGATATGATGATGATGAGGTGTT 684

Db 239 ThrAspIleThrAsnGlnLeuThrAsnValThrValGlyIle---AspSerGlyThrThr 257

QY 685 ATTAAGACATGATGCTGCAAACTTAATCTATGATGTAACCTTTTCAAGATGATGATAG 744

Db 258 ValTyrProHisGlnAlaGlyTyrValLysLeuAsnTyrGlyPheSerValProAsnSer 277

QY 745 GTGAATCTGTCATACGATGACAGTGGATATAGATAAGAATAACAGTTCATCAGATTTA 804

Db 278 AlaValLysGlyAspThrPheLysIleThrValProLysGluLeuAsnLeuAsnGlyVal 297

QY 805 ACGGATAGCTTTTACAAATACCAAAATAAAGATAATCTGGAGAAATCATCGCTACAGGT 864

Db 298 ThrSerThrAlaLysValProPheMetAlaGlyAsp---GlnValLeuAlaAsnGly 316

QY 865 ACTTATGATAACAATAAATAACCAATCACTATCTTACAGATTATGTAGATAAGTAT 924

Db 317 ValIleAspSer---AspGlyAsnValIleTyrThrPheThrAspTyrValAsnThrLys 335

QY 925 GAAATATTAAAGCACACCTTAAATTAACGTATACATGATTAATCAAGAGTTTCCAAAT 984

Db 336 AspAspValLysAlaThrLeuThrMetProAlaTyrIleAsp-----ProGlu 351

QY 985 AATAATACCAAGTTA---CATGTAGATAATAAAGCGCCCTTTCATCA-----GTAAAT 1035

Db 352 AsnValLysLysThrGlyAsnValThrLeuAlaThrGlyGlySerThrThrAlaAsn 371

QY 1036 AAAACAATTACGTTTGAATATCAAGACCTAACGAAATCGGACTGCTAACCTTCAAGT 1095

Db 372 LysThrValLeuValAspTyrGluLysTyrGlyLysPheTyrAsnLeuSerIleLysGly 391

QY 1096 ATGTTTCAAAATATAGATACGAAAAATCATACAGTTGTAGCAAAACGATTATATTAACCT 1155

Db 392 ThrIleAspGlnIleAspLysThrAsnAsnThrTyrArgGlnThrIleTyrValAsnPro 411

QY 1156 CTT-----CGTTATTCAGCCAGGAACAAATGTAATATTTTCAGGGAATGGTGATGAA 1209  
Db 412 SerGlyAspAsnValIleAlaProValLeuThrGlyAsnLeuLysProAsnThrAspSer 431  
QY 1210 GOTTCAACAATATATACGATAGCACAATAATTAAGTTTATAAGTTTGAAGTTGCGATATATCAA 1269  
Db 432 AsnAlaLeuIleAspGlnGlnAsnThrSerIleLysValTyrLysValAspAsnAlaAla 451  
QY 1270 AATTTACAGATPAGTACAGAAATTTATGATTCAGTGAATATGAAGATGTCAAAATGAT 1329  
Db 452 AspLeuSerGluSerTyrPheVal---AsnProGluAsnPheGluAspValThrAsnSer 470  
QY 1330 GATTATGCCAATTAGGAATAATTAATGATGTGAATATTAATTTGGT----- 1377  
Db 471 ValAsnIleThrPheProAsnProAsnGlnTyrLysValGluPheAsnThrProAspAsp 490  
QY 1378 AATATAGATTACCATATATTTAAGTTTATTAGTATTAATAGACCCCTAAT---AAGGAT 1434  
Db 491 GlnIleThrProTyrIleValValValAsnGlyHisIleAspProAsnSerLysGly 510  
QY 1435 GATTACAGCACTATACAGCAAACTGTGCAAACTGCAGACGACTATATAATGAGTACTGCT 1494  
Db 511 Asp-----LeuAlaLeuArgSerThrLeuTyrGlyTyrAsnSer 523  
QY 1495 GAG-----TTTAGAACAGCATCTTATGATATACAAATTTGCTTCTTACAAATTCAGGT 1548  
Db 524 AsnIleIleTyrArgSerMetSerTrpAspAsnGluValAlaPheAsnAsnGlySerGly 543  
QY 1549 CAAGACAAAGGT---GACTTGCCT-----CCTGAAAAAATTTATAAATCGGAGATTAC 1599  
Db 544 SerGlyAspGlyIleAspLysProValValProGluGlnProAspGluProGlyGluIle 563  
QY 1600 -----GTATGGGAAGATGTAGATAAGAT---GGTATTCAAAATACAAATGATAAT 1647  
Db 564 GluProIleProGluAspSerAspSerAspProGlySerAspSerGlySerAspSer 582

## RESULT 14

US-08-781-986A-5249  
; Sequence 5249, Application US/08781986A  
; Patent No 6737248

## GENERAL INFORMATION:

; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/781,986A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Benson, Bob

; REGISTRATION NUMBER: 30,446

; REFERENCE/DOCKET NUMBER: PB248PP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 5249:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 936 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-781-986A-5249

## Alignment Scores:

Pred. No.: 2,2e-25 Length: 936  
Score: 454.00 Matches: 154  
Percent Similarity: 44.7% Conservative: 105  
Best Local Similarity: 26.6% Mismatches: 234  
Query Match: 15.0% Indels: 86  
DB: 2 Gaps: 26

US-10-806-288-12 (1-1746) x US-08-781-986A-5249 (1-936)

QY 1 TCTAGTGTGAAGAAAAGAAGATGATGTGATCAATTAATCAATCAATTAATAACACCCGACAT 60  
Db 60 SerAsnGluSerLysSerAsnAspSerSerValSerAlaAlaProLysThrAspAsp 79  
QY 61 AATAACCAAAATAATTAATAAAGAAAGAAACGAAATCACTACGATGGCATAGAAAAACGCTCA 120  
Db 80 ThrAsnVal-----Ser 83  
QY 121 GAAGATAGAACAGAGTCAACAAATACTAGATGAAACGAAAGCAACATTTTACAAAAG 180  
Db 84 AspThrLysThrSerSerAsnThrAsn-----AsnGlyGluThrSerValAlaGln 100  
QY 181 ACCCTCAAGATAATACTCATCTTTACAGAAGAAGAGGTAAAGAAATCTCATCATCGCAA 240  
Db 101 AsnPro-----AlaGlnGlnGluThrThrGlnSerSerSerThrAsn 114  
QY 241 TCCTCAAAATTCATCAATTTGATCTGCCCAACACCATCTCACACACAAATAAATAGAGAA 300  
Db 115 AlaThrThrGluGluThrProValThrGlyAlaThrThrThrThrThrAsnGlnAla 134  
QY 301 GAATCTGTTCAACAAAGTGATAATGTAGACATTACACAGTATCAGATTTTGGCTAACTCT 360  
Db 135 AsnThrProAlaThrThrGlnSer---SerAsnThrAsnAlaGluGluLeuValAsn--- 152  
QY 361 AAAATAAAGAGAGTAACTGTAATCTGGTAAAGAAGAGATATCTATATAGACCAACCTAAT 420  
Db 153 -----GlnThrSerAsnGluThrThrSerAsnAspThrAsnThrVal----- 166  
QY 421 AAAGTAAAGAGATTCAACACAAAGTCAGCCGCTGCTGCTATACAAATATATAGATGAAAAA 480  
Db 167 -----SerSerValAsnSerProGlnAsnSerThrAsnAlaGluAsnVal 181  
QY 481 ATTTCAAAATCAAGATGAGTTATTAAAT---TTACCAATAAATGAATATGAAAAATAAGGCT 537  
Db 182 SerThrThrGlnAspThrSerThrGluAlaThrProSerAsn-----AsnGluSer 198  
QY 538 AGACCATATTTCAACACATCTGCCCAACCACTGATTAAACGTTAAACCGTAAAT----- 591  
Db 199 AlaProGlnSerThrAspAlaSerAsnLysAspValValAsnGlnAlaValAsnThrSer 218  
QY 592 -----CAATTAGCGCGGCAACAAAGGTTCAATGTTTAAACCATTTA 630  
Db 219 AlaProArgMetArgAlaPheSerLeuAlaAlaValAlaAlaAspAlaProValAlaGly 238  
QY 631 ATTAAGTTACTGATCAAA-----AGTATTACTGAAGATATGATAGTAGAGGTTCTT 684  
Db 239 ThrAspIleThrAsnGlnLeuThrAsnValThrValGlyIle---AspSerGlyThrThr 257  
QY 685 ATTAAGCACATGATGCTGAAAACCTTAATCTATGATGTAACTTTTGAAGTAGATGATAAG 744  
Db 258 ValTyrProHisGlnAlaGlyTyrValLysLeuAsnTyrGlyPheSerValProAsnSer 277  
QY 745 GTGAAATCTGGTATACGATGACAGTCAGTGATATAGATAGAAATACAGTTTCCATCAGATT 804  
Db 278 AlaValLysGlyAspThrPheLysIleThrValProLysGluLeuAsnLeuAsnGlyVal 297

```
QY 805 ACCGATAGCTTTCAATACCAAAAATAAAGATAATTTCTGGAGAAATCATCGCTACAGGT 864
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 298 ThrSerThrAlaLysValProPheMetAlaGlyAsp---GlnValLeuAlaAsnGly 316
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 865 ACTTATGATACAAAAATAACAAATCACCTATCTTTTACAGATTATGTAGATAGTAT 924
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 317 ValIleAspSer---AspGlyAsnValIleTyrThrPheThrAspTyrValAsnThrLys 335
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 925 GAAATATTAAAGACACACCTTAATTAACGTGCATACATTAATTAATCAATCAAGTTCCAAAT 984
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 336 AspAspValIleAlaThrLeuThrMetProAlaTyrIleAsp-----ProGlu 351
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 985 AATAATACCAAGTTA---GATGTAGATATATAAAGCGCCCTTCATCA-----GTAAAT 1035
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 352 AsnValIleLysThrGlyAsnValThrLeuAlaThrGlyIleGlySerThrThrAlaAsn 371
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1036 AAAACAATTAACGGTTGAATATCAAGACCTAACCAAAATCGGACTGCTAACCTTCAAAAGT 1095
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 372 LysThrValLeuValAspTyrGluLysTyrGlyLysPheTyrAsnLeuSerIleLysGly 391
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1096 ATGTTTACAATATAGATACGAAAAATCATACAGTTGAGCAAGAGTATTATTAACCTT 1155
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 392 ThrIleAspGlnIleAspLysThrAsnAsnThrTyrArgGlnThrIleTyrValAsnPro 411
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1156 CTT-----CGTTATTCCAGCCAGGAACAATGTAATATTTACAGGGAATGGTGATGAA 1209
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 412 SerGlyAspAsnValIleAlaProValLeuThrGlyAsnLeuLysProAsnThrAspSer 431
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1210 GGTTCACAATATTATAGACGATGACACAATAATTAAGTTTATAGGTTTGAGATATCA 1269
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 432 AsnAlaLeuIleAspGlnGlnAsnThrSerIleLysValTyrLysValAspAsnAlaAla 451
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1270 AATTACCAATAGTACAGAAATTTATGATACAGTGAATATGAAGATGTCACAAATGAT 1329
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 452 AspLeuSerGluSerTyrPheVal---AsnProGluAsnPheGluAspValThrAsnSer 470
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1330 GATTATGCCCAATTAGGAATAATAATGATGTGAATATTAATTTTGGT----- 1377
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 471 ValAsnIleThrPheProAsnProAsnGlnTyrLysValGluPheAsnThrProAspAsp 490
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1378 AATATAGATTTACCATATATTATAAGTTATTATGTAATAATATGACCCCTAAT---AAGGAT 1434
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 491 GlnIleThrThrProTyrIleValValAsnGlyHisIleAspProAsnSerLysGly 510
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1435 GATTACAGCACTATACAGCAAACTGTCACAACTGCACAGCACTATAATGATGATCTGGT 1494
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 511 Asp-----LeuAlaLeuArgSerThrLeuTyrGlyTyrAsnSer 523
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1495 GAG-----TTTAGACAGCATCCTATGATAATAACAATTCCTTCTCAAGTTCAAGT 1548
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 524 AsnIleIleThrArgSerMetSerTrpAspAsnGluValAlaPheAsnAsnGlySerGly 543
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1549 CAAGGACACAGGT---GACTTGGCCT-----CCTGAAAAAACTTTATAAAATCGGAGATTAC 1599
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 544 SerGlyAspGlyIleAspLysProValValProGluGlnProAspGluProGlyGluIle 563
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 1600 -----GTATGGGAAGATGTAGATAAAGAT---GGTATTCAAATAACAATGATAAT 1647
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 564 GluProIleProGluAspSerAspSerAspProGlySerAspGlySerAspSer 582
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
```

## RESULT 15

```
US-08-293-728-2
; Sequence 2, Application US/08293728D
; Patent No. 6008341
; GENERAL INFORMATION:
; APPLICANT: Timothy J.
; APPLICANT: Foster, Damien L.
; TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene
; FILE REFERENCE: 05344.105011
; CURRENT APPLICATION NUMBER: US/08/293,728D
; CURRENT FILING DATE: 1994-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 2
; LENGTH: 933
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-293-728-2
```

## Alignment Scores:

```
Pred. No.: 3,08e-25 Length: 933
Score: 452.00 Matches: 154
Percent Similarity: 44.7% Conservative: 105
Best Local Similarity: 26.6% Mismatches: 234
Query Match: 14.9% Indels: 86
DB: 2 Gaps: 26
```

US-10-806-288-12 (1-1746) x US-08-293-728-2 (1-933)

```
QY 1 TCTAGTGTGAAGAAGAAAGATGATGTGATCAATAATAACAGTCAATAAACAACCGACGAT 60
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 51 SerAsnGluSerLysSerAsnAspSerSerValSerAlaAlaProLysThrAspAsp 70
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 61 AATAACCAATAATAATTAAAAAGAAAGAAACGAATAACTACGATGGCATAGAAAAACGCTCA 120
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 71 ThrAsnVal-----Ser 74
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 121 GAAGATAGAACAGAGTCAACACAAATGTAGTGAAGAAACGAACCAACATTTTACAAAAG 180
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 75 AspThrLysThrSerSerAsnThrAsn-----AsnGlyGluThrSerValAlaGln 91
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 181 ACCCTTCAAGATAATACTCATCTTACAGAAAGAGGTAAAGAATCTCTCATCAGTCGAA 240
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 92 AsnPro-----AlaGlnGlnGluThrThrGlnSerSerSerThrAsn 105
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 241 TCCTCAAAATTCATCAATGATGATCTGCCCAACCAACCATCTCACACAACATAAATAGAGAA 300
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 106 AlaThrThrGluGluThrProValThrGlyGluAlaThrThrThrAsnGlnAla 125
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 301 GAATCTGTTCAACAAAGTGTATGATGTAGAAGATTACACAGTATCAGATTTTGTAACTCT 360
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 126 AsnThrProAlaThrThrGlnSer---SerAsnThrAsnAlaGluLeuValAsn--- 143
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 361 AAAATAAAGAGAGTTAACTGAATCTGTTGTAAGAAGAGAATACTATAGAACCACTTAAT 420
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 144 -----GlnThrSerAsnGluThrThrPheAsnAspThrAsnThrVal----- 157
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 421 AAAGTAAAAGAGAGATTCAACACACAGTACAGCTCTGGCTATACAAATATAGATGAAAAA 480
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 158 -----SerSerValAsnSerProGlnAsnSerThrAsnAlaGluAsnVal 172
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 481 ATTTCAAAATCAAGATCAGTTATTAAAT---TTACCAATAAATGAATATGAAAAATAAGCT 537
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 173 SerThrThrGlnAspThrSerThrGluAlaThrProSerAsn-----AsnGluSer 189
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 538 AGACCAATATTCTACAAACATCTGCCCAACCATCGATTAAACGTGTAAACCGTAAT----- 591
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 190 AlaProGlnSerThrAspAlaSerAsnLysAspValValAsnGlnAlaValAsnThrSer 209
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 592 -----CAATTAGCGCGGCAACAGGTTCGAATGTTTAACCATTTA 630
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 210 AlaProArgMetArgAlaPheSerLeuAlaAlaValAlaAlaAspAlaProAlaAlaGly 229
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 631 ATTAAAGTTACTGATCAA-----AGTATTACTGAAGGATATGATGATGAGGTTGTT 684
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 230 ThrAspIleThrAsnGlnLeuThrAsnValThrValGlyIle---AspSerGlyThrThr 248
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 685 ATTAAAGCACATGATCTGAAAACTTAACTATGATGTAACTTTTGAAGTAGATGATAAG 744
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 249 ValTyrProHisGlnAlaGlyTyrValLysLeuAsnTyrGlyPheSerValProAsnSer 268
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 745 GTGAATCTGTTGATACGATGACAGTGGATATAGATAAGAAATACAGTTCCTCAGATTTA 804
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 269 AlaValLysGlyAspThrPheLysIleThrValProLysGluLeuAsnLeuAsnGlyVal 288
Db ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : ||| ||| : : : |||
QY 805 ACGATAGCTTTTACAATACCAAAAAATAAAGATAATTTCTGGAGAAATCATCGCTACAGGT 864
```

```
Db 289 ThrSerThrAlaLysValProProIleMetAlaGlyAsp-----GlnValLeuAlaAsnGly 307
Qy 865 ACTTATGATAACAAATAAACAACACCTACCTATCTTTTACAGATTATGTAGTAAGTAT 924
Db 308 ValIleAspSer---AspGlyAsnValIleTyrPheThrAspTyrValAsnThrLys 326
Qy 925 GAAATATTAAGACACACTTAATTAACGTACATCATTAATAATCAAGTTCCTCAAT 984
Db 327 AspAspValLysAlaThrLeuThrMetProAlaTyrIleAsp-----ProGlu 342
Qy 985 AATAATACCAAGTTA---GATGTAGATATATAAAGCGCCCTTTCATCA-----GTAAAT 1035
Db 343 AsnValLysLysThrGlyAsnValThrLeuAlaThrGlyIleGlySerThrThralaAsn 362
Qy 1036 AAAACAATTCGTTGAATATCAAGACCTAACGAAATCGGACTGCTAACCTTCAAGT 1095
Db 363 LysThrValLeuValAspTyrGluLysTyrGlyLysPheTyrAsnLeuSerIleLysGly 382
Qy 1096 ATGTTTCAATATAGATACGAAATAATCATACAGTTGAGCAACGATTATATTAACCT 1155
Db 383 ThrIleAspGlnIleAspLysThrAsnAsnThrTyrArgGlnThrIleTyrValAsnPro 402
Qy 1156 CTT-----CGTTATTCAGCCAGGAAACAATGTAATATTTTCAGGGAATGGTGATCAA 1209
Db 403 SerGlyAspAsnValIleAlaProValLeuThrGlyAsnLeuLysProAsnThrAspSer 422
Qy 1210 GGTTCACAACTATATAGACGATAGCACAATAATTAAGTTTATAGGTTGGAGATAATCAA 1269
Db 423 AsnAlaLeuIleAspGlnGlnAsnThrSerIleLysValTyrLysValAspAsnAlaAla 442
Qy 1270 AATTACACAGATAGTAACAGAAATTTATGATTACAGTGAATATGAAGATGTACAAATGAT 1329
Db 443 AspLeuSerGluSerTyrPheVal---AsnProGluAsnPheGluAspValThrAsnSer 461
Qy 1330 GATTATGCCCAATTAGGAATAATAATGATGTGAATATTAATTTTGGT----- 1377
Db 462 ValAsnIleThrPheProAsnProAsnGlnTyrLysValGluPheAsnThrProAspAsp 481
Qy 1378 AATATAGATTCACCATATATTATTAAGTTTATAGTAAATATGACCTAAT---AAGGAT 1434
Db 482 GlnIleThrThrProTyrIleValValValAsnGlyHisIleAspProAsnSerLysGly 501
Qy 1435 GATTACACGACTATACAGCAAACTGTGCAATGTGACAGCTACATAAATGACTACTGCT 1494
Db 502 Asp-----LeuAlaLeuArgSerThrLeuTyrGlyTyrAsnSer 514
Qy 1495 GAG-----TTTGAACAGCATCCTATGATATAATCAATTCCTTCTTCAAGTTCAGGT 1548
Db 515 AsnIleIleTrpArgSerMetSerTrpAspAsnGluValAlaPheAsnAsnGlySerGly 534
Qy 1549 CAAGGACAAGCT---GACTTCCT-----CCTGAAAAAACTTATAAATCGGAGATTAC 1599
Db 535 SerGlyAspGlyIleAspLysProValValProGluGlnProAspGluProGlyGluIle 554
Qy 1600 -----GTATCGGAAGATGTAGATAAGAT---GTTATTTCAAAATACAAATGATAAT 1647
Db 555 GluProIleProGluAspSerAspSerAspProGlySerAspSerGlySerAspSer 573
```

Search completed: August 12, 2006, 08:14:31  
Job time : 105.5 secs

**This Page Blank (uspto)**